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(54) Title: NOVEL PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract: The present invention provides polynucleotides and secreted proteins encoded by the polynucleotides. The proteins include a variety of fusion proteins, including fusions comprising a signal peptide selected from the group consisting of signal peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide. The invention further provides therapeutic and diagnostic methods utilizing the polynucleotides, polypeptides, and antagonists of the polypeptides.

Description

NOVEL PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

BACKGROUND OF THE INVENTION

Within the field of genetic engineering, polynucleotides encoding proteins of interest have been identified and cloned by methods that require a detailed knowledge of the structure and/or function of the polynucleotide or the encoded protein. These methods include hybridization screening, polymerase chain reaction (PCR), and expression cloning.

With the more recent advent of large DNA sequence databases and the accompanying data analysis tools, identification of genes of interest is possible through the analysis of raw sequence data. Databases can be "mined" to locate sequences that resemble (are "homologous to") sequences of known function. Alignment of similar sequences can be used to place novel sequences within families of structurally similar sequences. These analytical tools can be combined with structural information obtained from, for example, X-ray crystallography to predict the higher order structure of a novel polypeptide. These analyses also facilitate prediction of polypeptide function. These recent technological advances have greatly increased the pace of gene discovery.

Genetic engineering has made available a number of genes and proteins of pharmaceutical or other economic importance. Such proteins include, for example, tissue plasminogen activator (t-PA) (U.S. Patent No. 4,766,075), coagulation factor VII (U.S. Patent No. 4,784,950), erythropoietin (U.S. Patent No. 4,703,008), platelet derived growth factor (U.S. Patent No. 4,889,919), and various industrial enzymes (e.g., U.S. Patents Nos. 5,965,384; 5,942,431; and 5,922,586).

Although estimates vary as to the amount of the human genome that has been identified to date, there remains a need in the art for further characterization of the human genome and the proteins encoded thereby. Previously unknown genes and proteins will be useful in the treatment and/or prevention of many human diseases, included diseases that have heretofore been refractory to treatment.

SUMMARY OF THE INVENTION

Within one aspect of the invention there is provided an isolated polypeptide comprising fifteen contiguous amino acid residues of a polypeptide as

shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422. Within one embodiment, the isolated polypeptide is from 15 to 2235 amino acid residues in length. Within another embodiment, the at least fifteen contiguous amino acid residues of SEQ ID NO:M are operably linked via a peptide bond or polypeptide linker to a second polypeptide selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag, and a peptide as shown in SEQ ID NO:423. Within another embodiment, the polypeptide comprises at least 30 contiguous residues of SEQ ID NO:M. Within a further embodiment, the polypeptide comprises at least 47 contiguous residues of SEQ ID NO:M. Within additional embodiments, the polypeptide is selected from the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 10, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 82, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 136, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 186, 202, 204, 206, 208, 210, 224, 230, 232, 234, 236, 240, 242, 250, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 310, 312, 314, 316, 322, 324, 328, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, and 420; the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, and 420; the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, and 416; or the group consisting of polypeptides of SEQ ID NOS: 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, and 416.

Within a second aspect of the invention there is provided an isolated, mature protein encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NO:N, wherein N is an odd integer from 1 to 421. Within certain embodiments, N is 3, 5, 7, 9, 11, 15, 17, 23, 27, 41, 47, 53, 61, 65, 67, 69, 71, 81, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 135, 137, 139, 155,

157, 161, 163, 165, 167, 173, 177, 179, 185, 201, 203, 205, 207, 209, 223, 229, 231, 233, 235, 239, 241, 249, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 309, 311, 313, 315, 321, 323, 327, 325, 335, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, 415, or 419; N is 3, 5, 7, 11, 15, 17, 23, 27, 41, 47, 53, 61, 65, 67, 69, 71, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 137, 139, 155, 157, 161, 163, 165, 167, 173, 177, 179, 201, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 321, 323, 325, 335, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, 415, or 419; N is 3, 5, 7, 11, 15, 17, 23, 27, 41, 47, 53, 65, 67, 69, 71, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 137, 139, 155, 157, 161, 163, 165, 167, 173, 177, 179, 201, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 321, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, or 415; or N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.

A third aspect of the invention provides isolated polynucleotides encoding the polypeptides disclosed above. Within certain embodiments of the invention the polynucleotides comprise a sequence of nucleotides as shown in SEQ ID NO:N, wherein N is an odd integer as defined above

Within a fourth aspect of the invention there is provided an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment encoding a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422; and a transcription terminator. Within certain embodiments, M is 4, 6, 8, 10, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 82, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 136, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 186, 202, 204, 206, 208, 210, 224, 230, 232, 234, 236, 240, 242, 250, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 310, 312, 314, 316, 322, 324, 328, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, or 420; M is 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, or 420; M is 4, 6, 8, 12, 16, 18, 24, 28, 42,

48, 54, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, or 416; or M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.

A fifth aspect of the invention provides a cultured cell comprising the expression vector disclosed above. The cultured cell can be used, *inter alia*, within a method of producing a polypeptide, the method comprising (a) culturing the cell under conditions whereby the sequence of nucleotides is expressed, and (b) recovering the polypeptide. The invention also provides a polypeptide produced by this method.

Within a sixth aspect of the ivention there is provided an isolated polynucleotide encoding a fusion protein, wherein the fusion protein comprises a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer as defined above, operably linked to a second polypeptide.

Within a seventh aspect of the invention there is provided an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment encoding a fusion protein as disclosed above; and a transcription terminator. The invention further provides a cultured cell comprising this expression vector, wherein the cell expresses the DNA segment and produces the encoded fusion protein. Also provided is a method of producing a protein comprising culturing the cell under conditions whereby the DNA segment is expressed, and recovering the second polypeptide. Within one embodiment the recovered second polypeptide is joined to a portion of a protein of SEQ ID NO: M, wherein M is an even integer as defined above.

Within a further aspect of the invention there is provided a computer-readable medium encoded with a data structure comprising SEQ ID NO:X, wherein X is an integer from 1 to 422.

Within an additional aspect of the invention there is provided an antibody that specifically binds to a protein selected from of the group consisting of SEQ ID NO:M, wherein M is an even integer as defined above.

These and other aspects of the invention will become evident upon reference to the following detailed description of the invention.

DETAILED DESCRIPTION OF THE INVENTION

Prior to setting forth the invention in detail, it may be helpful to the understanding thereof to define the following terms:

The term "affinity tag" is used herein to denote a polypeptide segment that can be attached to a second polypeptide to provide for purification of the second polypeptide or provide sites for attachment of the second polypeptide to a substrate. In principal, any peptide or protein for which an antibody or other specific binding agent is available can be used as an affinity tag. Affinity tags include a poly-histidine tract, protein A (Nilsson et al., *EMBO J.* 4:1075, 1985; Nilsson et al., *Methods Enzymol.* 198:3, 1991), glutathione S transferase (Smith and Johnson, *Gene* 67:31, 1988), Glu-Glu affinity tag (Grussenmeyer et al., *Proc. Natl. Acad. Sci. USA* 82:7952-7954, 1985; see SEQ ID NO:423), substance P, Flag™ peptide (Hopp et al., *Biotechnology* 6:1204-1210, 1988), maltose binding protein (Kellerman and Ferenci, Methods Enzymol. 90:459-463, 1982; Guan et al., Gene 67:21-30, 1987), streptavidin binding peptide, thioredoxin, ubiquitin, cellulose binding protein, T7 polymerase, immunoglobulin constant domain, or other antigenic epitope or binding domain. See, in general, Ford et al., *Protein Expression and Purification* 2: 95-107, 1991. Affinity tags can be used individually or in combination. DNAs encoding affinity tags and otehr reagents are available from commercial suppliers (e.g., Pharmacia Biotech, Piscataway, NJ; Eastman Kodak, New Haven, CT; New England Biolabs, Beverly, MA).

The term "allelic variant" is used herein to denote any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant is also used herein to denote a protein encoded by an allelic variant of a gene.

The terms "amino-terminal" and "carboxyl-terminal" are used herein to denote positions within polypeptides. Where the context allows, these terms are used with reference to a particular sequence or portion of a polypeptide to denote proximity or relative position. For example, a certain sequence positioned carboxyl-terminal to a reference sequence within a polypeptide is located proximal to the carboxyl terminus of the reference sequence, but is not necessarily at the carboxyl terminus of the complete polypeptide.

A "complement" of a polynucleotide molecule is a polynucleotide molecule having a complementary base sequence and reverse orientation as compared to a reference sequence. For example, the sequence 5' ATGCACGGG 3' is complementary to 5' CCCGTGCAT 3'.

"Corresponding to", when used in reference to a nucleotide or amino acid sequence, indicates the position in a second sequence that aligns with the reference position when two sequences are optimally aligned.

The term "degenerate nucleotide sequence" denotes a sequence of nucleotides that includes one or more degenerate codons (as compared to a reference polynucleotide molecule that encodes a polypeptide). Degenerate codons encompass different triplets of nucleotides, but encode the same amino acid residue (i.e., GAU and GAC triplets each encode Asp).

The term "expression vector" is used to denote a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of interest operably linked to additional segments that provide for its transcription, wherein said segments are arranged in a way that does not exist naturally. Such additional segments include promoter and terminator sequences, and may also include one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, etc. Expression vectors are generally derived from plasmid or viral DNA, or may contain elements of both.

The term "isolated", when applied to a polynucleotide, denotes that the polynucleotide has been removed from its natural genetic milieu and is thus free of other extraneous or unwanted coding sequences, and is in a form suitable for use within genetically engineered protein production systems. Such isolated molecules are those that are separated from their natural environment and include cDNA and genomic clones. Isolated DNA molecules of the present invention are free of other genes with which they are ordinarily associated, but may include naturally occurring 5' and 3' untranslated regions such as promoters and terminators. The identification of associated regions will be evident to one of ordinary skill in the art (see for example, Dynan and Tijan, *Nature* 316:774-78, 1985).

An "isolated" polypeptide or protein is a polypeptide or protein that is found in a condition other than its native environment, such as apart from blood and animal tissue. In a preferred form, the isolated polypeptide or protein is substantially free of other polypeptides or proteins, particularly other polypeptides or proteins of animal origin. It is preferred to provide the polypeptides or proteins in a highly purified form, i.e. greater than 95% pure, more preferably greater than 99% pure. When used in this context, the term "isolated" does not exclude the presence of the same polypeptide or protein in alternative physical forms, such as dimers or alternatively glycosylated or derivatized forms.

A "mature protein" is a protein that is produced by cellular processing of a primary translation product of a DNA sequence. Such processing may include

removal of a secretory signal peptide, sometimes in combination with a propeptide. Mature sequences can be predicted from full-length sequences using methods known in the art for predicting cleavage sites. See, for example, von Heijne (*Nuc. Acids Res.* 14:4683, 1986). The sequence of a mature protein can be determined experimentally by expressing a DNA sequence of interest in a eukaryotic host cell and determining the amino acid sequence of the final product. For proteins lacking secretory peptides, the primary translation product will be the mature protein.

"Operably linked", when referring to DNA segments, indicates that the segments are arranged so that they function in concert for their intended purposes, e.g., transcription initiates in the promoter and proceeds through the coding segment to the terminator. When referring to polypeptides, "operably linked" includes both covalently (e.g., by disulfide bonding) and non-covalently (e.g., by hydrogen bonding, hydrophobic interactions, or salt-bridge interactions) linked sequences, wherein the desired function(s) of the sequences are retained.

The term "ortholog" denotes a polypeptide or protein obtained from one species that is the functional counterpart of a polypeptide or protein from a different species. Sequence differences among orthologs are the result of speciation.

"Paralogs" are distinct but structurally related proteins made by an organism. Paralogs are believed to arise through gene duplication. For example, α-globin, β-globin, and myoglobin are paralogs of each other.

A "polynucleotide" is a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. Polynucleotides include RNA and DNA, and may be isolated from natural sources, synthesized *in vitro*, or prepared from a combination of natural and synthetic molecules. Sizes of polynucleotides are expressed as base pairs (abbreviated "bp"), nucleotides ("nt"), or kilobases ("kb"). Where the context allows, the latter two terms may describe polynucleotides that are single-stranded or double-stranded. When the term is applied to double-stranded molecules it is used to denote overall length and will be understood to be equivalent to the term "base pairs". It will be recognized by those skilled in the art that the two strands of a double-stranded polynucleotide may differ slightly in length and that the ends thereof may be staggered as a result of enzymatic cleavage; thus all nucleotides within a double-stranded polynucleotide molecule may not be paired. Such unpaired ends will in general not exceed 20 nt in length.

A "polypeptide" is a polymer of amino acid residues joined by peptide bonds, whether produced naturally or synthetically. Polypeptides of less than about 10 amino acid residues are commonly referred to as "peptides".

The term "promoter" is used herein for its art-recognized meaning to denote a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding regions of genes.

A "protein" is a macromolecule comprising one or more polypeptide chains. A protein may also comprise non-peptidic components, such as carbohydrate groups. Carbohydrates and other non-peptidic substituents may be added to a protein by the cell in which the protein is produced, and will vary with the type of cell. Proteins are defined herein in terms of their amino acid backbone structures; substituents such as carbohydrate groups are generally not specified, but may be present nonetheless.

A "secretory signal sequence" is a DNA sequence that encodes a polypeptide (a "secretory peptide") that, as a component of a larger polypeptide, directs the larger polypeptide through a secretory pathway of a cell in which it is synthesized. The larger polypeptide is commonly cleaved to remove the secretory peptide during transit through the secretory pathway.

The present invention is based in part upon the discovery of a group of novel, protein-enoding DNA molecules. These DNA molecules and the amino acid sequences that they encode are shown in SEQ ID NO:1 through SEQ ID NO:436. Sequence analysis predicts that each of the encoded proteins includes an amino-terminal secretory peptide. These secretory peptides are shown below in Table 1, wherein residue numbers are in reference to the indicated SEQ ID NO. As will be understood by those skilled in the art, the cleavage sites predicted by conventional models of secretory peptide cleavage (e.g., von Heijne, *Nuc. Acids Res.* 14:4683, 1986) are not always exact and may vary by as much as ± 5 residues. In addition, cleavage may occur at multiple sites within 5 residues of the indicated position. The mature form of any given protein may thus consists of a plurality of species differing at their amino termini.

Table 1

Protein	SEQ ID NO:	Residues 1-
AFP210015	2	14
AFP170681	4	26
AFP413680	6	28
AFP483037	8	14
AFP230872	10	27
AFP178828	12	14
AFP200134	14	23
AFP195796	16	22
AFP477303	18	18
AFP354334	20	25
AFP250287	22	17
AFP177000	24	26
AFP278176	26	21
AFP202885	28	18
AFP221312	30	23
AFP239757	32	22
AFP226311	34	20
AFP305901	36	20
AFP325549	38	20
AFP81988	40	14
AFP199200	42	20
AFP290395	44	23
AFP212675	46	20
AFP326051	48	17
AFP512441	50	18
AFP55098	52	15
AFP169796	54	21
AFP280706	56	25
AFP383165	58	23
AFP195467	60	26
AFP134225	62	22
AFP261193	64	28
AFP324422	66	28
AFP374312	68	28
AFP258118	70	24
AFP74517	72	25
AFP254653	74	18
AFP108666	76	21
AFP8766	78	15
AFP397185	80	20
AFP195042	82	21
AFP310695	84	26
AFP70022	86	19
AFP121670	88	22
AFP345861	90	15

AFP395942	92	16
AFP170291	94	21
AFP297548	96	22
AFP188135	98	28
AFP302388	100	19
AFP263430	102	17
AFP201273	104	18
AFP98983	106	25
AFP581958	108	20
AFP404202	110	19
AFP207203	112	15
AFP220790	114	19
AFP536326	116	23
AFP257473	118	22
AFP248380	120	16
AFP276202	122	20
AFP227568	124	23
AFP229039	126	20
AFP176297	128	17
AFP356885	130	17
AFP226938	132	16
AFP138504	134	29
AFP359196	136	24
AFP501809	138	27
AFP152733	140	15
AFP541394	142	23
AFP243183	144	20
AFP80739	146	18
AFP361806	148	26
AFP483930	150	21
AFP257336	152	25
AFP195800	154	23
AFP179530	156	19
AFP279267	158	14
AFP299766	160	29
AFP244615	162	16
AFP325761	164	22
AFP226024	166	22
AFP257094	168	27
AFP197103	170	27
AFP271855	172	17
AFP324816	174	29
AFP407963	176	25
AFP369635	178	17
AFP93743	180	28
AFP243230	182	15
AFP169316	184	21
AFP130852	186	15

AFP194191	188	22
AFP213472	190	21
AFP360430	192	22
AFP491309	194	21
AFP193428	196	23
AFP366534	198	22
AFP22706	200	27
AFP389012	202	14
AFP137186	204	24
AFP127023	206	21
AFP389687	208	16
AFP293220	210	25
AFP425535	212	25
AFP301494	214	25
AFP345421	216	19
AFP216667	218	26
AFP247951	220	29
AFP4464	222	22
AFP561930	224	28
AFP192851	226	22
AFP252759	228	20
AFP199044	230	20
AFP357958	232	28
AFP117501	234	15
AFP194554	236	23
AFP371069	238	23
AFP313600	240	19
AFP262739	242	18
AFP180730	244	27
AFP287227	246	28
AFP75785	248	26
AFP174843	250	15
AFP250422	252	15
AFP198645	254	17
AFP238111	256	16
AFP460626	258	24
AFP271081	260	14
AFP277752	262	16
AFP291338	264	15
AFP551038	266	22
AFP301579	268	20
AFP266188	270	16
AFP275580	272	28
AFP298054	274	21
AFP348226	276	23
AFP349106	278	23
AFP288248	280	15
AFP436476	282	19

AFP352125	284	14
AFP62060	286	25
AFP236718	288	21
AFP75775	290	25
AFP407487	292	23
AFP280451	294	27
AFP11675	296	29
AFP348656	298	16
AFP277451	300	19
AFP287436	302	14
AFP116043	304	28
AFP138740	306	26
AFP15192	308	17
AFP169968	310	27
AFP173341	312	23
AFP17588	314	23
AFP176427	316	20
AFP192633	318	14
AFP193013	320	15
AFP193881	322	16
AFP195562	324	16
AFP199922	326	18
AFP204736	328	17
AFP206179	330	27
AFP221877	332	23
AFP222758	334	26
AFP227032	336	24
AFP229269	338	27
AFP232213	340	25
AFP237679	342	21
AFP249599	344	28
AFP275215	346	21
AFP290397	348	26
AFP306591	350	18
AFP310297	352	20
AFP314720	354	19
AFP318671	356	29
AFP323575	358	21
AFP327160	360	20
AFP329002	362	29
AFP345415	364	24
AFP347179	366	24
AFP359138	368	23
AFP365372	370	17
AFP367284	372	23
AFP372822	374	26
AFP374595	376	29
AFP375952	378	25

AFP382913	380	17
AFP389184	382	23
AFP404208	384	20
AFP404279	386	29
AFP409112	388	26
AFP413111	390	19
AFP415635	392	15
AFP421092	394	17
AFP436666	396	25
AFP448623	398	19
AFP454192	400	20
AFP49026	402	28
AFP51688	404	28
AFP525341	406	16
AFP545268	408	15
AFP592620	410	22
AFP62197	412	23
AFP68229	414	25
AFP71288	416	15
AFP77851	418	27
AFP81957	420	15
AFP85168	422	27

A secretory peptide of a protein of the present invention can be used to direct the secretion of other proteins of interest from a host cell. Thus, the present invention provides, *inter alia*, fusions comprising such a secretory peptide of a protein disclosed herein operably linked to another protein of interest. The secretory peptide can be used to direct the secretion of other proteins of interest by joining a polynucleotide sequence encoding it, in the correct reading frame, to the 5' end of a sequence encoding the other protein of interest. Those skilled in the art will recognize that the resulting fused sequence may encode additional residues of a protein of the present invention at the amino terminus of the protein to be secreted. In the extreme case, the fusion may comprise an entire protein of the present invention fused to the amino terminus of a second protein, whereby secretion of the fusion protein is directed by the secretory peptide of the protein of the present invention. It will often be desirable to include a proteolytic cleavage site between the protein of the present invention (or portion thereof) and the other protein of interest. The joined polynucleotide sequences are then introduced into a host cell, which is cultured according to conventional methods. The protein of interest is then recovered from the culture media. Methods for introducing DNA into host cells, culturing the cells, and isolating recombinant proteins are known in the art. Representative methods are summarized below.

Within certain embodiments of the invention, the protein is selected from those listed in Table 2. Within related embodiments of the invention, the polynucleotide is selected from polynucleotides encoding the proteins listed in Table 2, i.e., for a protein of SEQ ID NO:M, the polynucleotide is SEQ ID NO:M-1.

Table 2

SEQ ID NO:	Protein	SEQ ID NO:	Protein
6	AFP413680	234	AFP117501
12	AFP178828	236	AFP194554
18	AFP477303	240	AFP313600
24	AFP177000	242	AFP262739
42	AFP199200	252	AFP250422
48	AFP326051	254	AFP198645
66	AFP324422	258	AFP460626
68	AFP374312	270	AFP266188
72	AFP74517	272	AFP275580
90	AFP345861	288	AFP236718
92	AFP395942	294	AFP280451
96	AFP297548	300	AFP277451
98	AFP188135	306	AFP138740
110	AFP404202	324	AFP195562
134	AFP138504	338	AFP229269
138	AFP501809	342	AFP237679
156	AFP179530	344	AFP249599
158	AFP279267	348	AFP290397
162	AFP244615	350	AFP306591
164	AFP325761	366	AFP347179
174	AFP324816	374	AFP372822
180	AFP93743	378	AFP375952
204	AFP137186	386	AFP404279
206	AFP127023	396	AFP436666
210	AFP293220	398	AFP448623
224	AFP561930	408	AFP545268
230	AFP199044	416	AFP71288

Higher order structures of the proteins of the present invention can be predicted by computer analysis using available software (e.g., the Insight II® viewer and homology modeling tools available from MSI, San Diego, CA; and King and Sternberg, *Protein Sci.* 5:2298-310, 1996). In addition, analytical algorithms permit the identification of homologies between newly discovered proteins and known proteins. Such homologies are indicative of related biological functions.

AFP254653 is 49% identical in sequence to human lysozyme C. Lysozyme C is a secreted bacteriolytic enzyme with similarity to the alpha-lactalbumins. Both are small alpha + beta proteins with six conserved cysteines forming a disulfide core comprising three disulfide bonds. AFP254653 may also exhibit bacteriolytic or other antimicrobial activity.

AFP581958 is 43% identical to wheat aluminum-induced protein, a member of the Bowman-Birk proteinase inhibitor family. All serine proteinases possess an exposed inhibitor loop that is stabilized by intermolecular interactions (usually disulfide bonds) between residues flanking the binding loop and the protein core. Interaction between inhibitor and enzyme produces a stable complex that disassociates very slowly, producing either an unaffected or a modified inhibitor that is cleaved at the scissile bond of the binding loop. AFP581958 may be a secreted serine proteinase.

AFP220790 is 42% identical to chicken lysozyme G, a bacteriolytic glycosyl hydrolase that hydrolizes peptidoglycan homopolymers of the prokaryote cell walls. AFP220790 may thus be a secreted bacteriolytic enzyme, and may exhibit other antimicrobial activity.

AFP271855 is 37% identical to bovine granulocyte peptide A precursor (antimicrobial BGP-A). Bovine and murine granulocyte peptide A precursor (also called antimicrobial BGP-A) are disclosed in WIPO publication WO 97/29765. Bovine GP-A was isolated from a bone marrow library (WO 97/29765). GP-A exhibits activity against Gram-positive and Gram-negative bacteria, fungi and viruses. AFP271855 may exhibit antimicrobial (including one or more of anti-bacterial, anti-fungal, and anti-viral) activity.

AFP298054 is 24% identical to human T1/ST2 ligand. The T1 gene is also known as ST2, DER4, and Fit-1. It encodes a member of the interleukin-1 (IL-1) receptor family. It is transcribed in two forms, a soluble form and a membrane-bound form. The classical IL-1 ligands (IL-1α, IL-1β, and IL-1ra) do not bind T1. A putative ligand for T1 was disclosed in 1996 (Gayle et al., *J. Biol. Chem.* 227:5784-5789, 1996). This protein binds T1 but is unable to initiate signal transduction by the membrane-bound form. The ligand is apparently a type I membrane protein. It has a predicted molecular weight (excluding the signal sequence and transmembrane domain) of about 22 kD, and has no sequence or hydrophobicity profile similarity to the beta-trefoil cytokines IL-1 or the FGFs. AFP298054 may be an antagonist that binds the receptor and regulates the activity of an as yet undiscovered IL-1 homolog.

Table 3 lists homologies between AFP sequences and sequences contained in the GenBank database, Derwent protein (PSP) or polynucleotide (PSN) databases, or Protein Identification Resource (PIR).

Table 3

Locus	Accession Number & Description
AFP130852	AE003823 (fly genomic)
AFP169968	AE003515 (fly genomic)
AFP174843	AF283518 (*Mus musculus* elongation factor sec)
AFP176427	AE003808 (fly genomic)
AFP178828	PSN_V61483
AFP179530	AE003708 (fly genomic)
AFP188135	AE003677 (fly genomic)
AFP195042	PIR_T41241 (yeast oxysterol-binding protein family)
AFP198645	AE003718 (fly genomic)
AFP199200	AF113691 (human clone FLB4739 PRO1238 mRNA)
AFP204736	AC069237 (human chromosome 3 clone RP11-175M9)
AFP229269	AF247177 (*Mus musculus* sphingosine-1-phosphate phosphohydrolase)
AFP230872	AF150741 (*Rattus norvegicus* prolactin-like protein J mRNA)
AFP279267	AE003559 (fly genomic)
AFP347179	AE003499 (fly genomic) Z1041035F6P
AFP357958	AF283518 (*Mus musculus* elongation factor sec mRNA)
AFP359196	AE003530 (fly genomic)
AFP374312	AE003538 (fly genomic)
AFP389687	AE003831 (fly genomic)
AFP395942	AB041564 (mouse brain cDNA; clone MNCb-0914)
AFP404202	AL137255 (human mRNA; cDNA DKFZp434B1813)
AFP413680	X14971 (mouse mRNA for alpha-adaptin, MMADAPA1)
AFP477303	AE003778 (fly genomic)
AFP62060	PSP_Y94938 (Human secreted protein clone ye78_1)
AFP71288	AL161655 (human chromosome 20 clone RP11-116E13)
AFP74517	PIR_T16263 (*C. elegans* hypothetical protein F35D11.3)

Table 4 lists AFP proteins for which regions of identity have been found in the GenBank database.

Table 4

Locus	Accession Number & Description
AFP127023	SK000740 (human cDNA FLJ20733; clone HEP08550; by homology: molybdopterin cofactor sulfurase)
AFP134225	AB020970 (human mRNA; partial cds and 3'UTR; up-regulated by BCG-CWS)
AFP195562	AK000382 (human cDNA FLJ20375; clone HUV00942)

AFP199044	HSU80813 (human nucleoside diphosphate kinase homolog DR-nm23)
AFP227032	AK001848 (human cDNA FLJ10986; clone PLACE1001869; weakly similar to L-RIBULOKINASE; EC 2.7.1.16)
AFP237679	AB000465 (human mRNA; exon 1; 2; 3; 4; clone:RES4-24B; in genomic region of Huntington's disease locus)
AFP262739	AK000135 (human cDNA FLJ20128; clone COL06181)
AFP369635	PSN_Z24827 (Human secreted protein gene 17 clone HNFIY77)
AFP81957	AF267730 (human 26S proteasome-associated UCH interacting protein 1; UIP1)
AFP93743	AK000066 (human cDNA FLJ20059; clone COL01349)

Table 5 lists AFP proteins for which longer regions of identity have been found in proteins contained in GenBank and other databases.

Table 5

Locus	Accession Number & Description
AFP117501	AK000505 (human cDNA FLJ20498; clone KAT08960)
AFP138740	HSM802370 (human mRNA; cDNA DKFZp434M1511)
AFP170291	AK000494 (human cDNA FLJ20487; clone KAT08245)
AFP170681	AK001698 (human cDNA FLJ10836; clone NT2RP4001228 close paralogue of human Kelch-like 1 protein (KLHL1) mRNA: AF252283)
AFP177000	AK000524 (human cDNA FLJ20517; clone KAT10235)
AFP193881	AK000382 (human cDNA FLJ20375; clone HUV00942)
AFP195796	AF251041 (human SGC32445 protein (SGC32445) mRNA; homology to PSP_W35393 Human TB2 gene product)
AFP202885	AB037808 (human mRNA for KIAA1387 protein)
AFP207203	AF250924 (human PNGase mRNA: peptide N-glycanase)
AFP226024	AK001952 (human cDNA FLJ11090; clone PLACE1005308)
AFP227568	AB019038 (human HMT-1 mRNA for beta-1;4 mannosyltransferase)
AFP244615	AK001009 (human cDNA FLJ10147; clone HEMBA1003369; weak homology: CENE_HUMAN CENTROMERIC PROTEIN E)
AFP250422	AF208849 (human BM-007 mRNA)
AFP266188	AK000272 (human cDNA FLJ20265; clone COLF9334; homology to major facilitator protein homolog, fission yeast: PIR_S62432)
AFP277451	AK001373 (human cDNA FLJ10511; clone NT2RP2000656)
AFP277752	AK000453 (human cDNA FLJ20446; clone KAT05231; weak homology to dinitrogenase reductase activating glycohydrolase (draG) *Archaeoglobus fulgidus*: PIR_C69465)
AFP280451	AL133355 (Human DNA sequence from clone RP11-541N10 on chromosome 10. Contains a novel gene and the 5' end of the gene for a novel protein; ortholog of mouse FISH protein)
AFP293220	AK001441 (human cDNA FLJ10579; clone NT2RP2003446)
AFP297548	AK000494 (human cDNA FLJ20487; clone KAT08245)
AFP306591	AL359700 (human chromosome 6 clone RP11-802L12)
AFP324816	AB032966 (human mRNA for KIAA1140 protein weak homology: Human O-linked GlcNAc transferase mRNA)

AFP356885	AK001544 (human cDNA FLJ10682; clone NT2RP3000072)
AFP389012	AK000428 (human cDNA FLJ20421; clone KAT02467; homologus to human bisphosphate 3'-nucleotidase mRNA: AF125042)
AFP436666	AK001608 (human cDNA FLJ10746; clone NT2RP3001679; likely human orthologue of *Rattus norvegicus* small rec (srec) mRNA: AF228917)
AFP501809	AK001963 (human cDNA FLJ11101; clone PLACE1005623)
AFP525341	AF189692 (human non-kinase Cdc42 effector protein SPEC2 mRNA)

A protein of the present invention can be prepared as a fusion protein by joining it to a second polypeptide or a plurality of additional polypeptides. Suitable second polypeptides include amino- or carboxyl-terminal extensions, such as linker peptides of up to about 20-25 residues and extensions that facilitate purification (affinity tags) as disclosed above. A protein of interest can be prepared as a fusion to a dimerizing protein as disclosed in U.S. Patents Nos. 5,155,027 and 5,567,584. Preferred dimerizing proteins in this regard include immunoglobulin constant region domains. Immunoglobulin-polypeptide fusions can be expressed in genetically engineered cells to produce a variety of multimeric analogs of a protein of interest. Fusion proteins can also comprise auxiliary domains that target the protein of interest to specific cells, tissues, or macromolecules (e.g., collagen). For example, a protein of interest can be targeted to a predetermined cell type by fusing it to a ligand that specifically binds to a receptor on the surface of a target cell. In this way, proteins can be targeted for therapeutic or diagnostic purposes. A protein can be fused to two or more moieties, such as an affinity tag for purification and a targeting domain. Protein fusions can also comprise one or more cleavage sites, particularly between domains. See, Tuan et al., *Connective Tissue Research* 34:1-9, 1996. Proteins of the present invention can also be used as targetting moieties within fusion proteins comprising, for example, cytokines, cytotoxins, or other biologically active polypeptide moieties.

Protein fusions of the present invention will usually contain not more than about 1,200 amino acid residues joined to the AFP protein. For example, an AFP protein can be fused to *E. coli* β-galactosidase (1,021 residues; see Casadaban et al., *J. Bacteriol.* 143:971-980, 1980), a 10-residue spacer, and a 4-residue factor Xa cleavage site. Such a protein comprising, for example, AFP345421 (SEQ ID NO:216), contains 2235 amino acid residues. In a second example, an AFP protein can be fused to maltose binding protein (approximately 370 residues), a 4-residue cleavage site, and a 6-residue polyhistidine tag.

As disclosed above, the proteins of the present invention or portions thereof can also be used to direct the secretion of a second protein. When such fusions

are designed so that the secreted protein retains a portion of the protein of the present invention, the fusion protein can be purified by means that exploit the properties of the protein of the present invention. Typical of such methods is immunoaffinity chromatography using an antibody directed against a protein of the present invention. When such a fusion is engineered to contain a cleavage site at the fusion point, the fusion can be cleaved and the protein of interest recovered free of extraneous sequence.

The present invention also provides polynucleotide molecules, including DNA and RNA molecules, that encode the proteins disclosed above. Those skilled in the art will readily recognize that, in view of the degeneracy of the genetic code, considerable sequence variation is possible among these polynucleotide molecules. The amino acid sequence information provided herein can be used by one of ordinary skill in the art to generate degenerate sequences comprising all nucleotide sequences encoding a particular polypeptide. Table 6 sets forth the one-letter codes used to denote degenerate nucleotide positions. "Resolutions" are the nucleotides denoted by a code letter. "Complement" indicates the code for the complementary nucleotide(s). For example, the code Y denotes either C or T, and its complement R denotes A or G, A being complementary to T, and G being complementary to C.

TABLE 6

Nucleotide	Resolutions	Complement	Resolutions
A	A	T	T
C	C	G	G
G	G	C	C
T	T	A	A
R	A|G	Y	C|T
Y	C|T	R	A|G
M	A|C	K	G|T
K	G|T	M	A|C
S	C|G	S	C|G
W	A|T	W	A|T
H	A|C|T	D	A|G|T
B	C|G|T	V	A|C|G
V	A|C|G	B	C|G|T
D	A|G|T	H	A|C|T
N	A|C|G|T	N	A|C|G|T

Degenerate codons encompassing all possible codons for a given amino acid are set forth in Table 7, below.

TABLE 7

Amino Acid	One-Letter Code	Codons	Degenerate Codon
Cys	C	TGC TGT	TGY
Ser	S	AGC AGT TCA TCC TCG TCT	WSN
Thr	T	ACA ACC ACG ACT	CAN
Pro	P	CCA CCC CCG CCT	CCN
Ala	A	GCA GCC GCG GCT	GCN
Gly	G	GGA GGC GGG GGT	GGN
Asn	N	AAC AAT	AAY
Asp	D	GAC GAT	GAY
Glu	E	GAA GAG	GAR
Gln	Q	CAA CAG	CAR
His	H	CAC CAT	CAY
Arg	R	AGA AGG CGA CGC CGG CGT	MGN
Lys	K	AAA AAG	AAR
Met	M	ATG	ATG
Ile	I	ATA ATC ATT	ATH
Leu	L	CTA CTC CTG CTT TTA TTG	YTN
Val	V	GTA GTC GTG GTT	GTN
Phe	F	TTC TTT	TTY
Tyr	Y	TAC TAT	TAY
Trp	W	TGG	TGG
Ter	.	TAA TAG TGA	TRR
Asn|Asp	B		RAY
Glu|Gln	Z		SAR
Any	X		NNN
Gap	-	---	

One of ordinary skill in the art will appreciate that some ambiguity is introduced in determining a degenerate codon, representative of all possible codons encoding each amino acid. For example, the degenerate codon for serine (WSN) can, in some circumstances, encode arginine (AGR), and the degenerate codon for arginine (MGN) can, in some circumstances, encode serine (AGY). A similar relationship

exists between codons encoding phenylalanine and leucine. Thus, some polynucleotides encompassed by the degenerate sequences may encode variant amino acid sequences, but one of ordinary skill in the art can easily identify such variant sequences by reference to the amino acid sequences disclosed in the accompanying Sequence Listing.

Methods for preparing DNA and RNA are well known in the art. Complementary DNA (cDNA) clones are prepared from RNA that is isolated from a tissue or cell that produces large amounts of the cognate mRNA. Such tissues and cells are identified by methods commonly known in the art, such as Northern blotting (Thomas, *Proc. Natl. Acad. Sci. USA* 77:5201, 1980). Databases of expressed sequence tags (ESTs) can be analyzed to produce an "electronic Northern" wherein sequences are assigned to specific cell or tissue sources on the basis of their abundance within libraries. Table 8, below, shows the results of such an analysis when, as the minimum significant abundance, it was required that at least 10% of all sequences for a given protein were from a single source and at least five individual clones had been identified from that source. Sequences shown in the accompanying Sequence Listing but not listed in Table 8 were widely distributed among various tissues or were represented by few clones.

Table 8

AFP152733	K562 cells
AFP169796	T-cells
AFP173341	testis
AFP17588	fetal liver or spleen
AFP194554	fetal liver or spleen
AFP199922	testis
AFP229269	placenta
AFP237679	fetal liver or spleen
AFP257094	adult brain
AFP258118	epidermal breast keratinocytes
AFP263430	breast
AFP276202	infant brain
AFP287436	testis
AFP290397	testis
AFP306591	fetal heart
AFP325761	K562 cells
AFP352125	testis
AFP359138	infant brain
AFP369635	germinal center B-cells
AFP409112	kidney
AFP483037	neonatal keratinocytes
AFP49026	peripheral blood eosinophils of asthma patients
AFP545268	K562 cells
AFP561930	fetal liver or spleen
AFP62060	testis
AFP62197	pregnant uterus
AFP93743	germinal center B-cells
AFP98983	fetal heart

A panel of cDNAs from human tissues was screened for AFP expression using PCR. The panel was made from first strand cDNAs obtained from Clontech laboratories, Inc., Palo Alto, CA and contained 20 first-strand cDNA samples from the human tissues shown in Table 9. The panel was set up in a 96-well format that further included a human genomic DNA (obtained from Clontech Laboratories, Inc.) positive control sample and a water-only well as a negative control sample. Each well contained approximately 0.2-100 pg/μl of cDNA, diluted with water to 17.5μl. The

PCR reactions were set up by adding oligonucleotide primers, DNA polymerase (Ex Taq™; TAKARA Shuzo Co. Ltd. Biomedicals Group, Japan or Advantage™ 2 cDNA polymerase mix; Clontech Laboratories, Inc.) with the appropriate supplied buffer, dNTP mix (TAKARA Shuzo Co. Ltd.), and a density increasing agent and tracking dye (RediLoad; Research Genetics, Inc., Huntsville, AL) to each sample on the panel. The amplification was carried out as follows: incubation at 94°C for 2 minutes; 35 cycles of 94°C for 30 seconds, 60°C for 20 seconds, and 72°C for 30 seconds; followed by incubation at 72°C for 5 minutes. About 10 μl of the PCR reaction product was subjected to standard agarose gel electrophoresis using a 4% agarose gel.

Table 9

Protein	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
AFP117501	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP127023	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	n	y	y	n	y	n	n
AFP137186	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP138504	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP138740	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP177000	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP178828	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP179530	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	y	n	y
AFP188135	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP194554	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP195562	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP198645	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n
AFP199044	n	n	n	y	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n
AFP199200	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP229269	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	n	y
AFP236718	n	y	y	y	y	y	y	n	n	y	n	n	n	y	n	n	n	y	y	y	n	y
AFP237679	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP244615	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP249599	n	y	y	n	n	y	y	y	n	n	n	n	n	n	y	n	n	n	n	n	n	y
AFP250422	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP262739	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP266188	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP275580	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	n	y	y	y	n	y
AFP277451	y	y	y	y	y	y	y	y	y	y	nd	y	y	y	y	y	n	y	y	y	n	n
AFP279267	y	y	y	y	y	y	y	y	n	y	y	y	n	y	y	y	y	y	y	y	n	n
AFP280451	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP290397	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP293220	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP297548	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	n	y
AFP306591	y	y	y	y	y	y	y	y	y	y	n	y	y	nd	y	nd	nd	y	y	y	n	y
AFP313600	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP324422	n	n	y	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	y	n	n	y

Table 9, continued

Protein	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
AFP324816	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP325761	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	n	n
AFP326051	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP345861	y	y	y	y	y	y	y	nd	nd	y	nd	y	nd	nd	y	y	y	y	y	y	n	n
AFP347179	y	y	y	y	y	y	y	y	y	y	y	y	n	y	y	y	n	y	y	y	n	y
AFP372822	y	y	y	y	y	y	y	y	n	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP374312	n	n	y	y	n	n	n	n	n	n	n	n	n	n	n	n	y	y	n	n	n	y
AFP375952	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	y
AFP395942	y	y	y	y	y	y	y	y	n	n	y	y	n	y	n	y	y	y	y	y	n	y
AFP404202	y	y	y	y	y	y	y	n	y	y	y	y	n	y	y	y	y	y	y	y	n	n
AFP404279	y	y	y	y	n	y	y	n	y	y	y	y	y	y	y	y	n	y	y	y	n	y
AFP413680	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	nd	y	y	y	n	y
AFP436666	y	y	y	y	y	y	y	y	n	y	y	y	n	y	y	y	y	y	y	y	n	n
AFP448623	y	n	y	n	n	y	n	n	n	n	n	n	n	n	y	n	n	y	y	n	n	y
AFP460626	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	nd	y	y	y	n	y
AFP477303	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP501809	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP545268	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y
AFP561930	y	y	y	y	y	y	y	nd	y	y	n	y	y	nd	y	y	y	y	nd	y	n	y
AFP71288	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	y
AFP74517	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	n
AFP93743	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	y	n	y

Tissues screened were: 1, brain; 2, heart; 3, kidney; 4, liver; 5, lung; 6, pancreas; 7, placenta; 8, skeletal muscle; 9, colon; 10, ovary; 11, peripheral blood leukocytes; 12, prostate; 13, small intestine; 14, spleen; 15, testis; 16, thymus; 17, bone marrow; 18, fetal liver; 19, lymph node; 20, tonsil; 21, H_2O; 22, genomic DNA. Y=yes; n=no; nd=not determined.

Total RNA can be prepared using guanidine HCl extraction followed by isolation by centrifugation in a CsCl gradient (Chirgwin et al., *Biochemistry* 18:52-94, 1979). Poly $(A)^+$ RNA is prepared from total RNA using the method of Aviv and Leder (*Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972). Complementary DNA (cDNA) is prepared from poly$(A)^+$ RNA using known methods. In the alternative, genomic DNA can be isolated. For some applications (e.g., expression in transgenic animals) it may be preferable to use a genomic clone, or to modify a cDNA clone to include at least one genomic intron. Methods for identifying and isolating cDNA and genomic clones are well known and within the level of ordinary skill in the art, and include the use of the sequences disclosed herein, sequences complementary thereto, or parts thereof, for probing or priming a library. Such methods include, for example, hybridization or polymerase chain reaction ("PCR", Mullis, U.S. Patent 4,683,202). Expression libraries can be probed with antibodies to a protein of interest, receptor fragments, or other specific binding partners.

The polynucleotides of the present invention can also be prepared by automated synthesis. Synthesis of polynucleotides is within the level of ordinary skill in the art, and suitable equipment and reagents are available from commercial suppliers. See, in general, Glick and Pasternak, Molecular Biotechnology, Principles & Applications of Recombinant DNA, ASM Press, Washington, D.C., 1994; Itakura et al., *Ann. Rev. Biochem.* 53: 323-56, 1984; and Climie et al., *Proc. Natl. Acad. Sci. USA* 87:633-7, 1990.

The present invention further provides antisense polynucleotides that are complementary to a segment of a polynucleotide as set forth in one of SEQ ID NO:N, wherein N is an odd integer from 1 to 435. Such antisense polynucleotides are designed to bind to the corresponding mRNA and inhibit its translation. Antisense polynucleotides are used to inhibit gene expression in cell culture or in a patient, and can be used as probes or primers for research or diagnostic purposes.

Probes and primers of the present invention comprise a suitable fragment, and may comprise up to the complete sequence, of a polynucleotide as shown in SEQ ID NO:N or the complement thereof, wherein N is an odd integer from 1 to 421. Probes will generally be at least 20 nucleotides in length, although somewhat shorter probes (14-17 nucleotides) can be used. PCR primers are at least 5 nucleotides in length, preferably 15 or more nt, more preferably 20-30 nt. Shorter polynucleotide probes and primers are referred to in the art as "oligonucleotides," and can be DNA or RNA. Probes will generally comprise an oligonucleotide linked to a label, such as a radionuclide.

Probes and primers as disclosed herein can be used for cloning allelic, orthologous, and paralogous sequences. Allelic variants of the disclosed sequences can be cloned by probing cDNA or genomic libraries from different individuals according to standard procedures. Orthologous sequences can be cloned using information and compositions provided by the present invention in combination with conventional cloning techniques. For example, a cDNA can be cloned using mRNA obtained from a tissue or cell type that expresses the protein. Suitable sources of mRNA can be identified by probing Northern blots with probes designed from the sequences disclosed herein. A library is then prepared from mRNA of a positive tissue or cell line. A cDNA can then be isolated by a variety of methods, such as by probing with a complete or partial human cDNA or with one or more sets of degenerate probes based on the disclosed sequences. A cDNA can also be cloned by PCR using primers designed from the sequences disclosed herein. Within an additional method, the cDNA library can be used to transform or transfect host cells, and expression of the cDNA of interest can be detected with an antibody to the encoded protein. Similar techniques can also be applied to the isolation of genomic clones. Orthologous and paralogous sequences can be identified from libraries by probing blots at low stringency and washing the blots at successively higher stringency until background is suitably reduced.

Probes and primers disclosed herein can be used to clone 5' non-coding regions of a corresponding gene. In view of the tissue-specific expression observed for certain proteins of the invention (Tables 8 and 9), promoters of these genes are expected to provide tissue-specific expression. Such promoter elements can thus be used to direct the tissue-specific expression of heterologous genes in, for example, transgenic animals or patients treated with gene therapy. Cloning of 5' flanking sequences also facilitates production of a protein of interest by "gene activation" as disclosed in U.S. Patent No. 5,641,670. Briefly, expression of an endogenous gene in a cell is altered by introducing into its locus a DNA construct comprising at least a targeting sequence, a regulatory sequence, an exon, and an unpaired splice donor site. The targeting sequence is a 5' non-coding sequence that permits homologous recombination of the construct with the endogenous locus, whereby the sequences within the construct become operably linked with the endogenous coding sequence. In this way, an endogenous promoter can be replaced or supplemented with other regulatory sequences to provide enhanced, tissue-specific, or otherwise regulated expression.

The polynucleotides of the present invention further include polynucleotides encoding the fusion proteins, including signal peptide fusions, disclosed above.

The present invention further provides a computer-readable medium encoded with a data structure that provides at least one of SEQ ID NO:1 through SEQ ID NO:436. Suitable forms of computer-readable media include magnetic media and optically-readable media. Examples of magnetic media include a hard or fixed drive, a random access memory (RAM) chip, a floppy disk, digital linear tape (DLT), a disk cache, and a ZIP® disk. Optically readable media are exemplified by compact discs (e.g., CD-read only memory (ROM), CD-rewritable (RW), and CD-recordable),digital versatile/video discs (DVD) (e.g., DVD-ROM, DVD-RAM, and DVD+RW), and carrier waves.

The polypeptides of the present invention, including full-length proteins, biologically active fragments, immunogenic fragments, and fusion proteins, can be produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacteria, fungal cells, and cultured higher eukaryotic cells. Eukaryotic cells, particularly cultured cells of multicellular organisms, are generally preferred for the production of proteins having higher eukaryotic-type post-translational modifications (e.g., γ-carboxylation) and for making proteins, especially secretory proteins, for pharmaceutical use in humans. Techniques for manipulating cloned DNA molecules and introducing exogenous DNA into a variety of host cells are disclosed by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989, and Ausubel et al., eds., *Current Protocols in Molecular Biology*, Green and Wiley and Sons, NY, 1993.

In general, a DNA sequence encoding a polypeptide of interest is operably linked to other genetic elements required for its expression, generally including a transcription promoter and terminator, within an expression vector. The vector will also commonly contain one or more selectable markers and one or more origins of replication, although those skilled in the art will recognize that within certain systems selectable markers can be provided on separate vectors, and replication of the exogenous DNA can be achieved through integration into the host cell genome. Selection of promoters, terminators, selectable markers, vectors and other elements is a matter of routine design within the level of ordinary skill in the art. Many such elements are described in the literature and are available through commercial suppliers.

To direct a polypeptide into the secretory pathway of a host cell, a secretory signal sequence (also known as a leader sequence, prepro sequence or pre sequence) is provided in the expression vector. The secretory signal sequence may be that of the protein of interest, or may be derived from another secreted protein (e.g., t-PA; see U.S. Patent No. 5,641,655) or synthesized *de novo*. The secretory signal sequence is operably linked to the DNA sequence encoding the protein of interest, i.e., the two sequences are joined in the correct reading frame and positioned to direct the newly synthesized protein into the secretory pathway of the host cell. Secretory signal sequences are commonly positioned 5' to the DNA sequence encoding the protein of interest, although certain secretory signal sequences may be positioned elsewhere in the DNA sequence of interest (see, e.g., Welch et al., U.S. Patent No. 5,037,743; Holland et al., U.S. Patent No. 5,143,830).

Cultured mammalian cells are suitable hosts for use within the present invention. Methods for introducing exogenous DNA into mammalian host cells include calcium phosphate-mediated transfection (Wigler et al., *Cell* 14:725, 1978; Corsaro and Pearson, *Somatic Cell Genetics* 7:603, 1981: Graham and Van der Eb, *Virology* 52:456, 1973), electroporation (Neumann et al., *EMBO J.* 1:841-845, 1982), DEAE-dextran mediated transfection (Ausubel et al., *ibid.*), and liposome-mediated transfection (Hawley-Nelson et al., *Focus* 15:73, 1993; Ciccarone et al., *Focus* 15:80, 1993). The production of recombinant polypeptides in cultured mammalian cells is disclosed by, for example, Levinson et al., U.S. Patent No. 4,713,339; Hagen et al., U.S. Patent No. 4,784,950; Palmiter et al., U.S. Patent No. 4,579,821; and Ringold, U.S. Patent No. 4,656,134. Suitable cultured mammalian cells include the COS-1 (ATCC No. CRL 1650), COS-7 (ATCC No. CRL 1651), BHK (ATCC No. CRL 1632), BHK 570 (ATCC No. CRL 10314), 293 (ATCC No. CRL 1573; Graham et al., *J. Gen. Virol.* 36:59-72, 1977) and Chinese hamster ovary (e.g. CHO-K1; ATCC No. CCL 61) cell lines. Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture Collection, Rockville, Maryland. In general, strong transcription promoters are preferred, such as promoters from SV-40 or cytomegalovirus. See, e.g., U.S. Patent No. 4,956,288. Other suitable promoters include those from metallothionein genes (U.S. Patent Nos. 4,579,821 and 4,601,978) and the adenovirus major late promoter. Within an alternative embodiment, adenovirus vectors can be employed. See, for example, Garnier et al., *Cytotechnol.* 15:145-55, 1994.

Drug selection is generally used to select for cultured mammalian cells into which foreign DNA has been inserted. Such cells are commonly referred to as "transfectants". Cells that have been cultured in the presence of the selective agent and

are able to pass the gene of interest to their progeny are referred to as "stable transfectants." An exemplary selectable marker is a gene encoding resistance to the antibiotic neomycin. Selection is carried out in the presence of a neomycin-type drug, such as G-418 or the like. Selection systems can also be used to increase the expression level of the gene of interest, a process referred to as "amplification." Amplification is carried out by culturing transfectants in the presence of a low level of the selective agent and then increasing the amount of selective agent to select for cells that produce high levels of the products of the introduced genes. An exemplary amplifiable selectable marker is dihydrofolate reductase, which confers resistance to methotrexate. Other drug resistance genes (e.g. hygromycin resistance, multi-drug resistance, puromycin acetyltransferase) can also be used.

Insect cells can be infected with recombinant baculovirus, commonly derived from *Autographa californica* nuclear polyhedrosis virus (AcNPV). See, King and Possee, The Baculovirus Expression System: A Laboratory Guide, London, Chapman & Hall; O'Reilly et al., Baculovirus Expression Vectors: A Laboratory Manual, New York, Oxford University Press., 1994; and Richardson, Ed., Baculovirus Expression Protocols. Methods in Molecular Biology, Humana Press, Totowa, NJ, 1995. Recombinant baculovirus can also be produced through the use of a transposon-based system described by Luckow et al. (*J. Virol.* 67:4566-4579, 1993). This system, which utilizes transfer vectors, is commercially available in kit form (Bac-to-Bac™ kit; Life Technologies, Rockville, MD). See also, Hill-Perkins and Possee, *J. Gen. Virol.* 71:971-976, 1990; Bonning et al., *J. Gen. Virol.* 75:1551-1556, 1994; and Chazenbalk and Rapoport, *J. Biol. Chem.* 270:1543-1549, 1995.

For protein production, the recombinant virus is used to infect host cells, typically a cell line derived from the fall armyworm, *Spodoptera frugiperda* (e.g., Sf9 or Sf21 cells) or *Trichoplusia ni* (e.g., High Five™ cells; Invitrogen, Carlsbad, CA). See, in general, Glick and Pasternak, Molecular Biotechnology: Principles and Applications of Recombinant DNA, ASM Press, Washington, D.C., 1994. See also, U.S. Patent No. 5,300,435. Serum-free media are used to grow and maintain the cells. Suitable media formulations are known in the art and can be obtained from commercial suppliers. The cells are grown up from an inoculation density of approximately 2-5 x 10^5 cells to a density of 1-2 x 10^6 cells, at which time a recombinant viral stock is added at a multiplicity of infection (MOI) of 0.1 to 10, more typically near 3. Procedures used are generally described in available laboratory manuals (e.g., King and Possee, *ibid.*; O'Reilly et al., *ibid.*; Richardson, *ibid.*). See also, Guarino et al., U.S. Patent No. 5,162,222 and WIPO publication WO 94/06463.

Fungal cells, including yeast cells, can also be used within the present invention. Yeast species of particular interest in this regard include *Saccharomyces cerevisiae*, *Pichia pastoris*, and *Pichia methanolica*. Methods for transforming *S. cerevisiae* cells with exogenous DNA and producing recombinant polypeptides therefrom are disclosed by, for example, Kawasaki, U.S. Patent No. 4,599,311; Kawasaki et al., U.S. Patent No. 4,931,373; Brake, U.S. Patent No. 4,870,008; Welch et al., U.S. Patent No. 5,037,743; and Murray et al., U.S. Patent No. 4,845,075. Transformed cells are selected by phenotype determined by the selectable marker, commonly drug resistance or the ability to grow in the absence of a particular nutrient (e.g., leucine). A preferred vector system for use in *Saccharomyces cerevisiae* is the *POT1* vector system disclosed by Kawasaki et al. (U.S. Patent No. 4,931,373), which allows transformed cells to be selected by growth in glucose-containing media. Suitable promoters and terminators for use in yeast include those from glycolytic enzyme genes (see, e.g., Kawasaki, U.S. Patent No. 4,599,311; Kingsman et al., U.S. Patent No. 4,615,974; and Bitter, U.S. Patent No. 4,977,092) and alcohol dehydrogenase genes. See also U.S. Patents Nos. 4,990,446; 5,063,154; 5,139,936 and 4,661,454.

Transformation systems for other yeasts, including *Hansenula polymorpha, Schizosaccharomyces pombe, Kluyveromyces lactis, Kluyveromyces fragilis, Ustilago maydis, Pichia pastoris, Pichia methanolica, Pichia guillermondii* and *Candida maltosa* are known in the art. See, for example, Gleeson et al., *J. Gen. Microbiol.* 132:3459-3465, 1986 and Cregg, U.S. Patent No. 4,882,279. Aspergillus cells may be utilized according to the methods of McKnight et al., U.S. Patent No. 4,935,349. Methods for transforming *Acremonium chrysogenum* are disclosed by Sumino et al., U.S. Patent No. 5,162,228. Methods for transforming Neurospora are disclosed by Lambowitz, U.S. Patent No. 4,486,533. Production of recombinant proteins in *Pichia methanolica* is disclosed in U.S. Patents No. 5,716,808, 5,736,383, 5,854,039, and 5,888,768; and WIPO publications WO 99/14347 and WO 99/14320.

Other higher eukaryotic cells, including plant cells and avian cells, can also be used as hosts according to methods commonly known in the art. For example, the use of *Agrobacterium rhizogenes* as a vector for expressing genes in plant cells has been reviewed by Sinkar et al., *J. Biosci. (Bangalore)* 11:47-58, 1987.

Prokaryotic host cells, including strains of the bacteria *Escherichia coli*, *Bacillus* and other genera are also useful host cells within the present invention. Techniques for transforming these hosts and expressing foreign DNA sequences cloned therein are well known in the art (see, e.g., Sambrook et al., ibid.). When expressing a polypeptide in bacteria such as *E. coli*, the polypeptide may be retained in the

cytoplasm, typically as insoluble granules, or may be directed to the periplasmic space by a bacterial secretion sequence. In the former case, the cells are lysed, and the granules are recovered and denatured using, for example, guanidine isothiocyanate or urea. The denatured polypeptide can then be refolded and dimerized by diluting the denaturant, such as by dialysis against a solution of urea and a combination of reduced and oxidized glutathione, followed by dialysis against a buffered saline solution. In the latter case, the polypeptide can be recovered from the periplasmic space in a soluble and functional form by disrupting the cells (by, for example, sonication or osmotic shock) to release the contents of the periplasmic space and recovering the protein, thereby obviating the need for denaturation and refolding.

Transformed or transfected host cells are cultured according to conventional procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media may also contain such components as growth factors or serum, as required. The growth medium will generally select for cells containing the exogenously added DNA by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression vector or co-transfected into the host cell.

It is preferred to purify the polypeptides and proteins of the present invention to ≥80% purity, more preferably to ≥90% purity, even more preferably ≥95% purity, and particularly preferred is a pharmaceutically pure state, that is greater than 99.9% pure with respect to contaminating macromolecules, particularly other proteins and nucleic acids, and free of infectious and pyrogenic agents. Preferably, a purified polypeptide or protein is substantially free of other polypeptides or proteins, particularly those of animal origin.

Expressed recombinant proteins (including single polypeptide chains, chimeric polypeptides, and polypeptide multimers) are purified by conventional protein purification methods, typically by a combination of chromatographic techniques. See, in general, Affinity Chromatography: Principles & Methods, Pharmacia LKB Biotechnology, Uppsala, Sweden, 1988; and Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York, 1994. Proteins comprising a polyhistidine affinity tag (typically about 6 histidine residues) are purified by affinity chromatography on a nickel chelate resin. See, for example, Houchuli et al., *Bio/Technol.* 6: 1321-1325, 1988. Proteins comprising a glu-glu tag can be purified by immunoaffinity chromatography essentially as disclosed by Grussenmeyer et al., *ibid.*

Proteins comprising other affinity tags can be purified by appropriate affinity chromatography methods, which are known in the art.

Proteins of the present invention and fragments thereof can also be prepared through chemical synthesis according to methods known in the art, including exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. See, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149, 1963; Stewart et al., Solid Phase Peptide Synthesis (2nd edition), Pierce Chemical Co., Rockford, IL, 1984; Bayer and Rapp, *Chem. Pept. Prot.* 3:3, 1986; and Atherton et al., Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, Oxford, 1989.

Using methods known in the art, the proteins of the present invention can be prepared in a variety of modified or derivatized forms. For example, the proteins can be prepared glycosylated or non-glycosylated; pegylated or non-pegylated; and may or may not include an initial methionine amino acid residue.

Biological activities of the proteins of the present invention can be measured *in vitro* using cultured cells or *in vivo* by administering molecules of the claimed invention to the appropriate animal model. Many such assays and models are known in the art. Guidance in initial assay selection is provided by structural predictions and sequence alignments. However, even if no functional prediction is made, the activity of a protein can be elucidated by known methods, including, for example, screening a variety of target cells for a biological response, other *in vitro* assays, expression in a host animal, or through the use of transgenic and/or "knockout" animals. Through the application of robotics, many *in vitro* assays can be adapted to rapid, high-throughput screeing of a large number of samples. Target cells for use in activity assays include, without limitation, vascular cells (especially endothelial cells and smooth muscle cells), hematopoietic (myeloid and lymphoid) cells, liver cells (including hepatocytes, fenestrated endothelial cells, Kupffer cells, and Ito cells), fibroblasts (including human dermal fibroblasts and lung fibroblasts), neurite cells (including astrocytes, glial cells, dendritic cells, and PC-12 cells), fetal lung cells, articular synoviocytes, pericytes, chondrocytes, osteoblasts, adipocytes, and prostate epithelial cells. Endothelial cells and hematopoietic cells are derived from a common ancestral cell, the hemangioblast (Choi et al., *Development* 125:725-732, 1998).

Biological activity can be measured with a silicon-based biosensor microphysiometer that measures the extracellular acidification rate or proton excretion associated with receptor binding and subsequent physiologic cellular responses. An exemplary such device is the Cytosensor™ Microphysiometer manufactured by Molecular Devices, Sunnyvale, CA. A variety of cellular responses, such as cell proliferation, ion transport, energy production, inflammatory response, regulatory and

receptor activation, and the like, can be measured by this method. See, for example, McConnell et al., *Science* 257:1906-1912, 1992; Pitchford et al., *Meth. Enzymol.* 228:84-108, 1997; Arimilli et al., *J. Immunol. Meth.* 212:49-59, 1998; and Van Liefde et al., *Eur. J. Pharmacol.* 346:87-95, 1998. The microphysiometer can be used for assaying adherent or non-adherent eukaryotic or prokaryotic cells. By measuring extracellular acidification changes in cell media over time, the microphysiometer directly measures cellular responses to various stimuli, including agonistic and antagonistic stimuli. Preferably, the microphysiometer is used to measure responses of a eukaryotic cell known to be responsive to the protein of interest, compared to a control eukaryotic cell that does not respond to the protein of interest. Responsive eukaryotic cells comprise cells into which a receptor for the protein of interest has been transfected, as well as naturally responsive cells. Differences in the response of cells exposed to the protein of interest, relative to a control not so exposed, are a direct measurement of protein-modulated cellular responses. Such responses can be assayed under a variety of stimuli. The present invention thus provides methods of identifying agonists and antagonists of proteins of interest, comprising providing cells responsive to a selected protein, culturing a first portion of the cells in the absence of a test compound, culturing a second portion of the cells in the presence of a test compound, and detecting a change in a cellular response of the second portion of the cells as compared to the first portion of the cells. The change in cellular response is shown as a measurable change in extracellular acidification rate. Culturing a third portion of the cells in the presence of the protein of interest and the absence of a test compound provides a positive control and a control to compare the agonist activity of a test compound with that of the protein of interest. Antagonists can be identified by exposing the cells to the protein of interest in the presence and absence of the test compound, whereby a reduction in protein-stimulated activity is indicative of antagonist activity in the test compound.

Assays measuring cell proliferation or differentiation are well known in the art. For example, assays measuring proliferation include such assays as chemosensitivity to neutral red dye (Cavanaugh et al., *Investigational New Drugs* 8:347-354, 1990), incorporation of radiolabelled nucleotides (as disclosed by, e.g., Raines and Ross, *Methods Enzymol.* 109:749-773, 1985; Wahl et al., *Mol. Cell Biol.* 8:5016-5025, 1988; and Cook et al., *Analytical Biochem.* 179:1-7, 1989), incorporation of 5-bromo-2'-deoxyuridine (BrdU) in the DNA of proliferating cells (Porstmann et al., *J. Immunol. Methods* 82:169-179, 1985), and use of tetrazolium salts (Mosmann, *J. Immunol. Methods* 65:55-63, 1983; Alley et al., *Cancer Res.* 48:589-601, 1988; Marshall et al., *Growth Reg.* 5:69-84, 1995; and Scudiero et al., *Cancer Res.* 48:4827-

4833, 1988). Differentiation can be assayed using suitable precursor cells that can be induced to differentiate into a more mature phenotype. Assays measuring differentiation include, for example, measuring cell-surface markers associated with stage-specific expression of a tissue, enzymatic activity, functional activity or morphological changes (Watt, *FASEB*, 5:281-284, 1991; Francis, *Differentiation* 57:63-75, 1994; Raes, Adv. Anim. Cell Biol. Technol. Bioprocesses, 161-171, 1989). Effects of a protein on tumor cell growth and metastasis can be analyzed using the Lewis lung carcinoma model, for example as described by Cao et al., *J. Exp. Med.* 182:2069-2077, 1995. Activity of a protein on cells of neural origin can be analyzed using assays that measure effects on neurite growth as disclosed below.

In vitro assays for pro- and anti-inflammatory activity are known in the art. Exemplary activity assays include mitogenesis assays in which IL-1 responsive cells (e.g., D10.N4.M cells) are incubated in the presence of IL-1 or a test protein for 72 hours at 37°C in a 5% CO_2 atmosphere. IL-2 (and optionally IL-4) is added to the culture medium to enhance sensitivity and specificity of the assay. ^{3}H-thymidine is then added, and incubation is continued for six hours. The amount of label incorporated is indicative of agonist activity. See, Hopkins and Humphreys, *J. Immunol. Methods* 120:271-276, 1989; Greenfeder et al., *J. Biol. Chem.* 270:22460-22466, 1995. Stimulation of cell proliferation can also be measured using thymocytes cultured in a test protein in combination with phytohemagglutinin. IL-1 is used as a control. Proliferation is detected as ^{3}H-thymidine incorporation or metabolic breakdown of (MTT) (Mosman, *ibid.*).

Protein activity may also be detected using assays designed to measure induction of one or more growth factors or other macromolecules. Preferred such assays include those for determining the presence of hepatocyte growth factor (HGF), epidermal growth factor (EGF), transforming growth factor alpha (TGFα), interleukin-6 (IL-6), VEGF, acidic fibroblast growth factor (aFGF), angiogenin, and other macromolecules produced by the liver. Suitable assays include mitogenesis assays using target cells responsive to the macromolecule of interest, receptor-binding assays, competition binding assays, immunological assays (e.g., ELISA), and other formats known in the art. Metalloprotease secretion is measured from treated primary human dermal fibroblasts, synoviocytes and chondrocytes. The relative levels of collagenase, gelatinase and stromalysin produced in response to culturing a target cell in the presence of a protein of interest is measured using zymogram gels (Loita and Stetler-Stevenson, *Cancer Biology* 1:96-106, 1990). Procollagen/collagen synthesis by dermal fibroblasts and chondrocytes in response to a test protein is measured using ^{3}H-proline incorporation into nascent secreted collagen. ^{3}H-labeled collagen is visualized by

SDS-PAGE followed by autoradiography (Unemori and Amento, *J. Biol. Chem.* 265: 10681-10685, 1990). Glycosaminoglycan (GAG) secretion from dermal fibroblasts and chondrocytes is measured using a 1,9-dimethylmethylene blue dye binding assay (Farndale et al., *Biochim. Biophys. Acta* 883:173-177, 1986). Collagen and GAG assays are also carried out in the presence of IL-1β or TGF-β to examine the ability of a protein to modify the established responses to these cytokines.

Monocyte activation assays are carried out (1) to look for the ability of a protein of interest to further stimulate monocyte activation, and (2) to examine the ability of a protein of interest to modulate attachment-induced or endotoxin-induced monocyte activation (Fuhlbrigge et al., *J. Immunol.* 138: 3799-3802, 1987). IL-1β and TNFα levels produced in response to activation are measured by ELISA (Biosource, Inc. Camarillo, CA). Monocyte/macrophage cells, by virtue of CD14 (LPS receptor), are exquisitely sensitive to endotoxin, and proteins with moderate levels of endotoxin-like activity will activate these cells.

Other metabolic effects of proteins can be measured by culturing target cells in the presence and absence of a protein and observing changes in adipogenesis, gluconeogenesis, glycogenolysis, lipogenesis, glucose uptake, or the like. Suitable assays are known in the art.

Hematopoietic activity of proteins can be assayed on various hematopoietic cells in culture. Preferred assays include primary bone marrow colony assays and later stage lineage-restricted colony assays, which are known in the art (e.g., Holly et al., WIPO Publication WO 95/21920). Marrow cells plated on a suitable semi-solid medium (e.g., 50% methylcellulose containing 15% fetal bovine serum, 10% bovine serum albumin, and 0.6% PSN antibiotic mix) are incubated in the presence of test polypeptide, then examined microscopically for colony formation. Known hematopoietic factors are used as controls. Mitogenic activity of a protein of interest on hematopoietic cell lines can be measured as disclosed above.

Cell migration is assayed essentially as disclosed by Kähler et al. (*Arteriosclerosis, Thrombosis, and Vascular Biology* 17:932-939, 1997). A protein is considered to be chemotactic if it induces migration of cells from an area of low protein concentration to an area of high protein concentration. A typical assay is performed using modified Boyden chambers with a polystryrene membrane separating the two chambers (Transwell; Corning Costar Corp.). The test sample, diluted in medium containing 1% BSA, is added to the lower chamber of a 24-well plate containing Transwells. Cells are then placed on the Transwell insert that has been pretreated with 0.2% gelatin. Cell migration is measured after 4 hours of incubation at 37°C. Non-migrating cells are wiped off the top of the Transwell membrane, and cells

attached to the lower face of the membrane are fixed and stained with 0.1% crystal violet. Stained cells are then extracted with 10% acetic acid and absorbance is measured at 600 nm. Migration is then calculated from a standard calibration curve. Cell migration can also be measured using the matrigel method of Grant et al. ("Angiogenesis as a component of epithelial-mesenchymal interactions" in Goldberg and Rosen, *Epithelial-Mesenchymal Interaction in Cancer*, Birkhäuser Verlag, 1995, 235-248; Baatout, *Anticancer Research* 17:451-456, 1997).

Proteins can be assayed for the ability to modulate axon guidance and growth. Suitable assays that detect changes in neuron growth patterns include, for example, those disclosed in Hastings, WIPO Publication WO 97/29189 and Walter et al., *Development* 101:685-96, 1987. Assays to measure the effects on neuron growth are well known in the art. For example, the C assay (e.g., Raper and Kapfhammer, *Neuron* 4:21-9, 1990 and Luo et al., *Cell* 75:217-27, 1993) can be used to determine collapsing activity of a protein of interest on growing neurons. Other methods that can assess protein-induced inhibition of neurite extension or divert such extension are also known. See, Goodman, *Annu. Rev. Neurosci.* 19:341-77, 1996. Conditioned media from cells expressing a protein of interest, or aggregates of such cells, can by placed in a gel matrix near suitable neural cells, such as dorsal root ganglia (DRG) or sympathetic ganglia explants, which have been co-cultured with nerve growth factor. Compared to control cells, protein-induced changes in neuron growth can be measured (as disclosed by, for example, Messersmith et al., *Neuron* 14:949-59, 1995 and Puschel et al., *Neuron* 14:941-8, 1995). Neurite outgrowth can be measured using neuronal cell suspensions grown in the presence of molecules of the present invention. See, for example, O'Shea et al., *Neuron* 7:231-7, 1991 and DeFreitas et al., *Neuron* 15:333-43, 1995.

Cell adhesion activity is assayed essentially as disclosed by LaFleur et al. (*J. Biol. Chem.* 272:32798-32803, 1997). Briefly, microtiter plates are coated with the test protein, non-specific sites are blocked with BSA, and cells (such as smooth muscle cells, leukocytes, or endothelial cells) are plated at a density of approximately 10^4 - 10^5 cells/well. The wells are incubated at 37°C (typically for about 60 minutes), then non-adherent cells are removed by gentle washing. Adhered cells are quantitated by conventional methods (e.g., by staining with crystal violet, lysing the cells, and determining the optical density of the lysate). Control wells are coated with a known adhesive protein, such as fibronectin or vitronectin.

Assays for angiogenic activity are also known in the art. For example, the effect of a protein of interest on primordial endothelial cells in angiogenesis can be assayed in the chick chorioallantoic membrane angiogenesis assay (Leung, *Science*

246:1306-1309, 1989; Ferrara, *Ann. NY Acad. Sci.* 752:246-256, 1995). Briefly, a small window is cut into the shell of an eight-day old fertilized egg, and a test substance is applied to the chorioallantoic membrane. After 72 hours, the membrane is examined for neovascularization. Other suitable assays include microinjection of early stage quail (*Coturnix coturnix japonica*) embryos as disclosed by Drake et al. (*Proc. Natl. Acad. Sci. USA* 92:7657-7661, 1995); the rodent model of corneal neovascularization disclosed by Muthukkaruppan and Auerbach (*Science* 205:1416-1418, 1979), wherein a test substance is inserted into a pocket in the cornea of an inbred mouse; and the hampster cheek pouch assay (Höckel et al., *Arch. Surg.* 128:423-429, 1993). Induction of vascular permeability, which is indicative of angiogenic activity, is measured in assays designed to detect leakage of protein from the vasculature of a test animal (e.g., mouse or guinea pig) after administration of a test compound (Miles and Miles, *J. Physiol.* 118:228-257, 1952; Feng et al., *J. Exp. Med.* 183:1981-1986, 1996). *In vitro* assays for angiogenic activity include the tridimensional collagen gel matrix model (Pepper et al. *Biochem. Biophys. Res. Comm.* 189:824-831, 1992 and Ferrara et al., *Ann. NY Acad. Sci.* 732:246-256, 1995), which measures the formation of tube-like structures by microvascular endothelial cells; and matrigel models (Grant et al., "Angiogenesis as a component of epithelial-mesenchymal interactions" in Goldberg and Rosen, *Epithelial-Mesenchymal Interaction in Cancer*, Birkhäuser Verlag, 1995, 235-248; Baatout, *Anticancer Research* 17:451-456, 1997), which are used to determine effects on cell migration and tube formation by endothelial cells seeded in matrigel, a basement membrane extract enriched in laminin. It is preferred to carry out angiogenesis assays in the presence and absence of vascular endothelial growth factor (VEGF) to assess possible combinatorial effects. It is also preferred to use VEGF as a control within *in vivo* assays.

Receptor binding can be measured by the competition binding method of Labriola-Tompkins et al., *Proc. Natl. Acad. Sci. USA* 88:11182-11186, 1991. In an exemplary assay for IL-1 receptor binding, membranes pepared from EL-4 thymoma cells (Paganelli et al., *J. Immunol.* 138:2249-2253, 1987) are incubated in the presence of the test protein for 30 minutes at 37°C. Labeled IL-1α or IL-1β is then added and the incubation is continued for 60 minutes. The assay is terminated by membrane filtration. The amount of bound label is determined by conventional means (e.g., γ counter). In an alternative assay, the ability of a test protein to compete with labeled IL-1 for binding to cultured human dermal fibroblasts is measured according to the method of Dower et al. (*Nature* 324:266-268, 1986). Briefly, cells are incubated in a round-bottomed, 96-well plate in a suitable culture medium (e.g., RPMI 1640 containing 1% BSA, 0.1% Na azide, and 20 mM HEPES pH 7.4) at 8°C on a rocker

platform in the presence of labeled IL-1. Various concentrations of test protein are added. After the incubation (typically about two hours), cells are separated from unbound label by centrifuging 60-µl aliquots through 200 µl of phthalate oils in 400-µl polyethylene centrifuge tubes and excising the tips of the tubes with a razor blade as disclosed by Segal and Hurwitz, *J. Immunol.* 118:1338-1347, 1977. Receptor binding assays for other cell types are known in the art. See, for example, Bowen-Pope and Ross, *Methods Enzymol.* 109:69-100, 1985.

Receptor binding can also be measured using immobilized receptors or ligand-binding receptor fragments. For example, an immobilized receptor can be exposed to its labeled ligand and unlabeled test protein, whereby a reduction in labeled ligand binding compared to a control is indicative of receptor-binding activity in the test protein. Within another format, a receptor or ligand-binding receptor fragment is immobilized on a biosensor (e.g., BIACore™, Pharmacia Biosensor, Piscataway, NJ) and binding is determined. Antagonists of the native ligand will exhibit receptor binding but will exhibit essentially no activity in appropriate activity assays or will reduce the ligand-mediated response when combined with the native ligand. In view of the low level of receptor occupancy required to produce a response to some ligands (e.g., IL-1), a large excess of antagonist (typically a 10- to 1000-fold molar excess) may be necessary to neutralize ligand activity.

Receptor activation can be detected in target cells by: (1) measurement of adenylate cyclase activity (Salomon et al., *Anal. Biochem.* 58:541-48, 1974; Alvarez and Daniels, *Anal. Biochem.* 187:98-103, 1990); (2) measurement of change in intracellular cAMP levels using conventional radioimmunoassay methods (Steiner et al., *J. Biol. Chem.* 247:1106-13, 1972; Harper and Brooker, *J. Cyc. Nucl. Res.* 1:207-18, 1975); or (3) through use of a cAMP scintillation proximity assay (SPA) method (such as available from Amersham Corp., Arlington Heights, IL).

Proteins can be tested for serine protease activity or proteinase inhibitory activity using conventional assays. Substrate cleavage is conveniently assayed using a tetrapeptide that mimics the cleavage site of the natural substrate and which is linked, via a peptide bond, to a carboxyl-terminal para-nitro-anilide (pNA) group. The protease hydrolyzes the bond between the fourth amino acid residue and the pNA group, causing the pNA group to undergo a dramatic increase in absorbance at 405 nm. Suitable substrates can be synthesized according to known methods or obtained from commercial suppliers. Inhibitory activity is measured by adding a test sample to a reaction mixture containing enzyme and substrate, and comparing the observed enzyme activity to a control (without the test sample). A variety of such assays are known in the art, including assays measuring inhibition of trypsin,

chymotrypsin, plasmin, cathepsin G, and human leukocyte elastase. See, for example, Petersen et al., *Eur. J. Biochem.* 235:310-316, 1996. In a typical procedure, the inhibitory activity of a test compound is measured by incubating the test compound with the proteinase, then adding an appropriate substrate, typically a chromogenic peptide substrate. See, for example, Norris et al. (*Biol. Chem. Hoppe-Seyler* 371:37-42, 1990). Various concentrations of the inhibitor are incubated in the presence of trypsin, plasmin, and plasma kallikrein in a low-salt buffer at pH 7.4, 25°C. After 30 minutes, the residual enzymatic activity is measured by the addition of a chromogenic substrate (e.g., S2251 (D-Val-Leu-Lys-Nan) or S2302 (D-Pro-Phe-Arg-Nan), available from Kabi, Stockholm, Sweden) and a 30-minute incubation. Inhibition of enzyme activity is indicated by a decrease in absorbance at 405 nm or fluorescence Em at 460 nm. From the results, the apparent inhibition constant K_i is calculated. When a serine protease is prepared as an active precursor (e.g., comprising N-terminal residues 1-109 of SEQ ID NO:2), it is activated by cleavage with a suitable protease (e.g., furin (Steiner et al., J. Biol. Chem. 267:23435-23438, 1992)) prior to assay. Assays of this type are well known in the art. See, for example, Lottenberg et al., Thrombosis Research 28:313-332, 1982; Cho et al., Biochem. 23:644-650, 1984; Foster et al., Biochem. 26:7003-7011, 1987). The inhibition of coagulation factors (e.g., factor VIIa, factor Xa) can be measured using chromogenic substrates or in conventional coagulation assays (e.g., clotting time of normal human plasma; Dennis et al., *J. Biol. Chem.* 270:25411-25417, 1995).

Blood coagulation and chromogenic assays, which can be used to detect both procoagulant, anticoagulant, and thrombolytic activities, are known in the art. For example, pro- and anticoagulant activities can be measured in a one-stage clotting assay using platelet-poor or factor-deficient plasma (Levy and Edgington, *J. Exp. Med.* 151:1232-1243, 1980; Schwartz et al., *J. Clin. Invest.* 67:1650-1658, 1981). As disclosed by Anderson et al. (*Proc. Natl. Acad. Sci. USA* 96:11189-11193, 1999), the effect of a test compound on platelet activation can be determined by a change in turbidity, and the procoagulant activity of activated platelets can be determined in a phospholipid-dependent coagulation assay. Activation of thrombin can be determined by hydrolysis of peptide p-nitroanilide substrates as disclosed by Lottenberg et al. (*Thrombosis Res.* 28:313-332, 1982). Other procoagulant, anticoagulant, and thrombolytic activities can be measured using appropriate chromogenic substrates, a variety of which are available from commercial suppliers. See, for example, Kettner and Shaw, *Methods Enzymol.* 80:826-842, 1981.

Anti-microbial activity of proteins is evaluated by techniques that are known in the art. For example, anti-microbial activity can be assayed by evaluating the

sensitivity of microbial cell cultures to test agents and by evaluating the protective effect of test agents on infected mice. See, for example, Musiek et al., *Antimicrob. Agents Chemothr.* 3:40, 1973. Antiviral activity can also be assessed by protection of mammalian cell cultures. Known techniques for evaluating anti-microbial activity include, for example, Barsum et al., *Eur. Respir. J.* 8:709-714, 1995; Sandovsky-Losica et al., *J. Med. Vet. Mycol (England)* 28:279-287, 1990; Mehentee et al., *J. Gen. Microbiol (England)* 135(:2181-2188, 1989; and Segal and Savage, *J. Med. Vet. Mycol.* 24:477-479, 1986. Assays specific for anti-viral activity include, for example, those described by Daher et al., *J. Virol.* 60:1068-1074, 1986.

The assays disclosed above can be modified by those skilled in the art to detect the presence of agonists and antagonists of a selected protein of interest.

Expression of a polynucleotide encoding a protein of interest in animals provides models for further study of the biological effects of overproduction or inhibition of protein activity *in vivo*. Polynucleotides and antisense polynucleotides can be introduced into test animals, such as mice, using viral vectors or naked DNA, or transgenic animals can be produced.

One *in vivo* approach for assaying proteins of the present invention utilizes viral delivery systems. Exemplary viruses for this purpose include adenovirus, herpesvirus, retroviruses, vaccinia virus, and adeno-associated virus (AAV). Adenovirus, a double-stranded DNA virus, is currently the best studied gene transfer vector for delivery of heterologous nucleic acids. For review, see Becker et al., *Meth. Cell Biol.* 43:161-89, 1994; and Douglas and Curiel, *Science & Medicine* 4:44-53, 1997. The adenovirus system offers several advantages. Adenovirus can (i) accommodate relatively large DNA inserts; (ii) be grown to high-titer; (iii) infect a broad range of mammalian cell types; and (iv) be used with many different promoters including ubiquitous, tissue specific, and regulatable promoters. Because adenoviruses are stable in the bloodstream, they can be administered by intravenous injection.

By deleting portions of the adenovirus genome, larger inserts (up to 7 kb) of heterologous DNA can be accommodated. These inserts can be incorporated into the viral DNA by direct ligation or by homologous recombination with a co-transfected plasmid. In an exemplary system, the essential E1 gene is deleted from the viral vector, and the virus will not replicate unless the E1 gene is provided by the host cell (e.g., the human 293 cell line). When intravenously administered to intact animals, adenovirus primarily targets the liver. If the adenoviral delivery system has an E1 gene deletion, the virus cannot replicate in the host cells. However, the host's tissue (e.g., liver) will express and process (and, if a signal sequence is present, secrete) the

heterologous protein. Secreted proteins will enter the circulation in the highly vascularized liver, and effects on the infected animal can be determined.

An alternative method of gene delivery comprises removing cells from the body and introducing a vector into the cells as a naked DNA plasmid. The transformed cells are then re-implanted in the body. Naked DNA vectors are introduced into host cells by methods known in the art, including transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter. See, Wu et al., *J. Biol. Chem.* 263:14621-14624, 1988; Wu et al., *J. Biol. Chem.* 267:963-967, 1992; and Johnston and Tang, *Meth. Cell Biol.* 43:353-365, 1994.

Transgenic mice, engineered to express a gene encoding a protein of interest, and mice that exhibit a complete absence of gene function, referred to as "knockout mice" (Snouwaert et al., *Science* 257:1083, 1992), can also be generated (Lowell et al., *Nature* 366:740-742, 1993). These mice can be employed to study the gene of interest and the protein encoded thereby in an *in vivo* system. Transgenic mice are particularly useful for investigating the role of proteins in early development in that they allow the identification of developmental abnormalities or blocks resulting from the over- or underexpression of a specific factor. See also, Maisonpierre et al., *Science* 277:55-60, 1997 and Hanahan, *Science* 277:48-50, 1997. Preferred promoters for transgenic expression include promoters from metallothionein and albumin genes. As disclosed above, the human sequences provided herein can be used to clone orthologous polynucleotides, which may be preferred for use in generating transgenic and knockout animals.

Antisense methodology can be used to inhibit gene transcription to examine the effects of such inhibition *in vivo*. Polynucleotides that are complementary to a segment of a protein-encoding polynucleotide are designed to bind to the encoding mRNA and to inhibit translation of such mRNA. Such antisense oligonucleotides can also be used to inhibit expression of protein-encoding genes in cell culture.

Biological activities of test proteins can also be measured in animal models by administering the test protein, by itself or in combination with other agents, including other proteins. Using such models facilitates the assay of the test protein by itself or as an inhibitor or modulator of another agent, and also facilitates the measurement of combinatorial effects of bioactive compounds.

Anti-inflammatory activity can be tested in animal models of inflammatory disease. For example, animal models of psoriasis include the analysis of histological alterations in adult mouse tail epidermis (Hofbauer et al, *Brit. J. Dermatol.*

118:85-89, 1988; Bladon et al., *Arch Dermatol. Res.* 277:121-125, 1985). In this model, anti-psoriatic activity is indicated by the induction of a granular layer and orthokeratosis in areas of scale between the hinges of the tail epidermis. Typically, a topical ointment comprising a test compound is applied daily for seven consecutive days, then the animal is sacrificed, and tail skin is examined histologically. An additional model is provided by grafting psoriatic human skin to congenitally athymic (nude) mice (Krueger et al., *J. Invest. Dermatol.* 64:307-312, 1975). Such grafts have been shown to retain the characteristic histology for up to eleven weeks. As in the mouse tail model, the test composition is applied to the skin at predetermined intervals for a period of one to several weeks, at which time the animals are sacrificed and the skin grafts examined histologically. A third model has been disclosed by Fretland et al. (*Inflammation* 14:727-739, 1990). Briefly, inflammation is induced in guinea pig epidermis by topically applying phorbol ester (phorbol-12-myristate-13-acetate; PMA), typically at ca. 2 g/ml in acetone, to one ear and vehicle to the contralateral ear. Test compounds are applied concurrently with the PMA, or may be given orally. Histological analysis is performed at 96 hours after application of PMA. This model duplicates many symptoms of human psoriasis, including edema, inflammatory cell diapedesis and infiltration, high LTB_4 levels and epidermal proliferation.

Cerebral ischemia can be studied in a rat model as disclosed by Relton et al. (*ibid.*) and Loddick et al. (*ibid.*).

The effect of a test protein on primordial endothelial cells in angiogenesis can be assayed in the chick chorioallantoic membrane angiogenesis assay (Leung, *Science* 246:1306-1309, 1989; Ferrara, *Ann. NY Acad. Sci.* 752:246-256, 1995). Briefly, a small window is cut into the shell of an eight-day old fertilized egg, and a test substance is applied to the chorioallantoic membrane. After 72 hours, the membrane is examined for neovascularization. Embryo microinjection of early stage quail (*Coturnix coturnix japonica*) embryos can also be used (Drake et al., *Proc. Natl. Acad. Sci. USA* 92:7657-7661, 1995). Briefly, a solution containing the protein is injected into the interstitial space between the endoderm and the splanchnic mesoderm of early-stage embryos using a micropipette and micromanipulator system. After injection, embryos are placed ventral side down on a nutrient agar medium and incubated for 7 hours at 37°C in a humidified CO_2/air mixture (10%/90%). Vascular development is assessed by microscopy of fixed, whole-mounted embryos and sections.

Stimulation of coronary collateral growth can be measured in known animal models, including a rabbit model of peripheral limb ischemia and hind limb ischemia and a pig model of chronic myocardial ischemia (Ferrara et al., *Endocrine*

Reviews 18:4-25, 1997). Test proteins are assayed in the presence and absence of VEGF and basic FGF to test for combinatorial effects. These models can be modified by the use of adenovirus or naked DNA for gene delivery as disclosed in more detail above, resulting in local expression of the test protein(s).

Angiogenic activity can also be tested in a rodent model of corneal neovascularization as disclosed by Muthukkaruppan and Auerbach, *Science* 205:1416-1418, 1979, wherein a test substance is inserted into a pocket in the cornea of an inbred mouse. For use in this assay, proteins are combined with a solid or semi-solid, biocompatible carrier, such as a polymer pellet. Angiogenesis is followed microscopically. Vascular growth into the corneal stroma can be detected in about 10 days.

Angiogenic activity can also be tested in the hampster cheek pouch assay (Höckel et al., *Arch. Surg.* 128:423-429, 1993). A test substance is injected subcutaneiously into the cheek pouch, and after five days the pouch is examined under low magnification to determine the extent of neovascularization. Tissue sections can also be examined histologically.

Induction of vascular permeability is measured in assays designed to detect leakage of protein from the vasculature of a test animal (e.g., mouse or guinea pig) after administration of a test compound (Miles and Miles, *J. Physiol.* 118:228-257, 1952; Feng et al., *J. Exp. Med.* 183:1981-1986, 1996).

Wound-healing models include the linear skin incision model of Mustoe et al. (*Science* 237:1333, 1987). In a typical procedure, a 6-cm incision is made in the dorsal pelt of an adult rat, then closed with wound clips. Test substances and controls (in solution, gel, or powder form) are applied before primary closure. It is preferred to limit administration to a single application, although additional applications can be made on succeeding days by careful injection at several sites under the incision. Wound breaking strength is evaluated between 3 and 21 days post wounding. In a second model, multiple, small, full-thickness excisions are made on the ear of a rabbit. The cartilage in the ear splints the wound, removing the variable of wound contraction from the evaluation of closure. Experimental treatments and controls are applied. The geometry and anatomy of the wound site allow for reliable quantification of cell ingrowth and epithelial migration, as well as quantitative analysis of the biochemistry of the wounds (e.g., collagen content). See, Mustoe et al., *J. Clin. Invest.* 87:694, 1991. The rabbit ear model can be modified to create an ischemic wound environment, which more closely resembles the clinical situation (Ahn et al., *Ann. Plast. Surg.* 24:17, 1990). Within a third model, healing of partial-thickness skin wounds in pigs or guinea pigs is evaluated (LeGrand et al., *Growth Factors* 8:307, 1993). Experimental

treatments are applied daily on or under dressings. Seven days after wounding, granulation tissue thickness is determined. This model is preferred for dose-response studies, as it is more quantitative than other *in vivo* models of wound healing. A full thickness excision model can also be employed. Within this model, the epidermis and dermis are removed down to the panniculus carnosum in rodents or the subcutaneous fat in pigs. Experimental treatments are applied topically on or under a dressing, and can be applied daily if desired. The wound closes by a combination of contraction and cell ingrowth and proliferation. Measurable endpoints include time to wound closure, histologic score, and biochemical parameters of wound tissue. Impaired wound healing models are also known in the art (e.g., Cromack et al., *Surgery* 113:36, 1993; Pierce et al., *Proc. Natl. Acad. Sci. USA* 86:2229, 1989; Greenhalgh et al., *Amer. J. Pathol.* 136:1235, 1990). Delay or prolongation of the wound healing process can be induced pharmacologically by treatment with steroids, irradiation of the wound site, or by concomitant disease states (e.g., diabetes). Linear incisions or full-thickness excisions are most commonly used as the experimental wound. Endpoints are as disclosed above for each type of wound. Subcutaneous implants can be used to assess compounds acting in the early stages of wound healing (Broadley et al., *Lab. Invest.* 61:571, 1985; Sprugel et al., *Amer. J. Pathol.* 129: 601, 1987). Implants are prepared in a porous, relatively non-inflammatory container (e.g., polyethylene sponges or expanded polytetrafluoroethylene implants filled with bovine collagen) and placed subcutaneously in mice or rats. The interior of the implant is empty of cells, producing a "wound space" that is well-defined and separable from the preexisting tissue. This arrangement allows the assessment of cell influx and cell type as well as the measurement of vasculogenesis/angiogenesis and extracellular matrix production.

Inhibition of tumor metastasis can be assessed in mice into which cancerous cells or tumor tissue have been introduced by implantation or injection (e.g., Brown, *Advan. Enzyme Regul.* 35:293-301, 1995; Conway et al., *Clin. Exp. Metastasis* 14:115-124, 1996).

Effects on fibrinolysis can be measured in a rat model wherein the enzyme batroxobin and radiolabeled fibrinogen are administered to test animals. Inhibition of fibrinogen activation by a test compound is seen as a reduction in the circulating level of the label as compared to animals not receiving the test compound. See, Lenfors and Gustafsson, *Semin. Thromb. Hemost.* 22:335-342, 1996.

The invention further provides polypeptides that comprise an epitope-bearing portion of a protein as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 436. An "epitope" is a region of a protein to which an antibody can bind. See, for example, Geysen et al., *Proc. Natl. Acad. Sci. USA* 81:3998-4002, 1984.

Epitopes can be linear or conformational, the latter being composed of discontinuous regions of the protein that form an epitope upon folding of the protein. Linear epitopes are generally at least 6 amino acid residues in length. Relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for example, Sutcliffe et al., *Science* 219:660-666, 1983. Antibodies that recognize short, linear epitopes are particularly useful in analytic and diagnostic applications that employ denatured protein, such as Western blotting (Tobin, *Proc. Natl. Acad. Sci. USA* 76:4350-4356, 1979). Antibodies to short peptides may also recognize proteins in native conformation and will thus be useful for monitoring protein expression and protein isolation, and in detecting proteins in solution, such as by ELISA or in immunoprecipitation studies.

Antigenic, epitope-bearing polypeptides of the present invention are useful for raising antibodies, including monoclonal antibodies, that specifically bind to the corresponding protein. Antigenic, epitope-bearing polypeptides contain a sequence of at least six, preferably at least nine, more preferably from 15 to about 30 contiguous amino acid residues of a protein. Within certain embodiments of the invention, the polypeptides comprise 40, 50, 100, or more contiguous residues of a protein as shown in SEQ ID NO:M, up to the entire predicted mature protein or the primary translation product. It is preferred that the amino acid sequence of the epitope-bearing polypeptide is selected to provide substantial solubility in aqueous solvents, that is the sequence includes relatively hydrophilic residues, and hydrophobic residues are substantially avoided. Table 10 lists preferred hexapeptides for use as antigens. Within Table 10, each the amino termini of the hexapeptides are specified. Those skilled in the art will recognize that longer polypeptides comprising these hexapeptides can also be used and will often be preferred.

Table 10

Protein	Hexapeptide N-termini				
AFP210015	389	405	97	388	359
AFP170681	51	334	113	49	140
AFP413680	221	207	220	206	198
AFP483037	219	218	82	216	215
AFP230872	189	188	73	156	68
AFP178828	211	210	209	208	207
AFP200134	150	149	146	132	145
AFP195796	99	97	111	208	240

AFP477303	64	126	63	54	112
AFP354334	269	268	267	266	265
AFP250287	34	33	48	2	143
AFP177000	133	132	104	37	68
AFP278176	234	145	284	91	291
AFP202885	134	244	170	133	243
AFP221312	31	29	28	51	43
AFP239757	329	200	556	107	328
AFP226311	293	74	250	86	184
AFP305901	340	194	451	192	120
AFP325549	293	74	250	86	184
AFP81988	151	167	147	165	173
AFP199200	150	149	148	92	147
AFP290395	31	29	28	329	326
AFP212675	67	66	65	204	396
AFP326051	49	56	23	78	95
AFP512441	94	93	41	39	38
AFP55098	140	34	139	120	32
AFP169796	177	173	156	32	155
AFP280706	33	54	32	31	53
AFP383165	25	82	52	24	178
AFP195467	113	112	71	2	80
AFP134225	114	280	113	455	417
AFP261193	120	66	65	85	119
AFP324422	147	145	66	65	85
AFP374312	125	124	79	123	77
AFP258118	64	63	116	115	62
AFP74517	1	72	124	123	22
AFP254653	134	36	62	14	23
AFP108666	79	76	74	49	48
AFP8766	140	34	139	120	298
AFP397185	265	35	264	34	48
AFP195042	192	535	191	259	533
AFP310695	49	75	190	5	94
AFP70022	38	64	179	83	37
AFP121670	184	183	121	118	182
AFP345861	151	89	75	135	149

AFP395942	60	14	59	13	21
AFP170291	144	72	56	55	63
AFP297548	145	73	57	56	64
AFP188135	152	148	158	147	144
AFP302388	478	431	416	414	429
AFP263430	92	23	64	91	110
AFP201273	373	384	163	372	44
AFP98983	3	2	35	34	32
AFP581958	71	66	80	26	25
AFP404202	1	31	115	30	92
AFP207203	427	258	204	426	48
AFP220790	139	92	51	187	91
AFP536326	87	146	105	73	103
AFP257473	270	205	203	245	244
AFP248380	283	62	54	272	100
AFP276202	50	48	35	46	33
AFP227568	199	23	238	363	224
AFP229039	226	91	116	161	225
AFP176297	261	382	183	119	182
AFP356885	622	45	525	175	466
AFP226938	118	108	117	79	107
AFP138504	77	255	75	254	292
AFP359196	4	76	3	2	37
AFP501809	141	139	9	169	2
AFP152733	258	204	48	47	257
AFP541394	31	29	28	235	232
AFP243183	272	110	106	3	2
AFP80739	398	397	224	223	155
AFP361806	4	78	139	3	76
AFP483930	107	124	123	88	45
AFP257336	124	42	122	182	158
AFP195800	40	39	65	38	96
AFP179530	57	251	249	315	55
AFP279267	106	62	216	187	59
AFP299766	127	168	165	29	126
AFP244615	171	196	326	255	179
AFP325761	138	137	2	144	109

AFP226024	79	317	159	140	45
AFP257094	71	116	115	3	144
AFP197103	200	198	215	195	177
AFP271855	92	44	42	18	27
AFP324816	9	252	120	8	63
AFP407963	202	201	156	200	155
AFP369635	98	398	255	97	254
AFP93743	4	254	3	294	293
AFP243230	28	129	128	127	44
AFP169316	294	170	293	36	157
AFP130852	82	59	117	145	66
AFP194191	363	112	271	69	267
AFP213472	103	102	69	2	37
AFP360430	177	75	183	74	130
AFP491309	107	106	69	2	37
AFP193428	129	87	343	60	128
AFP366534	72	4	2	59	39
AFP22706	229	227	65	64	188
AFP389012	216	27	289	34	17
AFP137186	2	1	182	216	43
AFP127023	86	56	131	178	55
AFP389687	57	56	117	370	369
AFP293220	186	194	105	146	182
AFP425535	264	181	163	370	149
AFP301494	159	4	2	84	25
AFP345421	500	592	639	652	849
AFP216667	92	435	329	422	47
AFP247951	27	34	33	25	94
AFP4464	365	363	362	55	209
AFP561930	108	107	104	52	66
AFP192851	300	276	299	298	496
AFP252759	311	310	64	21	157
AFP199044	143	2	209	206	125
AFP357958	167	338	165	324	362
AFP117501	135	87	362	86	418
AFP194554	318	170	54	105	169
AFP371069	332	1	283	365	279

AFP313600	341	340	240	48	176
AFP262739	25	24	142	23	207
AFP180730	58	37	30	27	36
AFP287227	596	592	591	374	525
AFP75785	128	127	136	99	71
AFP174843	152	323	150	309	347
AFP250422	100	140	99	138	182
AFP198645	145	144	143	64	56
AFP238111	123	50	20	137	35
AFP460626	153	151	71	150	70
AFP271081	68	112	39	202	67
AFP277752	109	106	220	238	92
AFP291338	347	342	97	362	339
AFP551038	134	131	186	130	173
AFP301579	105	153	130	152	67
AFP266188	121	235	61	180	120
AFP275580	193	77	192	2	148
AFP298054	148	234	146	233	144
AFP348226	148	103	85	309	59
AFP349106	208	118	117	207	116
AFP288248	376	342	340	339	312
AFP436476	18	39	139	38	99
AFP352125	53	59	163	142	104
AFP62060	247	187	73	426	72
AFP236718	100	99	249	248	184
AFP75775	201	90	239	173	199
AFP407487	148	103	85	59	58
AFP280451	141	294	6	209	139
AFP11675	58	56	90	64	89
AFP348656	160	159	158	103	149
AFP277451	118	2	1	146	241
AFP287436	53	59	223	142	104
AFP116043	212	239	138	186	183
AFP138740	264	263	31	72	232
AFP15192	47	46	216	85	212
AFP169968	64	117	63	2	81
AFP173341	65	64	102	101	100

AFP17588	43	42	2	41	1
AFP176427	311	290	308	155	288
AFP192633	58	56	162	349	44
AFP193013	47	90	87	46	68
AFP193881	274	295	402	273	292
AFP195562	274	295	339	473	273
AFP199922	57	55	74	180	50
AFP204736	89	58	43	28	23
AFP206179	74	80	73	71	70
AFP221877	32	31	30	50	75
AFP222758	44	43	75	42	19
AFP227032	47	55	46	65	54
AFP229269	147	127	146	63	60
AFP232213	44	41	28	27	40
AFP237679	2	1	34	58	55
AFP249599	48	47	45	43	42
AFP275215	82	80	70	2	55
AFP290397	149	148	2	1	29
AFP306591	45	44	84	83	65
AFP310297	23	31	37	47	30
AFP314720	47	44	26	25	23
AFP318671	55	54	51	64	63
AFP323575	75	73	72	70	18
AFP327160	37	68	47	67	96
AFP329002	78	77	76	75	74
AFP345415	41	40	133	106	39
AFP347179	30	4	29	86	177
AFP359138	77	2	76	75	74
AFP365372	13	1	62	69	79
AFP367284	61	60	36	5	59
AFP372822	49	48	25	8	24
AFP374595	154	153	165	3	56
AFP375952	36	35	53	52	69
AFP382913	67	32	30	20	66
AFP389184	24	31	78	30	39
AFP404208	69	68	67	39	36
AFP404279	81	31	72	30	62

AFP409112	97	96	56	94	55
AFP413111	65	85	96	64	94
AFP415635	35	26	25	34	32
AFP421092	27	1	46	57	35
AFP436666	5	95	59	4	58
AFP448623	14				
AFP454192	106	104	83	114	112
AFP49026	49	104	76	48	138
AFP51688	51	86	50	85	43
AFP525341	18	17	16	79	14
AFP545268	65	64	75	21	74
AFP592620	22	21	29	20	28
AFP62197	134	84	133	20	104
AFP68229	161	171	192	170	232
AFP71288	67	49	65	48	46
AFP77851	123	121	33	103	53
AFP81957	89	66	63	25	40
AFP85168	61	31	39	27	46

As used herein, the term "antibodies" includes polyclonal antibodies, monoclonal antibodies, antigen-binding fragments thereof such as $F(ab')_2$ and Fab fragments, single chain antibodies, and the like, including genetically engineered antibodies. Non-human antibodies can be humanized by grafting only non-human CDRs onto human framework and constant regions, or by incorporating the entire non-human variable domains (optionally "cloaking" them with a human-like surface by replacement of exposed residues, wherein the result is a "veneered" antibody). In some instances, humanized antibodies may retain non-human residues within the human variable region framework domains to enhance proper binding characteristics. Through humanizing antibodies, biological half-life may be increased, and the potential for adverse immune reactions upon administration to humans is reduced. One skilled in the art can generate humanized antibodies with specific and different constant domains (i.e., different Ig subclasses) to facilitate or inhibit various immune functions associated with particular antibody constant domains.

Alternative techniques for generating or selecting antibodies useful herein include *in vitro* exposure of lymphocytes to an immunogenic polypeptide, and selection of antibody display libraries in phage or similar vectors (for instance, through use of an immobilized or labeled polypeptide). Human antibodies can be produced in

transgenic, non-human animals that have been engineered to contain human immunoglobulin genes as disclosed in WIPO Publication WO 98/24893. It is preferred that the endogenous immunoglobulin genes in these animals be inactivated or eliminated, such as by homologous recombination.

Antibodies are defined to be specifically binding if they bind to a target polypeptide with an affinity at least 10-fold greater than the binding affinity to control (non-target) polypeptide. It is preferred that the antibodies exhibit a binding affinity (K_a) of 10^6 M^{-1} or greater, preferably 10^7 M^{-1} or greater, more preferably 10^8 M^{-1} or greater, and most preferably 10^9 M^{-1} or greater. The affinity of a monoclonal antibody can be readily determined by one of ordinary skill in the art (see, for example, Scatchard, *Ann. NY Acad. Sci.* 51: 660-672, 1949).

Methods for preparing polyclonal and monoclonal antibodies are well known in the art (see for example, Hurrell, J. G. R., Ed., *Monoclonal Hybridoma Antibodies: Techniques and Applications*, CRC Press, Inc., Boca Raton, FL, 1982). As would be evident to one of ordinary skill in the art, polyclonal antibodies can be generated from a variety of warm-blooded animals such as horses, cows, goats, sheep, dogs, chickens, rabbits, mice, and rats. The immunogenicity of a polypeptide immunogen may be increased through the use of an adjuvant such as alum (aluminum hydroxide) or Freund's complete or incomplete adjuvant. Polypeptides useful for immunization also include fusion polypeptides, such as fusions of a polypeptide of interest or a portion thereof with an immunoglobulin polypeptide or with maltose binding protein. The polypeptide immunogen may be a full-length molecule or a portion thereof. If the polypeptide portion is "hapten-like", such portion may be advantageously joined or linked to a macromolecular carrier (such as keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA) or tetanus toxoid) for immunization.

A variety of assays known to those skilled in the art can be utilized to detect antibodies that specifically bind to a polypeptide of interest. Exemplary assays are described in detail in *Antibodies: A Laboratory Manual*, Harlow and Lane (Eds.), Cold Spring Harbor Laboratory Press, 1988. Representative examples of such assays include concurrent immunoelectrophoresis, radio-immunoassays, radio-immunoprecipitations, enzyme-linked immunosorbent assays (ELISA), dot blot assays, Western blot assays, inhibition or competition assays, and sandwich assays.

Antibodies can be used, for example, to isolate target polypeptides by affinity purification, for diagnostic assays for determining circulating or localized levels of target polypeptides, for tissue typing, for cell sorting, for screening expression libraries; for generating anti-idiotypic antibodies, and as neutralizing antibodies or as antagonists to block protein activity *in vitro* and *in vivo*.

The present invention also provides reagents for use in diagnostic and therapeutic applications. Such reagents include polynucleotide probes and primers; antibodies, including antibody fragments, single-chain antibodies, and other genetically engineered forms; soluble receptors and other polypeptide binding partners; and the proteins of the invention themselves, including fragments thereof. Those skilled in the art will recognize that diagnostic reagents will commonly be labeled to provide a detectable signal or other second function. Thus, polypeptides, antibodies, receptors, and other binding partners disclosed herein can be directly or indirectly conjugated to drugs, toxins, radionuclides, enzymes, enzyme substrates, cofactors, inhibitors, fluorescent markers, chemiluminescent markers, magnetic particles, and the like, and these conjugates used for *in vivo* diagnostic or therapeutic applications. Cytotoxic molecules, for example, can be directly or indirectly attached to the binding partner (e.g., by chemical coupling or as a fusion protein), and include bacterial or plant toxins (e.g., diphtheria toxin, *Pseudomonas* exotoxin, ricin, saporin, abrin, and the like); therapeutic radionuclides (e.g., iodine-131, rhenium-188 or yttrium-90) which can be directly attached to a polypeptide or antibody or indirectly attached through means of a chelating moiety; and cytotoxic drugs (e.g., adriamycin). Methods for preparing labeled reagents are known in the art. Within an alternative embodiment, the detectable signal or other function can be provided by a second member of a complement-anticomplement pair, which second member binds to the diagnostic reagent. For example, a first (unlabeled) antibody can be used to bind to a cell-surface polypeptide, after which a second, labeled antibody which binds to the first antibody is added. Other complement-anticomplement pairs are known in the art and include biotin/streptavidin.

Diagnostic reagents as disclosed herein can be used *in vivo* or *in vitro*. *In vitro* diagnostic assays include assays of tissue and fluid samples. Assays for protein in serum, for example, may be used to detect metabolic abnormalities characterized by over- or under-production of the protein, such as cancers, immune system abnormalities, infections, organ failure, metabolic imbalances, inborn errors of metabolism and other disease states. Proteins of the present invention can also be used in the detection of circulating autoantibodies, which are indicative of autoimmune disorders. Those skilled in the art will recognize that conditions related to protein underexpression or overexpression may be amenable to treatment by therapeutic manipulation of the relevant protein level(s). Proteins in serum can be quantitated by known methods known in the art, which include the use of antibodies in a variety of formats. Non-antibody binding partners, such as ligand-binding receptor fragments (commonly referred to as "soluble receptors") can also be used.

In general, diagnostic methods employing oligonucleotide probes or primers comprise the steps of (a) obtaining a genetic sample from a patient; (b) incubating the genetic sample with an oligonucleotide probe or primer as disclosed above, under conditions wherein the probe or primer will hybridize to a complementary polynucleotide sequence, to produce a first reaction product; and (c) comparing the first reaction product to a control reaction product. A difference between the first reaction product and the control reaction product is indicative of a genetic abnormality in the patient. Genetic samples for use within such methods include genomic DNA, cDNA, and RNA. Suitable assay methods in this regard include molecular genetic techniques known to those in the art, such as restriction fragment length polymorphism (RFLP) analysis, short tandem repeat (STR) analysis employing PCR techniques, ligation chain reaction (Barany, *PCR Methods and Applications* 1:5-16, 1991), ribonuclease protection assays, and other genetic linkage analysis techniques known in the art (Sambrook et al., *ibid.*; Ausubel et. al., *ibid.*; A.J. Marian, *Chest* 108:255-65, 1995). Ribonuclease protection assays (see, e.g., Ausubel et al., *ibid.*, ch. 4) comprise the hybridization of an RNA probe to a patient RNA sample, after which the reaction product (RNA-RNA hybrid) is exposed to RNase. Hybridized regions of the RNA are protected from digestion. Within PCR assays, a patient genetic sample is incubated with a pair of oligonucleotide primers, and the region between the primers is amplified and recovered. Changes in size, amount, or sequence of recovered product are indicative of mutations in the patient. Another PCR-based technique that can be employed is single strand conformational polymorphism (SSCP) analysis (Hayashi, *PCR Methods and Applications* 1:34-38, 1991). Chromosomal localization data can be used to correlate AFP gene locations with known genetic disorders using, for example, the OMIM™ Database, Johns Hopkins University, 2000 (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM).

Relative chromosomal sublocalization shown in Table 11 was determined using the Draft Human Genome Browser (Kent, J., University of California Santa Cruz, http://genome.ucsc.edu/goldenPath/hgTracks.html) displaying the draft assembly of the July 17, 2000 version of the human genome. Table 11 also correlates AFP sequences with corresponding sequences in public databases by GenBank Accession Number, source clone ID number, and EST accession number. Also see Table 5, above.

Table 11

AFP	GenBank Acc. No.	Source Clone ID No.	EST Acc. No.	Chr.	Band	Start	Stop
AFP127023	AP001155	RP11-594B10	*	18	18q12	35729370	35952786
AFP138504	AP001931	RP11-691N7	*	11	11p11.11	53438038	53888802
AFP138740	AC024059	RP11-79j21	AW580814	15	15q22.1	58185489	58481462
AFP138740	*	*	AW580814	15		58258653	58308652
AFP177000	AL118506	RP4-591C20	*	20	20q12	48950838	49160243
AFP178828	AC007686	CTD-2289B16;RP11-116N21;RP11-7F17	*	14	14q23.3	62132030	62313415
AFP179530	AC011475	CTC-539A10	*	12	12q12	41234876	41456630
AFP188135	AC013740	*	*	9	9q31.2	91150313	91361876
AFP194554	AC024888	RP11-901L	*	16	16q22.1	71944378	72167142
AFP199044	AC012180	RP11-31I10	*	16	16q11.2	44574019	44904017
AFP.199200	CNS01DV7	BAC-R-1070N10	*	14		82330266	82541053
AFP229269	AL161670	BAC-R-804M7	*	14	14q21.3	46135365	46299284
AFP236718	AC010319	CTD-2521M24	*	19	19p13.3	4839920	5087628
AFP237679	Z69709	*	*	4	4p16.3	4521455	4544888
AFP244615	*	*	AI494556;AW850553	3	3q13.12	116466893	116517043
AFP249599	AL157714	RP11-541H12	*	1	1q22-23.3	161893354	162136704
AFP250422	AC012046	RP11-312P12	*	10	10q22.1	81289799	81650062
AFP262739	AC005884	hRPK.264_B_14	*	17	17q23.3	64245127	64365313
AFP275580	AC016773	*	*	3	3q21.3	141329005	141513510
AFP277451	AC055822	RP11-707M3	*	8	8q13.3	75395740	75583383
AFP279267	*	*	AI566086	10	10q11.1	52859924	52861338
AFP280451	AL133355	RP11-541N10	*	10	10q24.32	115276306	115467187
AFP290397	*	*	AA421069	15	15q15.3	48427462	48427830
AFP293220	AC012476	RP11-532F12	*	15	15p11.1	17263661	17480097
AFP297548	*	*	W52728	11	11q11	57918740	57927327
AFP306591	AQ079258	2366B9	AW118928	6	6p22.3	19812023	19812791
AFP313600	AC005037	NH0469M07	*	2	2q33.1	205320800	205511307
AFP324816	AC011687	RP11-15I20	*	2	2p21	49054619	49249783
AFP325761	AC012485	RP11-5O24	*	2	2p24.3	17554756	17765537

AFP326051	AL132639	BAC-R-407N17	AI525611	14	14p11.1	19959493	20153358
AFP345861	AC015936	CTD-2534I21	*	17	17q21.2	44087441	44286594
AFP347179	AC025740	*	*	12	12q24.23	125918909	126134148
AFP372822	AL022240	3.28E+21	*	1	1q12-21.2	138667522	138765140
AFP374312	*	*	AI253088	11	11q23.3	128134250	128134589
AFP375952	*	*	AI741157	16	16p13.3	3479999	3500834
AFP395942	AC004235	*	*	16	16p13.3	4189155	4222465
AFP404202	*	*	AI133727	7		142961410	143641730
AFP404279	*	*	AI341602	4	4p16.3	1512179	1514256
AFP413680	AC006942	cosmid-R31181	*	19	19q13.33	59897688	59940397
AFP436666	*	*	AI814257	8	8p21.3	18993217	19003942
AFP448623	*	*	AI140615	5	5q33.1	173540737	173547400
AFP460626	AC009131	RP11-502K10	*	16	16q22.1	70222075	70471703
AFP477303	AC008686	CTB-5E10	*	19	19p13.13	16491516	16677574
AFP501809	*	*	AW583171	6	6p21.1	50554924	50564907
AFP545268	AL138695	RP11-342J4	*	13	13q21.1	60450247	60714738
AFP561930	AL136221	RP11-391H12	*	13	13q34	108494503	108794286
AFP71288	*	*	AA493506	6	6q22.33	137477811	137478427
AFP74517	HS1056L3	RP5-1056L3	*	1	1p35.1-36.13	*	*
AFP93743	AC067942	RP11-791G16	*	4	4q21.22	77419530	77633569

If a mammal has an insufficiency of a protein of interest (due to, for example, a mutated or absent gene), the corresponding wild-type gene can be introduced into the cells of the mammal. In one embodiment, a gene encoding a protein of interest is introduced into the animal using a viral vector. Such vectors include an attenuated or defective DNA virus, such as, but not limited to, herpes simplex virus (HSV), papillomavirus, Epstein Barr virus (EBV), adenovirus, adeno-associated virus (AAV), and the like. Defective viruses, which entirely or almost entirely lack viral genes, are preferred. A defective virus is not infective after introduction into a cell. Use of defective viral vectors allows for administration to cells in a specific, localized area, without concern that the vector can infect other cells. Examples of particular vectors include, but are not limited to, a defective herpes simplex virus 1 (HSV1) vector (Kaplitt et al., *Molec. Cell. Neurosci.* 2:320-30, 1991); an attenuated adenovirus vector, such as the vector described by Stratford-Perricaudet et al. (*J. Clin. Invest.* 90:626-30, 1992); and a defective adeno-associated virus vector (Samulski et al., *J. Virol.* 61:3096-101, 1987; Samulski et al., *J. Virol.* 63:3822-28, 1989).

Within another embodiment, a gene of interest is introducted into an animal by liposome-mediated transfection ("lipofection") essentially as disclosed above. Lipofection can be used to introduce exogenous genes into specific organs.

A gene of interest can also be introduced into an animal for gene therapy as a naked DNA plasmid using the methods disclosed above.

In another embodiment, polypeptide-toxin fusion proteins or antibody/fragment-toxin fusion proteins may be used for targeted cell or tissue inhibition or ablation, such as in cancer therapy. Of particular interest in this regard are conjugates of an AFP protein and a cytotoxin, which can be used to target the cytotoxin to a tumor or other tissue that is undergoing undesired angiogenesis or neovascularization.

In another embodiment, AFP-cytokine fusion proteins or antibody/fragment-cytokine fusion proteins may be used for enhancing *in vitro* cytotoxicity (for instance, that mediated by monoclonal antibodies against tumor targets) and for enhancing *in vivo* killing of target tissues (for example, blood and bone marrow cancers). See, generally, Hornick et al., *Blood* 89:4437-4447, 1997). In general, cytokines are toxic if administered systemically. The described fusion proteins enable targeting of a cytokine to a desired site of action, such as a cell having binding sites for an AFP protein, thereby providing an elevated local concentration of cytokine. Polypeptides, antibodies, or receptors target an undesirable cell or tissue

(e.g., a tumor), and the fused cytokine mediates improved target cell lysis by effector cells. Suitable cytokines for this purpose include, for example, interleukin-2 and granulocyte-macrophage colony-stimulating factor (GM-CSF).

In another embodiment, polypeptide-toxin fusion proteins or other binding partner-linked toxins may be used for targeted cell or tissue inhibition or ablation (for instance, to treat cancer cells or tissues). Target cells (i.e., those displaying a receptor for a polypeptide of interest) bind the polypeptide-toxin conjugate, which is then internalized, killing the cell. The effects of receptor-specific cell killing (target ablation) are revealed by changes in whole animal physiology or through histological examination. Thus, ligand-dependent, receptor-directed cyotoxicity can be used to enhance understanding of the physiological significance of a protein ligand. A preferred such toxin is saporin. Mammalian cells have no receptor for saporin, which is non-toxic when it remains extracellular. Alternatively, if the polypeptide of interest has multiple functional domains (i.e., an activation domain or a ligand binding domain, plus a targeting domain), a fusion protein including only the targeting domain may be suitable for directing a detectable molecule, a cytotoxic molecule or a complementary molecule to a cell or tissue type of interest. In instances where the domain-only fusion protein includes a complementary molecule, the anti-complementary molecule can be conjugated to a detectable or cytotoxic molecule. Such domain-complementary molecule fusion proteins thus represent a generic targeting vehicle for cell- or tissue-specific delivery of generic anti-complementary-detectable/cytotoxic molecule conjugates.

The bioactive conjugates described herein can be delivered intravenously, intraarterially or intraductally, or may be introduced locally at the intended site of action.

For pharmaceutical use, the proteins of the present invention are formulated according to conventional methods. Routes of delivery include topical, mucosal, and parenteral, the latter including intravenous and subcutaneous delivery. Intravenous administration will be by bolus injection or infusion over a typical period of one to several hours. In general, pharmaceutical formulations will include a protein of the present invention in combination with a pharmaceutically acceptable vehicle, such as saline, buffered saline, 5% dextrose in water or the like. Formulations may further include one or more excipients, diluents, fillers, emulsifiers, preservatives, solubilizers, buffering agents, wetting agents, stabilizers, colorings, penetration enhancers, albumin to prevent protein loss on vial surfaces, etc. Topical formulations are typically provided as liquids, ointments, salves, gels, emulsions and the like. Methods of formulation are well known in the art and are disclosed, for example, in

Remington: The Science and Practice of Pharmacy, Gennaro, ed., Mack Publishing Co., Easton, PA, 19th ed., 1995. Therapeutic doses will be determined by the clinician according to accepted standards, taking into account the nature and severity of the condition to be treated, patient traits, etc. Proteins of the present invention will generally be formulated to provide a dose of from 0.01 μg to 100 mg per kg patient weight per day, more commonly from 0.1 μg to 10 mg/kg/day, still more commonly from 0.1 μg to 1.0 mg/kg/day. Determination of dose is within the level of ordinary skill in the art. The proteins may be administered for acute treatment, over one week or less, often over a period of one to three days or may be used in chronic treatment, over several months or years. In general, a therapeutically effective amount is an amount sufficient to produce a clinically significant change in the targetted condition.

Within the laboratory research field, the proteins of the present invention can be used as molecular weight standards, or as standards in the analysis of cell phenotype, and as reagents for the study of cells, receptors, and other binding molecules. Such reagents will generally further comprise a second moiety, such as a label, binding partner, or toxin, that facilitates the detection of the protein when bound to its target. Many such systems are known in the art and are summarized above. Receptors and other cell-surface binding sites for proteins of the present invention can be identified by exposing a population of cells to a labelled protein under physiologic conditions, whereby the protein binds to the surface of the cell. Cells bearing receptors for a protein of interest can also be identified using the protein joined to a toxin, whereby receptor-bearing cells are killed by the toxin.

AFP proteins and antagonists thereof can be used as standards in assays of protein and protein inhibitors in both clinical and research settings. Such assays can comprise any of a number of standard formats, include radioreceptor assays and ELISAs. Protein standards can be prepared in labeled form using a radioisotope, enzyme, fluorophore, or other compound that produces a detectable signal. The proteins can be packaged in kit form, such kits comprising one or more vials containing the AFP protein and, optionally, a diluent, an antibody, a labeled binding protein, etc. Assay kits can be used in the research laboratory to detect protein and inhibitor activities produced by cultured cells or test animals.

Proteins of the present invention may also be used as protein and amino acid supplements, including hydrolysates. Specific uses in this regard include use as animal feed supplements and as cell culture components. Proteins rich in a particular amino acid can be used as a source of that amino acid.

Polynucleotides and polypeptides of the present invention will additionally find use as educational tools as a laboratory practicum kits for courses

related to genetics and molecular biology, protein chemistry and antibody production and analysis. Due to their unique polynucleotide and polypeptide sequences, molecules of AFP protein or polynucleotide can be used as standards or as "unknowns" for testing purposes. For example, AFP polynucleotides can be used as aids in teaching students how to prepare expression constructs for bacterial, viral, and/or mammalian expression, including fusion constructs, wherein an AFP polynucleotide is the gene to be expressed; for determining the restriction endonuclease cleavage sites of the polynucleotides (which can be determined from the sequence using conventional computer software, such as MapDraw™ (DNASTAR, Madison, WI)); determining mRNA and DNA localization of AFP polynucleotides in tissues (e.g., by Northern and Southern blotting as well as polymerase chain reaction); and for identifying related polynucleotides and polypeptides by nucleic acid hybridization.

AFP polypeptides can be used educationally as aids to teach preparation of antibodies; identifying proteins by Western blotting; protein purification; determining the weight of expressed AFP polypeptides as a ratio to total protein expressed; identifying peptide cleavage sites; coupling amino and carboxyl terminal tags; amino acid sequence analysis, as well as, but not limited to monitoring biological activities of both the native and tagged protein (i.e., receptor binding, signal transduction, proliferation, and differentiation) *in vitro* and *in vivo*. AFP polypeptides can also be used to teach analytical skills such as mass spectrometry, circular dichroism to determine conformation, in particular the locations of the disulfide bonds, x-ray crystallography to determine the three-dimensional structure in atomic detail, nuclear magnetic resonance spectroscopy to reveal the structure of proteins in solution. For example, a kit containing an AFP protein can be given to the student to analyze. Since the amino acid sequence would be known by the professor, the protein can be given to the student as a test to determine the skills or develop the skills of the student, the teacher would then know whether or not the student has correctly analyzed the polypeptide. Since every polypeptide is unique, the educational utility of zcub5 would be unique unto itself.

Antibodies that bind specifically to an AFP polypeptide can be used as a teaching aid to instruct students how to prepare affinity chromatography columns to purify the cognate polypeptide, cloning and sequencing the polynucleotide that encodes an antibody and thus as a practicum for teaching a student how to design humanized antibodies. The AFP polynucleotide, polypeptide or antibody would then be packaged by reagent companies and sold to universities so that the students gain skill in art of molecular biology. Because each polynucleotide and protein is unique, each polynucleotide and protein creates unique challenges and learning experiences for

students in a lab practicum. Such educational kits containing an AFP polynucleotide, polypeptide or antibody are considered within the scope of the present invention.

The invention is further illustrated by the following non-limiting examples.

EXAMPLES

Example 1

A protein of the present invention ("AFP") is produced in *E. coli* using a His_6 tag/maltose binding protein (MBP) double affinity fusion system as generally disclosed by Pryor and Leiting, *Prot. Expr. Pur.* 10:309-319, 1997. A thrombin cleavage site is placed at the junction between the affinity tag and AFP sequences.

The fusion construct is assembled in the vector pTAP98, which comprises sequences for replication and selection in *E. coli* and yeast, the *E. coli* tac promoter, and a unique SmaI site just downstream of the MBP-His_6-thrombin site coding sequences. The AFP cDNA is amplified by PCR using primers each comprising 40 bp of sequence homologous to vector sequence and 25 bp of sequence that anneals to the cDNA. The reaction is run using Taq DNA polymerase (Boehringer Mannheim, Indianapolis, IN) for 30 cycles of 94°C, 30 seconds; 60°C, 60 seconds; and 72°C, 60 seconds. One microgram of the resulting fragment is mixed with 100 ng of SmaI-cut pTAP98, and the mixture is transformed into yeast to assemble the vector by homologous recombination (Oldenburg et al., *Nucl. Acids. Res.* 25:451-452, 1997). Ura^+ transformants are selected.

Plasmid DNA is prepared from yeast transformants and transformed into *E. coli* MC1061. Pooled plasmid DNA is then prepared from the MC1061 transformants by the miniprep method after scraping an entire plate. Plasmid DNA is analyzed by restriction digestion.

E. coli strain BL21 is used for expression of AFP. Cells are transformed by electroporation and grown on minimal glucose plates containing casamino acids and ampicillin.

Protein expression is analyzed by gel electrophoresis. Cells are grown in liquid glucose media containing casamino acids and ampicillin. After one hour at 37°C, IPTG is added to a final concentration of 1mM, and the cells are grown for an additional 2-3 hours at 37°C. Cells are disrupted using glass beads, and extracts are prepared.

Example 2

Larger scale cultures of AFP transformants are prepared by the method of Pryor and Leiting (*ibid.*). 100-ml cultures in minimal glucose media containing casamino acids and 100 μg/ml ampicillin are grown at 37°C in 500-ml baffled flasks to $OD_{600} \approx 0.5$. Cells are harvested by centrifugation and resuspended in 100 ml of the same media at room temperature. After 15 minutes, IPTG is added to 0.5 mM, and cultures are incubated at room temperature (ca. 22.5°C) for 16 to 20 hours with shaking at 125 rpm. The culture is harvested by centrifugation, and cell pellets are stored at -70°C.

Example 3

For larger-scale protein preparation, 500-ml cultures of *E. coli* BL21 expressing the AFP-MBP-His_6 fusion protein are prepared essentially as disclosed in Example 2. Cell pellets are resuspended in 100 ml of binding buffer (20 mM Tris, pH 7.58, 100 mM NaCl, 20 mM NaH_2PO_4, 0.4 mM 4-(2-Aminoethyl)-benzenesulfonyl fluoride hydrochloride [Pefabloc® SC; Boehringer-Mannheim], 2 μg/ml Leupeptin, 2 μg/ml Aprotinin). The cells are lysed in a French press at 30,000 psi, and the lysate is centrifuged at 18,000 x g for 45 minutes at 4°C to clarify it. Protein concentration is estimated by gel electrophoresis with a BSA standard.

Recombinant AFP fusion protein is purified from the lysate by affinity chromatography. Immobilized cobalt resin (Talon® resin; Clontech Laboratories, Inc., Palo Alto, CA) is equilibrated in binding buffer. One ml of packed resin per 50 mg protein is combined with the clarified supernatant in a tube, and the tube is capped and sealed, then placed on a rocker overnight at 4°C. The resin is then pelleted by centrifugation at 4°C and washed three times with binding buffer. Protein is eluted with binding buffer containing 0.2 M imidazole. The resin and elution buffer are mixed for at least one hour at 4°C, the resin is pelleted, and the supernatant is removed. An aliquot is analyzed by gel electrophoresis, and concentration is estimated. Amylose resin is equilibrated in amylose binding buffer (20 mM Tris-HCl, pH 7.0, 100 mM NaCl, 10 mM EDTA) and combined with the supernatant from the Talon resin at a ratio of 2 mg fusion protein per ml of resin. Binding and washing steps are carried out as disclosed above. Protein is eluted with amylose binding buffer containing 10 mM maltose using as small a volume as possible to minimize the need for subsequent concentration. The eluted protein is analyzed by gel electrophoresis and staining with Coomassie blue using a BSA standard, and by Western blotting using an anti-MBP antibody.

Example 4

An expression plasmid containing all or part of a polynucleotide encoding AFP is constructed via homologous recombination. An AFP coding sequence comprising the ORF with 5' and 3' ends corresponding to the vector sequences flanking the insertion point is prepared by PCR. The primers for PCR each include from 5' to 3' end: 40 bp of flanking sequence from the vector and 17 bp corresponding to the amino or carboxyl termini from the open reading frame of AFP.

Ten µl of the 100 µl PCR reaction mixture is run on a 0.8% low-melting-temperature agarose (SeaPlaque GTG®; FMC BioProducts, Rockland, ME) gel with 1 x TBE buffer for analysis. The remaining 90 µl of the reaction mixture is precipitated with the addition of 5 µl 1 M NaCl and 250 µl of absolute ethanol. The plasmid pZMP6, which has been cut with SmaI, is used for recombination with the PCR fragment. Plamid pZMP6 is a mammalian expression vector containing an expression cassette having the cytomegalovirus immediate early promoter, multiple restriction sites for insertion of coding sequences, a stop codon, and a human growth hormone terminator; an *E. coli* origin of replication; a mammalian selectable marker expression unit comprising an SV40 promoter, enhancer and origin of replication, a DHFR gene, and the SV40 terminator; and URA3 and CEN-ARS sequences required for selection and replication in *S. cerevisiae*. It was constructed from pZP9 (deposited at the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209, under Accession No. 98668) with the yeast genetic elements taken from pRS316 (available from the American Type Culture Collection, 10801 University Boulevard, Manassas, VA, under Accession No. 77145), an internal ribosome entry site (IRES) element from poliovirus, and the extracellular domain of CD8 truncated at the C-terminal end of the transmembrane domain.

One hundred microliters of competent yeast (*S. cerevisiae*) cells are independently combined with 10 µl of the various DNA mixtures from above and transferred to a 0.2-cm electroporation cuvette. The yeast/DNA mixtures are electropulsed using power supply (BioRad Laboratories, Hercules, CA) settings of 0.75 kV (5 kV/cm), ∞ ohms, 25 µF. To each cuvette is added 600 µl of 1.2 M sorbitol, and the yeast is plated in two 300-µl aliquots onto two URA-D plates (1.8% agar in 2% D-glucose, 0.67% yeast nitrogen base without amino acids, 0.056% -Ura -Trp -Thr powder [made by combining 4.0 g L-adenine, 3.0 g L-arginine, 5.0 g L-aspartic acid, 2.0 g L-histidine, 6.0 g L-isoleucine, 8.0 g L-leucine, 4.0 g L-lysine, 2.0 g L-methionine, 6.0 g L-phenylalanine, 5.0 g L-serine, 5.0 g L-tyrosine, and 6.0 g L-valine], and 0.5% 200X tryptophan, threonine solution [3.0% L-threonine, 0.8% L-tryptophan in H_2O]) and incubated at 30°C. After about 48 hours, the Ura^+ yeast

transformants from a single plate are resuspended in 1 ml H_2O and spun briefly to pellet the yeast cells. The cell pellet is resuspended in 1 ml of lysis buffer (2% Triton X-100, 1% SDS, 100 mM NaCl, 10 mM Tris, pH 8.0, 1 mM EDTA). Five hundred microliters of the lysis mixture is added to an Eppendorf tube containing 300 µl acid-washed glass beads and 200 µl phenol-chloroform, vortexed for 1 minute intervals two or three times, and spun for 5 minutes in an Eppendorf centrifuge at maximum speed. Three hundred microliters of the aqueous phase is transferred to a fresh tube, and the DNA is precipitated with 600 µl ethanol (EtOH), followed by centrifugation for 10 minutes at 4°C. The DNA pellet is resuspended in 10 µl H_2O.

Transformation of electrocompetent *E. coli* host cells (Electromax DH10B™ cells; obtained from Life Technologies, Inc., Gaithersburg, MD) is done with 0.5-2 ml yeast DNA prep and 40 µl of cells. The cells are electropulsed at 1.7 kV, 25 µF, and 400 ohms. Following electroporation, 1 ml SOC (2% Bacto™ Tryptone (Difco, Detroit, MI), 0.5% yeast extract (Difco), 10 mM NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 10 mM $MgSO_4$, 20 mM glucose) is plated in 250-µl aliquots on four LB AMP plates (LB broth (Lennox), 1.8% Bacto™ Agar (Difco), 100 mg/L Ampicillin).

Individual clones harboring the correct expression construct for AFP are identified by restriction digest to verify the presence of the AFP insert and to confirm that the various DNA sequences have been joined correctly to one another. The inserts of positive clones are subjected to sequence analysis. Larger scale plasmid DNA is isolated using a commercially available kit (QIAGEN Plasmid Maxi Kit, Qiagen, Valencia, CA) according to manufacturer's instructions. The correct construct is designated pZMP6/AFP.

Recombinant protein is produced in BHK cells transfected with pZMP6/AFP. BHK 570 cells (ATCC CRL-10314) are plated in 10-cm tissue culture dishes and allowed to grow to approximately 50 to 70% confluence overnight at 37°C, 5% CO_2, in DMEM/FBS media (DMEM, Gibco/BRL High Glucose; Life Technologies), 5% fetal bovine serum (Hyclone, Logan, UT), 1 mM L-glutamine (JRH Biosciences, Lenexa, KS), 1 mM sodium pyruvate (Life Technologies). The cells are then transfected with pZMP6/AFP by liposome-mediated transfection using a 3:1 (w/w) liposome formulation of the polycationic lipid 2,3-dioleyloxy-N-[2(sperminecarboxamido)ethyl]-N,N-dimethyl-1-propaniminium-trifluoroacetate and the neutral lipid dioleoyl phosphatidylethanolamine in membrane-filtered water (Lipofectamine™ Reagent; Life Technologies, Garithersburg, MD), in serum free (SF) media (DMEM supplemented with 10 mg/ml transferrin, 5 mg/ml insulin, 2 mg/ml fetuin, 1% L-glutamine and 1% sodium pyruvate). The plasmid is diluted into 15-ml tubes to a total final volume of 640 µl with SF media. 35 µl of the lipid mixture is

mixed with 605 μl of SF medium, and the resulting mixture is allowed to incubate approximately 30 minutes at room temperature. Five milliliters of SF media is then added to the DNA:lipid mixture. The cells are rinsed once with 5 ml of SF media, aspirated, and the DNA:lipid mixture is added. The cells are incubated at 37°C for five hours, then 6.4 ml of DMEM/10% FBS, 1% PSN media is added to each plate. The plates are incubated at 37°C overnight, and the DNA:lipid mixture is replaced with fresh 5% FBS/DMEM media the next day. On day 5 post-transfection, the cells are split into T-162 flasks in selection medium (DMEM + 5% FBS, 1% L-Gln, 1% NaPyr, 1 μM methotrexate). Approximately 10 days post-transfection, two 150-mm culture dishes of methotrexate-resistant colonies from each transfection are trypsinized, and the cells are pooled and plated into a T-162 flask and transferred to large-scale culture.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

We claim:

1. An isolated polypeptide comprising fifteen contiguous amino acid residues of a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422.

2. The isolated polypeptide of claim 1 wherein M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.

3. The isolated polypeptide of claim 1 or claim 2 which is from 15 to 2235 amino acid residues in length.

4. The isolated polypeptide of claim 3 which is operably linked via a peptide bond or polypeptide linker to a second polypeptide selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag, and a peptide as shown in SEQ ID NO:423.

5. The isolated polypeptide of any of claims 1-4 comprising at least 30 contiguous residues of SEQ ID NO:M.

6. The isolated polypeptide of any of claims 1-5 comprising at least 47 contiguous residues of SEQ ID NO:M.

7. An isolated, mature protein encoded by a sequence selected from the group consisting of SEQ ID NO:N, wherein N is an odd integer from 1 to 421.

8. The protein of claim 7 wherein N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.

9. An isolated polynucleotide comprising a sequence of nucleotides as shown in SEQ ID NO:N, wherein N is an odd integer from 1 to 421.

10. The isolated polynucleotide of claim 9 wherein N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.

11. An expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment encoding a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422; and

a transcription terminator.

12. The expression vector of claim 11 wherein M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.

13. A cultured cell comprising the expression vector of claim 11 or claim 12.

14. A method of producing a polypeptide comprising culturing the cell of claim 13 under conditions whereby said sequence of nucleotides is expressed, and recovering said polypeptide.

15. A polypeptide produced by the method of claim 14.

16. An isolated polynucleotide encoding a fusion protein, said protein comprising a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide.

17. An expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment encoding a fusion protein, said protein comprising a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide; and

a transcription terminator.

18. A cultured cell comprising the expression vector of claim 17, wherein the cell expresses the DNA segment and produces the encoded fusion protein.

19. A method of producing a protein comprising culturing the cell of claim 18 under conditions whereby said DNA segment is expressed, and recovering said second polypeptide.

20. An antibody that specifically binds to a protein selected from of the group consisting of SEQ ID NO:M, wherein M is an even integer from 2 to 422.

SEQUENCE LISTING

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<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1233)

<221> misc_feature
<222> (1)...(1233)
<223> n = A,T,C or G

<400> 3
atg gag cat ttc atg gaa gta atc aga aac cag gaa ttt gta tta tta 48
Met Glu His Phe Met Glu Val Ile Arg Asn Gln Glu Phe Val Leu Leu
1 5 10 15

cca gcc agc gaa att gca aag ctc ttg gct agt gat gac atg aac att 96
Pro Ala Ser Glu Ile Ala Lys Leu Leu Ala Ser Asp Asp Met Asn Ile
20 25 30

cct aat gag gag aca ata ttg aat gca ctt ctt act tgg gtc cgt cat 144
Pro Asn Glu Glu Thr Ile Leu Asn Ala Leu Leu Thr Trp Val Arg His
35 40 45

gat ttg gaa cag aga cgg aaa gat cta agt aaa ctt ttg gct tat att 192
Asp Leu Glu Gln Arg Arg Lys Asp Leu Ser Lys Leu Leu Ala Tyr Ile
50 55 60

agg cta cct ctt ctt gca cca cag ttc ctg gca gac atg gaa aat aat 240
Arg Leu Pro Leu Leu Ala Pro Gln Phe Leu Ala Asp Met Glu Asn Asn
65 70 75 80

gta ctt ttt cgg gat gat ata gaa tgt cag aaa ctc att atg gaa gca 288
Val Leu Phe Arg Asp Asp Ile Glu Cys Gln Lys Leu Ile Met Glu Ala
85 90 95

atg aag tac cat tta tta cca gag aga cga ccc atg tta caa agt cct 336
Met Lys Tyr His Leu Leu Pro Glu Arg Arg Pro Met Leu Gln Ser Pro
100 105 110

cgg aca aaa cct agg aag tca act gtt ggt aca tta ttt gca gtt ggg 384
Arg Thr Lys Pro Arg Lys Ser Thr Val Gly Thr Leu Phe Ala Val Gly
115 120 125

gga atg gat tca aca aaa gga gca aca agc att gaa aag tat gat ctc 432
Gly Met Asp Ser Thr Lys Gly Ala Thr Ser Ile Glu Lys Tyr Asp Leu
130 135 140

cgt aca aat atg tgg act cca gta gca aat atg aat ggg agg ngg cta 480
Arg Thr Asn Met Trp Thr Pro Val Ala Asn Met Asn Gly Arg Xaa Leu
145 150 155 160

cag ttc ggt gtt gca gtg cta gat gac aaa ctg tat gtg gtt gga gga 528
Gln Phe Gly Val Ala Val Leu Asp Asp Lys Leu Tyr Val Val Gly Gly
165 170 175

aga gat gga ctg aag act ttg aat act gta gag tgc tac aac ccc aaa 576
Arg Asp Gly Leu Lys Thr Leu Asn Thr Val Glu Cys Tyr Asn Pro Lys
180 185 190

aca aaa act tgg agt gtg atg cca cct atg tcc aca cat aga cat ggc 624
Thr Lys Thr Trp Ser Val Met Pro Pro Met Ser Thr His Arg His Gly
195 200 205

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ctt ggt gtg gct gta ctg gaa ggt ccc atg tat gcc gta gga gga cat      672
Leu Gly Val Ala Val Leu Glu Gly Pro Met Tyr Ala Val Gly Gly His
    210                 215                 220

gat ggc tgg agc tat ctg aac aca gtg gaa aga tgg gac cct cag gct      720
Asp Gly Trp Ser Tyr Leu Asn Thr Val Glu Arg Trp Asp Pro Gln Ala
225                 230                 235                 240

cgc cag tgg aat ttt gtt gcc act atg tct acc cct agg agt aca gta      768
Arg Gln Trp Asn Phe Val Ala Thr Met Ser Thr Pro Arg Ser Thr Val
                245                 250                 255

ggt gtg gca gta cta agt gga aaa ctt tat gca gtt ggt ggt cgt gat      816
Gly Val Ala Val Leu Ser Gly Lys Leu Tyr Ala Val Gly Gly Arg Asp
            260                 265                 270

gga agt tct tgt ctc aaa tca gta gaa tgt ttt gat cct cat act aat      864
Gly Ser Ser Cys Leu Lys Ser Val Glu Cys Phe Asp Pro His Thr Asn
        275                 280                 285

aag tgg aca ctg tgt gca cag atg tca aaa agg aga ggt ggc gta gga      912
Lys Trp Thr Leu Cys Ala Gln Met Ser Lys Arg Arg Gly Gly Val Gly
    290                 295                 300

gtg acg acc tgg aat gga ctg ctg tat gct ata ggg ggg cac gat gct      960
Val Thr Thr Trp Asn Gly Leu Leu Tyr Ala Ile Gly Gly His Asp Ala
305                 310                 315                 320

ccc gca tcc aac ttg act tcc aga ctc tca gac tgt gtg gaa aga tat     1008
Pro Ala Ser Asn Leu Thr Ser Arg Leu Ser Asp Cys Val Glu Arg Tyr
                325                 330                 335

gat ccc aaa aca gac atg tgg act gca gta gca tcc atg agc atc agc     1056
Asp Pro Lys Thr Asp Met Trp Thr Ala Val Ala Ser Met Ser Ile Ser
            340                 345                 350

aga gat gca gtg ggg gtc tgt tta ctt ggt gat aag tta tat gct gtt     1104
Arg Asp Ala Val Gly Val Cys Leu Leu Gly Asp Lys Leu Tyr Ala Val
        355                 360                 365

ggg ggg tat gat gga cag gca tac ctt aat acc gtg gag gct tat gat     1152
Gly Gly Tyr Asp Gly Gln Ala Tyr Leu Asn Thr Val Glu Ala Tyr Asp
    370                 375                 380
```

ccc cag aca aat gag tgg acc cag gtt gct cca ctg tgc cta gga aga 1200
Pro Gln Thr Asn Glu Trp Thr Gln Val Ala Pro Leu Cys Leu Gly Arg
385 390 395 400

gct gga gct tgt gtt gtg act gta aaa tta taa 1233
Ala Gly Ala Cys Val Val Thr Val Lys Leu *
405 410

<210> 4
<211> 410
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(410)
<223> Xaa = Any Amino Acid

<400> 4
Met Glu His Phe Met Glu Val Ile Arg Asn Gln Glu Phe Val Leu Leu
1 5 10 15
Pro Ala Ser Glu Ile Ala Lys Leu Leu Ala Ser Asp Asp Met Asn Ile
20 25 30
Pro Asn Glu Glu Thr Ile Leu Asn Ala Leu Leu Thr Trp Val Arg His
35 40 45
Asp Leu Glu Gln Arg Arg Lys Asp Leu Ser Lys Leu Leu Ala Tyr Ile
50 55 60
Arg Leu Pro Leu Leu Ala Pro Gln Phe Leu Ala Asp Met Glu Asn Asn
65 70 75 80
Val Leu Phe Arg Asp Asp Ile Glu Cys Gln Lys Leu Ile Met Glu Ala
85 90 95
Met Lys Tyr His Leu Leu Pro Glu Arg Arg Pro Met Leu Gln Ser Pro
100 105 110
Arg Thr Lys Pro Arg Lys Ser Thr Val Gly Thr Leu Phe Ala Val Gly
115 120 125
Gly Met Asp Ser Thr Lys Gly Ala Thr Ser Ile Glu Lys Tyr Asp Leu
130 135 140
Arg Thr Asn Met Trp Thr Pro Val Ala Asn Met Asn Gly Arg Xaa Leu
145 150 155 160
Gln Phe Gly Val Ala Val Leu Asp Asp Lys Leu Tyr Val Val Gly Gly
165 170 175
Arg Asp Gly Leu Lys Thr Leu Asn Thr Val Glu Cys Tyr Asn Pro Lys

180 185 190
Thr Lys Thr Trp Ser Val Met Pro Pro Met Ser Thr His Arg His Gly
195 200 205
Leu Gly Val Ala Val Leu Glu Gly Pro Met Tyr Ala Val Gly Gly His
210 215 220
Asp Gly Trp Ser Tyr Leu Asn Thr Val Glu Arg Trp Asp Pro Gln Ala
225 230 235 240
Arg Gln Trp Asn Phe Val Ala Thr Met Ser Thr Pro Arg Ser Thr Val
245 250 255
Gly Val Ala Val Leu Ser Gly Lys Leu Tyr Ala Val Gly Gly Arg Asp
260 265 270
Gly Ser Ser Cys Leu Lys Ser Val Glu Cys Phe Asp Pro His Thr Asn
275 280 285
Lys Trp Thr Leu Cys Ala Gln Met Ser Lys Arg Arg Gly Gly Val Gly
290 295 300
Val Thr Thr Trp Asn Gly Leu Leu Tyr Ala Ile Gly Gly His Asp Ala
305 310 315 320
Pro Ala Ser Asn Leu Thr Ser Arg Leu Ser Asp Cys Val Glu Arg Tyr
325 330 335
Asp Pro Lys Thr Asp Met Trp Thr Ala Val Ala Ser Met Ser Ile Ser
340 345 350
Arg Asp Ala Val Gly Val Cys Leu Leu Gly Asp Lys Leu Tyr Ala Val
355 360 365
Gly Gly Tyr Asp Gly Gln Ala Tyr Leu Asn Thr Val Glu Ala Tyr Asp
370 375 380
Pro Gln Thr Asn Glu Trp Thr Gln Val Ala Pro Leu Cys Leu Gly Arg
385 390 395 400
Ala Gly Ala Cys Val Val Thr Val Lys Leu
405 410

<210> 5
<211> 1644
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1644)

<400> 5
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Met Leu Arg Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile
1 5 10 15

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gtc ctg aag gtg gcc atc ctg gcc gag aag tac gcc gtg gac tac agc      96
Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser
            20                  25                  30

tgg tac gtg gac acc atc ctc aac ctc atc cgc att gcg ggc gac tac     144
Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr
        35                  40                  45

gtg agt gag gag gtg tgg tac cgt gtg cta cag atc gtc acc aac cgt     192
Val Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg
    50                  55                  60

gat gac gtc cag ggc tat gcc gcc aag acc gtc ttt gag gcg ctc cag     240
Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln
65                  70                  75                  80

gcc cct gcc tgt cac gag aac atg gtg aag gtt ggc ggc tac atc ctt     288
Ala Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu
                85                  90                  95

ggg gag ttt ggg aac ctg att gct ggg gac ccc cgc tcc agc ccc cca     336
Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro
            100                 105                 110

gtg cag ttc tcc ctg ctc cac tcc aag ttc cat ctg tgc agc gtg gcc     384
Val Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala
        115                 120                 125

acg cgg gcg ctg ctg ctg tcc acc tac atc aag ttc atc aac ctc ttc     432
Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Phe
    130                 135                 140

ccc gag acc aag gcc acc atc cag ggc gtc ctg cgg gcc ggc tcc cag     480
Pro Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln
145                 150                 155                 160

ctg cgc aat gct gac gtg gag ctg cag cag cga gcc gtg gag tac ctc     528
Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu
                165                 170                 175

acc ctc agc tca gtg gcc agc acc gac gtc ctg gcc acg gtg ctg gag     576
Thr Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu
            180                 185                 190
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gag atg ccg ccc ttc ccc gag cgc gag tcg tcc atc ctg gcc aag ctg 624
Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu
195 200 205

aaa cgc aag aag ggg cca ggg gcc ggc agc gcc ctg gac gat ggc cgg 672
Lys Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg
210 215 220

agg gac ccc agc agc aac gac atc aac ggg ggc atg gag ccc acc ccc 720
Arg Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro
225 230 235 240

agc act gtg tcg acg ccc tcg ccc tcc gcc gac ctc ctg ggg ctg cgg 768
Ser Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg
245 250 255

gca gcc cct ccc ccg gca gca ccc ccg gct tct gca gga gca ggg aac 816
Ala Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn
260 265 270

ctt ctg gtg gac gtc ttc gat ggc ccg gcc gcc cag ccc agc ctg ggg 864
Leu Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly
275 280 285

ccc acc ccc gag gag gcc ttc ctc agc cca ggt cct gag gac atc ggc 912
Pro Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly
290 295 300

cct ccc att ccg gaa gcc gat gag ttg ctg aat aag ttt gtg tgt aag 960
Pro Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys
305 310 315 320

aac aac ggg gtc ctg ttc gag aac cag ctg ctg cag atc gga gtc aag 1008
Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys
325 330 335

tca gag ttc cga cag aac ctg ggc cgc atg tat ctc ttc tat ggc aac 1056
Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn
340 345 350

aag acc tcg gtg cag ttc cag aat ttc tca ccc act gtg gtt cac ccg 1104
Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro
355 360 365

gga gac ctc cag act cag ctg gct gtg cag acc aag cgc gtg gcg gcg 1152
Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala
370 375 380

cag gtg gac ggc ggc gcg cag gtg cag cag gtg ctc aat atc gag tgc 1200
Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys
385 390 395 400

ctg cgg gac ttc ctg acg ccc ccg ctg ctg tcc gtg cgc ttc cgg tac 1248
Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr
405 410 415

ggt ggc gcc ccc cag gcc ctc acc ctg aag ctc cca gtg acc atc aac 1296
Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn
420 425 430

aag ttc ttc cag ccc acc gag atg gcg gcc cag gat ttc ttc cag cgc 1344
Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg
435 440 445

tgg aag cag ctg agc ctc cct caa cag gag gcg cag aaa atc ttc aaa 1392
Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys
450 455 460

gcc aac cac ccc atg gac gca gaa gtt act aag gcc aag ctt ctg ggg 1440
Ala Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly
465 470 475 480

ttt ggc tct gct ctc ctg gac aat gtg gac ccc aac cct gag aac ttc 1488
Phe Gly Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe
485 490 495

gtg ggg gcg ggg atc atc cag act aaa gcc ctg cag gtg ggc tgt ctg 1536
Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu
500 505 510

ctt cgg ctg gag ccc aat gcc cag gcc cag atg tac cgg ctg acc ctg 1584
Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu
515 520 525

cgc acc agc aag gag ccc gtc tcc cgt cac ctg tgt gag ctg ctg gca 1632
Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala
530 535 540

```
cag cag ttc tga                                                1644
Gln Gln Phe  *
545


      <210> 6
      <211> 547
      <212> PRT
      <213> Homo sapiens

      <400> 6
Met Leu Arg Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile
 1               5                  10                  15
Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser
            20                  25                  30
Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr
        35                  40                  45
Val Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg
    50                  55                  60
Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln
65                  70                  75                  80
Ala Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu
                85                  90                  95
Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro
            100                 105                 110
Val Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala
        115                 120                 125
Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Phe
    130                 135                 140
Pro Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln
145                 150                 155                 160
Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu
                165                 170                 175
Thr Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu
            180                 185                 190
Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu
        195                 200                 205
Lys Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg
    210                 215                 220
Arg Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro
225                 230                 235                 240
Ser Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg
                245                 250                 255
Ala Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn
```

260 265 270
Leu Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly
275 280 285
Pro Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly
290 295 300
Pro Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys
305 310 315 320
Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys
325 330 335
Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn
340 345 350
Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro
355 360 365
Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala
370 375 380
Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys
385 390 395 400
Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr
405 410 415
Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn
420 425 430
Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg
435 440 445
Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys
450 455 460
Ala Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly
465 470 475 480
Phe Gly Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe
485 490 495
Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu
500 505 510
Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu
515 520 525
Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala
530 535 540
Gln Gln Phe
545

<210> 7
<211> 711
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)...(711)

<400> 7
atg gca gcc ttt gca gtg gaa cct cag ggg ccc gcg tta gga tct gaa 48
Met Ala Ala Phe Ala Val Glu Pro Gln Gly Pro Ala Leu Gly Ser Glu
1 5 10 15

cca atg atg ctg ggt tca ccc aca tct cca aag cca gga gtt aat gcc 96
Pro Met Met Leu Gly Ser Pro Thr Ser Pro Lys Pro Gly Val Asn Ala
20 25 30

cag ttc tta cct gga ttt tta atg ggg gat ttg cca gct ccg gtg act 144
Gln Phe Leu Pro Gly Phe Leu Met Gly Asp Leu Pro Ala Pro Val Thr
35 40 45

cca caa cct cga tca att agt ggc cct tca gta gga gta atg gaa atg 192
Pro Gln Pro Arg Ser Ile Ser Gly Pro Ser Val Gly Val Met Glu Met
50 55 60

aga tca cct tta ctt gca ggt ggg tca cca cca caa cca gtt gta cca 240
Arg Ser Pro Leu Leu Ala Gly Gly Ser Pro Pro Gln Pro Val Val Pro
65 70 75 80

gct cat aaa gat aaa agt ggc gct cca cca gtt aga agt ata tat gat 288
Ala His Lys Asp Lys Ser Gly Ala Pro Pro Val Arg Ser Ile Tyr Asp
85 90 95

gac att tct agc cca gga ctt gga tca aca cct tta act tca aga aga 336
Asp Ile Ser Ser Pro Gly Leu Gly Ser Thr Pro Leu Thr Ser Arg Arg
100 105 110

cag atg tct aat aca gga aat tgg atg cat att cgt tat caa tct aaa 384
Gln Met Ser Asn Thr Gly Asn Trp Met His Ile Arg Tyr Gln Ser Lys
115 120 125

ctg cag gct cgg aaa gcc tta agc aaa gat ggg agg att ttt gga gaa 432
Leu Gln Ala Arg Lys Ala Leu Ser Lys Asp Gly Arg Ile Phe Gly Glu
130 135 140

tcc atc atg att ggt gta aaa cca tgt att gac aaa agt gtt atg gaa 480
Ser Ile Met Ile Gly Val Lys Pro Cys Ile Asp Lys Ser Val Met Glu
145 150 155 160

```
agc agt gac aga tgt gct tta tca tct cca tct tta gcc ttt aca cca     528
Ser Ser Asp Arg Cys Ala Leu Ser Ser Pro Ser Leu Ala Phe Thr Pro
                165                 170                 175

cca atc aaa act cta ggt aca cca aca caa cct gga agt act cct agg     576
Pro Ile Lys Thr Leu Gly Thr Pro Thr Gln Pro Gly Ser Thr Pro Arg
            180                 185                 190

att tct acc atg aga cct ctt gct aca gca tac aaa gcc tct act agt     624
Ile Ser Thr Met Arg Pro Leu Ala Thr Ala Tyr Lys Ala Ser Thr Ser
        195                 200                 205

gat tat cag gtt att tct gac aga caa acg cca aaa aaa gat gaa agt     672
Asp Tyr Gln Val Ile Ser Asp Arg Gln Thr Pro Lys Lys Asp Glu Ser
    210                 215                 220

ctt gta tcc aaa gca atg gag tac atg ttt ggc tgg tag                 711
Leu Val Ser Lys Ala Met Glu Tyr Met Phe Gly Trp  *
225                 230                 235


      &lt;210&gt; 8
      &lt;211&gt; 236
      &lt;212&gt; PRT
      &lt;213&gt; Homo sapiens

      &lt;400&gt; 8
Met Ala Ala Phe Ala Val Glu Pro Gln Gly Pro Ala Leu Gly Ser Glu
 1               5                  10                  15
Pro Met Met Leu Gly Ser Pro Thr Ser Pro Lys Pro Gly Val Asn Ala
            20                  25                  30
Gln Phe Leu Pro Gly Phe Leu Met Gly Asp Leu Pro Ala Pro Val Thr
        35                  40                  45
Pro Gln Pro Arg Ser Ile Ser Gly Pro Ser Val Gly Val Met Glu Met
    50                  55                  60
Arg Ser Pro Leu Leu Ala Gly Gly Ser Pro Pro Gln Pro Val Val Pro
65                  70                  75                  80
Ala His Lys Asp Lys Ser Gly Ala Pro Pro Val Arg Ser Ile Tyr Asp
                85                  90                  95
Asp Ile Ser Ser Pro Gly Leu Gly Ser Thr Pro Leu Thr Ser Arg Arg
            100                 105                 110
Gln Met Ser Asn Thr Gly Asn Trp Met His Ile Arg Tyr Gln Ser Lys
        115                 120                 125
Leu Gln Ala Arg Lys Ala Leu Ser Lys Asp Gly Arg Ile Phe Gly Glu
```

```
    130                 135                 140
Ser Ile Met Ile Gly Val Lys Pro Cys Ile Asp Lys Ser Val Met Glu
145                 150                 155                 160
Ser Ser Asp Arg Cys Ala Leu Ser Ser Pro Ser Leu Ala Phe Thr Pro
                165                 170                 175
Pro Ile Lys Thr Leu Gly Thr Pro Thr Gln Pro Gly Ser Thr Pro Arg
            180                 185                 190
Ile Ser Thr Met Arg Pro Leu Ala Thr Ala Tyr Lys Ala Ser Thr Ser
        195                 200                 205
Asp Tyr Gln Val Ile Ser Asp Arg Gln Thr Pro Lys Lys Asp Glu Ser
    210                 215                 220
Leu Val Ser Lys Ala Met Glu Tyr Met Phe Gly Trp
225                 230                 235
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<210> 9
<211> 636
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(636)

<400> 9

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atg cag cta tca ctg act caa gcg cgc acc tgg aag ggt ctg ttg ctg       48
Met Gln Leu Ser Leu Thr Gln Ala Arg Thr Trp Lys Gly Leu Leu Leu
 1               5                  10                  15

ttg gtg tca tgc atg atc ctg tgg ata tct gtg act ccc aca cca tat       96
Leu Val Ser Cys Met Ile Leu Trp Ile Ser Val Thr Pro Thr Pro Tyr
            20                  25                  30

gac cag atg tcc aat gag gag ctg tat gac aat ctg ctt tcc tgt tct      144
Asp Gln Met Ser Asn Glu Glu Leu Tyr Asp Asn Leu Leu Ser Cys Ser
        35                  40                  45

cat cgc acc cat gta gtt gcc cga aaa atg tat aaa att tta gac tta      192
His Arg Thr His Val Val Ala Arg Lys Met Tyr Lys Ile Leu Asp Leu
    50                  55                  60

aat gta gct gag aga aga tgt ttt aag aat aaa aga aac aac acc tgc      240
Asn Val Ala Glu Arg Arg Cys Phe Lys Asn Lys Arg Asn Asn Thr Cys
 65                  70                  75                  80
```

```
cac acc act tct acc cat act gca aaa aca aat gaa gat ctt ctg aaa      288
His Thr Thr Ser Thr His Thr Ala Lys Thr Asn Glu Asp Leu Leu Lys
                 85                  90                  95

gtc atc atc agt gtt tcg aat gca tgg ata tat cca ctg aaa atg ctc      336
Val Ile Ile Ser Val Ser Asn Ala Trp Ile Tyr Pro Leu Lys Met Leu
            100                 105                 110

ata cct gca gtg ttg act cat ttg ggc tcc tat gat ggt atg atg gca      384
Ile Pro Ala Val Leu Thr His Leu Gly Ser Tyr Asp Gly Met Met Ala
        115                 120                 125

aga gcc ata gag ctt aac tat gga aat caa aaa att ctg gag gga gca      432
Arg Ala Ile Glu Leu Asn Tyr Gly Asn Gln Lys Ile Leu Glu Gly Ala
    130                 135                 140

aaa ttt tta ctc agc agg att cag cct gga att gaa gaa aat gac tat      480
Lys Phe Leu Leu Ser Arg Ile Gln Pro Gly Ile Glu Glu Asn Asp Tyr
145                 150                 155                 160

cct gtc tgg tca agc tta aaa gaa ttg agg tct tcc aat aaa agc att      528
Pro Val Trp Ser Ser Leu Lys Glu Leu Arg Ser Ser Asn Lys Ser Ile
                165                 170                 175

cac ctt ttt gca ttt tgt aaa ttc ttc tac tgc ttg cgc aaa gat aca      576
His Leu Phe Ala Phe Cys Lys Phe Phe Tyr Cys Leu Arg Lys Asp Thr
            180                 185                 190

aag aag att aag gat tat ctc cag atc ttg agg cct aac att att aaa      624
Lys Lys Ile Lys Asp Tyr Leu Gln Ile Leu Arg Pro Asn Ile Ile Lys
        195                 200                 205

aac aag tgg taa                                                      636
Asn Lys Trp  *
    210
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<210> 10
<211> 211
<212> PRT
<213> Homo sapiens

<400> 10

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Met Gln Leu Ser Leu Thr Gln Ala Arg Thr Trp Lys Gly Leu Leu Leu
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1 5 10 15
Leu Val Ser Cys Met Ile Leu Trp Ile Ser Val Thr Pro Thr Pro Tyr
20 25 30
Asp Gln Met Ser Asn Glu Glu Leu Tyr Asp Asn Leu Leu Ser Cys Ser
35 40 45
His Arg Thr His Val Val Ala Arg Lys Met Tyr Lys Ile Leu Asp Leu
50 55 60
Asn Val Ala Glu Arg Arg Cys Phe Lys Asn Lys Arg Asn Asn Thr Cys
65 70 75 80
His Thr Thr Ser Thr His Thr Ala Lys Thr Asn Glu Asp Leu Leu Lys
85 90 95
Val Ile Ile Ser Val Ser Asn Ala Trp Ile Tyr Pro Leu Lys Met Leu
100 105 110
Ile Pro Ala Val Leu Thr His Leu Gly Ser Tyr Asp Gly Met Met Ala
115 120 125
Arg Ala Ile Glu Leu Asn Tyr Gly Asn Gln Lys Ile Leu Glu Gly Ala
130 135 140
Lys Phe Leu Leu Ser Arg Ile Gln Pro Gly Ile Glu Glu Asn Asp Tyr
145 150 155 160
Pro Val Trp Ser Ser Leu Lys Glu Leu Arg Ser Ser Asn Lys Ser Ile
165 170 175
His Leu Phe Ala Phe Cys Lys Phe Phe Tyr Cys Leu Arg Lys Asp Thr
180 185 190
Lys Lys Ile Lys Asp Tyr Leu Gln Ile Leu Arg Pro Asn Ile Ile Lys
195 200 205
Asn Lys Trp
210

<210> 11
<211> 651
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(651)

<400> 11
atg tcc gcc ggg ggc ttc gcg gcg ccg ggg cac gcg gcg ggg ggt ccg 48
Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro
1 5 10 15

cct ccg ccg ccc cca cct ctg gga ccc cat tcc aac cgg acc acc cca 96
Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro

20 25 30

cct gag tca gcc ccc cag aac ggt ccg tcc cct atg gcc gct ctc atg 144
Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met
35 40 45

tcg gtg gca gat act ctg ggc aca gcg cac tcg ccc aag gat ggc agt 192
Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser
50 55 60

tcc gtg cac tct acc act gcg tcg gcg cgg cga aac agc agc agc cca 240
Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro
65 70 75 80

gtc tcg ccg gcc tcc gtg ccg ggg cag cgc cgc ttg gca tca cgt aac 288
Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn
85 90 95

ggg gac ctg aat tta cag gtg gcg ccc ccg ccg cct agc gcc cac ccg 336
Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Pro Ser Ala His Pro
100 105 110

ggc atg gac caa gtg cac ccc caa aac att ccg gat tcc ccc atg gcc 384
Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala
115 120 125

aac agc gga ccc ctc tgc tgc acc att tgc cac gaa cgt ttg gag gat 432
Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp
130 135 140

acg cat ttc gtt cag tgc cct tcc gtc ccc agc cac aaa ttt tgc ttc 480
Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe
145 150 155 160

cct tgc tct aga gag agt atc aag gcc cag ggg gcc acc ggc gag gtg 528
Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val
165 170 175

tat tgc ccc agc gga gag aaa tgc ccc cta gtc ggg tcg aat gta cct 576
Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro
180 185 190

tgg gcc ttc atg cag ggc gaa atc gcg act atc tta gct ggg gat gtt 624
Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val

195 200 205

aaa gtg aaa aag gag aga gac cct tga 651
Lys Val Lys Lys Glu Arg Asp Pro *
210 215

<210> 12
<211> 216
<212> PRT
<213> Homo sapiens

<400> 12
Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro
1 5 10 15
Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro
20 25 30
Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met
35 40 45
Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser
50 55 60
Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro
65 70 75 80
Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn
85 90 95
Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Pro Ser Ala His Pro
100 105 110
Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala
115 120 125
Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp
130 135 140
Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe
145 150 155 160
Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val
165 170 175
Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro
180 185 190
Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val
195 200 205
Lys Val Lys Lys Glu Arg Asp Pro
210 215

<210> 13
<211> 468

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(468)

<400> 13
atg gcc tta att att cgt cca tcc aca gat ttc acg ttt ctg ttt cta 48
Met Ala Leu Ile Ile Arg Pro Ser Thr Asp Phe Thr Phe Leu Phe Leu
1 5 10 15

ccc tgt acg tca gtt gga tta ttt aat ttt ctg tgt agt aga ttc tac 96
Pro Cys Thr Ser Val Gly Leu Phe Asn Phe Leu Cys Ser Arg Phe Tyr
20 25 30

ctg acc aag ttc aat aaa gaa aat aat tgt gta tta cct cat tca aaa 144
Leu Thr Lys Phe Asn Lys Glu Asn Asn Cys Val Leu Pro His Ser Lys
35 40 45

gtt tca ttc cag ggc ttt ata tta caa gtt ggc agt gga gca gct gca 192
Val Ser Phe Gln Gly Phe Ile Leu Gln Val Gly Ser Gly Ala Ala Ala
50 55 60

gag cca tcc cga ggc aca gga agc tct ggg ccc tcc tct caa cat cca 240
Glu Pro Ser Arg Gly Thr Gly Ser Ser Gly Pro Ser Ser Gln His Pro
65 70 75 80

tta tct caa gct cat cga cag gga aac ttc gtg gac att gtt gat gcc 288
Leu Ser Gln Ala His Arg Gln Gly Asn Phe Val Asp Ile Val Asp Ala
85 90 95

aag ttg aag att cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac 336
Lys Leu Lys Ile Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr
100 105 110

gtc cac tca tcc aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag 384
Val His Ser Ser Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu
115 120 125

gtc ttt tta gag ctc aag gat ggt cag cag att cct gtg ttc aag ctc 432
Val Phe Leu Glu Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu
130 135 140

agt ggg gaa aac ggt gat gaa gtg aaa aag gag tag 468
Ser Gly Glu Asn Gly Asp Glu Val Lys Lys Glu *
145 150 155

<210> 14
<211> 155
<212> PRT
<213> Homo sapiens

<400> 14
Met Ala Leu Ile Ile Arg Pro Ser Thr Asp Phe Thr Phe Leu Phe Leu
1 5 10 15
Pro Cys Thr Ser Val Gly Leu Phe Asn Phe Leu Cys Ser Arg Phe Tyr
20 25 30
Leu Thr Lys Phe Asn Lys Glu Asn Asn Cys Val Leu Pro His Ser Lys
35 40 45
Val Ser Phe Gln Gly Phe Ile Leu Gln Val Gly Ser Gly Ala Ala Ala
50 55 60
Glu Pro Ser Arg Gly Thr Gly Ser Ser Gly Pro Ser Ser Gln His Pro
65 70 75 80
Leu Ser Gln Ala His Arg Gln Gly Asn Phe Val Asp Ile Val Asp Ala
85 90 95
Lys Leu Lys Ile Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr
100 105 110
Val His Ser Ser Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu
115 120 125
Val Phe Leu Glu Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu
130 135 140
Ser Gly Glu Asn Gly Asp Glu Val Lys Lys Glu
145 150 155

<210> 15
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(765)

<400> 15
atg gtg tcc tgg atc atc tct cgc ctg gtg gtg ctc atc ttt ggc acc 48
Met Val Ser Trp Ile Ile Ser Arg Leu Val Val Leu Ile Phe Gly Thr

```
 1               5                   10                  15

ctg tac cca gcc tat tct tcc tac aag gcc gtg aag aca aaa aac gtg      96
Leu Tyr Pro Ala Tyr Ser Ser Tyr Lys Ala Val Lys Thr Lys Asn Val
                20                  25                  30

aag gaa tat gtg aaa tgg atg atg tac tgg atc gtc ttt gcc ttc ttc     144
Lys Glu Tyr Val Lys Trp Met Met Tyr Trp Ile Val Phe Ala Phe Phe
            35                  40                  45

acc acg gcc gag acg ctc acg gat ata gtg ctc tcc tgg ttc ccc ttc     192
Thr Thr Ala Glu Thr Leu Thr Asp Ile Val Leu Ser Trp Phe Pro Phe
    50                  55                  60

tac ttt gaa ctg aag atc gcc ttc gtg ata tgg ctg ctg tcc cct tac     240
Tyr Phe Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr
65                  70                  75                  80

acc aag ggc tcc agc gtg ctc tac cgc aag ttc gtg cac cca acg ctg     288
Thr Lys Gly Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu
                85                  90                  95

tcc aac aag gag aag gag atc gac gag tac atc acg cag gcc cga gac     336
Ser Asn Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp
            100                 105                 110

aag agc tat gag acc atg atg agg gtg ggc aag agg ggc ctg aac ctt     384
Lys Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu
        115                 120                 125

gcc gcc aat gct gca gtc aca gct gcc gcc aag ggc cag ggg gtg ctg     432
Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val Leu
    130                 135                 140

tca gag aag ctc cgc agc ttc agc atg cag gac ctg acc ctg atc cgg     480
Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu Ile Arg
145                 150                 155                 160

gac gag gac gca ctg ccc ctg cag agg cct gac ggc cgc ctc cga ccc     528
Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg Leu Arg Pro
                165                 170                 175

agc cct ggc agc ctc ctg gac acc atc gag gac tta gga gat gac cct     576
Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu Gly Asp Asp Pro
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180 185 190

gcc ctg agt cta agg tcc agc aca aac ccg gca gat tcc cgg aca gag 624
Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala Asp Ser Arg Thr Glu
195 200 205

gct tct gag gat gac atg gga gac aaa gct ccc aag agg gcc aaa ccc 672
Ala Ser Glu Asp Asp Met Gly Asp Lys Ala Pro Lys Arg Ala Lys Pro
210 215 220

atc aaa aaa gcg ccc aaa gct gag cca ctg gct tcc aag aca ctg aag 720
Ile Lys Lys Ala Pro Lys Ala Glu Pro Leu Ala Ser Lys Thr Leu Lys
225 230 235 240

acc cgg ccc aag aag aag acc tct ggc ggg ggc gac tca gct tga 765
Thr Arg Pro Lys Lys Lys Thr Ser Gly Gly Gly Asp Ser Ala *
245 250

<210> 16
<211> 254
<212> PRT
<213> Homo sapiens

<400> 16
Met Val Ser Trp Ile Ile Ser Arg Leu Val Val Leu Ile Phe Gly Thr
1 5 10 15
Leu Tyr Pro Ala Tyr Ser Ser Tyr Lys Ala Val Lys Thr Lys Asn Val
20 25 30
Lys Glu Tyr Val Lys Trp Met Met Tyr Trp Ile Val Phe Ala Phe Phe
35 40 45
Thr Thr Ala Glu Thr Leu Thr Asp Ile Val Leu Ser Trp Phe Pro Phe
50 55 60
Tyr Phe Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr
65 70 75 80
Thr Lys Gly Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu
85 90 95
Ser Asn Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp
100 105 110
Lys Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu
115 120 125
Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val Leu
130 135 140
Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu Ile Arg

145 150 155 160
Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg Leu Arg Pro
165 170 175
Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu Gly Asp Asp Pro
180 185 190
Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala Asp Ser Arg Thr Glu
195 200 205
Ala Ser Glu Asp Asp Met Gly Asp Lys Ala Pro Lys Arg Ala Lys Pro
210 215 220
Ile Lys Lys Ala Pro Lys Ala Glu Pro Leu Ala Ser Lys Thr Leu Lys
225 230 235 240
Thr Arg Pro Lys Lys Lys Thr Ser Gly Gly Gly Asp Ser Ala
245 250

<210> 17
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(408)

<221> misc_feature
<222> (1)...(408)
<223> n = A,T,C or G

<400> 17
atg gcc cat agg ggc gtg tca gct gtg gtc gtg gga gct gac cgc gtg 48
Met Ala His Arg Gly Val Ser Ala Val Val Val Gly Ala Asp Arg Val
1 5 10 15

gtt gcc aac ggn gac aca gcc aac aag gtg ggc acc tac cag ctg gcc 96
Val Ala Asn Xaa Asp Thr Ala Asn Lys Val Gly Thr Tyr Gln Leu Ala
20 25 30

att gtc gcc aag cac cat ggc att ccc ttc tac gtg gct gcc ccc agc 144
Ile Val Ala Lys His His Gly Ile Pro Phe Tyr Val Ala Ala Pro Ser
35 40 45

tct tca tgt gac ctc cgt ctg gag acc ggc aag gag atc att att gaa 192
Ser Ser Cys Asp Leu Arg Leu Glu Thr Gly Lys Glu Ile Ile Ile Glu
50 55 60

```
gag cga ccg ggc cag gag ctg acc gat gtt aat ggg gtc cgg att gca      240
Glu Arg Pro Gly Gln Glu Leu Thr Asp Val Asn Gly Val Arg Ile Ala
 65                 70                  75                  80

gca cct ggg att gga gtt tgg aat cct gcc ttc gat gtc acc ccc cac      288
Ala Pro Gly Ile Gly Val Trp Asn Pro Ala Phe Asp Val Thr Pro His
                85                  90                  95

gac ctc atc act ggt ggc atc atc aca gaa ctg ggg gtc ttt gcc cct      336
Asp Leu Ile Thr Gly Gly Ile Ile Thr Glu Leu Gly Val Phe Ala Pro
            100                 105                 110

gag gag ctc cgg aca gcc cta acc acc acc atc tct tcc agg gat gga      384
Glu Glu Leu Arg Thr Ala Leu Thr Thr Thr Ile Ser Ser Arg Asp Gly
        115                 120                 125

acc cta gat gga ccc cag atg taa                                      408
Thr Leu Asp Gly Pro Gln Met  *
    130                 135
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<210> 18
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(135)
<223> Xaa = Any Amino Acid

<400> 18

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Met Ala His Arg Gly Val Ser Ala Val Val Val Gly Ala Asp Arg Val
 1               5                  10                  15
Val Ala Asn Xaa Asp Thr Ala Asn Lys Val Gly Thr Tyr Gln Leu Ala
            20                  25                  30
Ile Val Ala Lys His His Gly Ile Pro Phe Tyr Val Ala Ala Pro Ser
        35                  40                  45
Ser Ser Cys Asp Leu Arg Leu Glu Thr Gly Lys Glu Ile Ile Ile Glu
    50                  55                  60
Glu Arg Pro Gly Gln Glu Leu Thr Asp Val Asn Gly Val Arg Ile Ala
65                  70                  75                  80
Ala Pro Gly Ile Gly Val Trp Asn Pro Ala Phe Asp Val Thr Pro His
                85                  90                  95
```

```
Asp Leu Ile Thr Gly Gly Ile Ile Thr Glu Leu Gly Val Phe Ala Pro
            100                 105                 110
Glu Glu Leu Arg Thr Ala Leu Thr Thr Thr Ile Ser Ser Arg Asp Gly
        115                 120                 125
Thr Leu Asp Gly Pro Gln Met
    130                 135

      <210> 19
      <211> 828
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)..(828)

      <400> 19
atg ggg aat ttc aga ggt cat gcc ctc cct gga acc ttc ttt ttt att       48
Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
 1               5                  10                  15

att ggt ctt tgg tgg tgt aca aag agt att ctg aag tat atc tgc aaa       96
Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
            20                  25                  30

aag caa aag cga acc tgc tat ctt ggt tcc aaa aca tta ttc tat cga      144
Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
        35                  40                  45

ttg gaa att ttg gag gga att aca ata gtt ggc atg gct tta act ggc      192
Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
    50                  55                  60

atg gct ggg gag cag ttt att cct gga ggg ccc cat ctg atg tta tat      240
Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
65                  70                  75                  80

gac tat aaa caa ggt cac tgg aat caa ctc ctg ggc tgg cat cat ttc      288
Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
                85                  90                  95

acc atg tat ttc ttc ttt ggg ctg ttg ggt gtg gca gat atc tta tgt      336
Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
            100                 105                 110
```

```
ttc acc atc agt tca ctt cct gtg tcc tta acc aag tta atg ttg tca      384
Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser
        115                 120                 125

aat gcc tta ttt gtg gag gcc ttt atc ttc tac aac cac act cat ggc      432
Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly
    130                 135                 140

cgg gaa atg ctg gac atc ttt gtg cac cag ctg ctg gtt ttg gtc gtc      480
Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val
145                 150                 155                 160

ttt ctg aca ggc ctc gtt gcc ttc cta gag ttc ctt gtt cgg aac aat      528
Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn
                165                 170                 175

gta ctt ctg gag cta ttg cgg tca agt ctc att ctg ctt cag ggg agc      576
Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser
            180                 185                 190

tgg ttc ttt cag att gga ttt gtc ctg tat ccc ccc agt gga ggt cct      624
Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro
        195                 200                 205

gca tgg gat ctg atg gat cat gaa aat att ttg ttt ctc acc ata tgc      672
Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys
    210                 215                 220

ttt tgt tgg cat tat gca gta acc att gtc atc gtt gga atg aat tat      720
Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr
225                 230                 235                 240

gct ttc att acc tgg ttg gtt aaa tct aga ctt aag agg ctc tgc tcc      768
Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser
                245                 250                 255

tca gaa gtt gga ctt ctg aaa aat gct gaa cga gaa caa gaa tca gaa      816
Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
            260                 265                 270

gaa gaa atg tga                                                      828
Glu Glu Met  *
        275
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<210> 20
<211> 275
<212> PRT
<213> Homo sapiens

<400> 20

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Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
 1               5                  10                  15
Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
            20                  25                  30
Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
        35                  40                  45
Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
    50                  55                  60
Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
65                  70                  75                  80
Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
                85                  90                  95
Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
            100                 105                 110
Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser
        115                 120                 125
Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly
    130                 135                 140
Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val
145                 150                 155                 160
Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn
                165                 170                 175
Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser
            180                 185                 190
Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro
        195                 200                 205
Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys
    210                 215                 220
Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr
225                 230                 235                 240
Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser
                245                 250                 255
Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
            260                 265                 270
Glu Glu Met
        275
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<210> 21
<211> 1623
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1623)

<221> misc_feature
<222> (1)...(1623)
<223> n = A,T,C or G

<400> 21
atg gag cgg gag gcg ttg ccg tgg ggc ctc gag ccc cag gat gtg cag 48
Met Glu Arg Glu Ala Leu Pro Trp Gly Leu Glu Pro Gln Asp Val Gln
1 5 10 15

agt tct gac gaa atg agg agc ccc gaa ggt aac ctc aga ggc aac atg 96
Ser Ser Asp Glu Met Arg Ser Pro Glu Gly Asn Leu Arg Gly Asn Met
20 25 30

agt gag aat gag gaa gag gaa att tct cag caa gaa ggc agt ggg gac 144
Ser Glu Asn Glu Glu Glu Glu Ile Ser Gln Gln Glu Gly Ser Gly Asp
35 40 45

tat gaa gtc gaa gag ata cca ttt ggg ctt gaa ccc cag agc cct ggg 192
Tyr Glu Val Glu Glu Ile Pro Phe Gly Leu Glu Pro Gln Ser Pro Gly
50 55 60

ttt gag cca caa agc cca gag ttt gaa ccc caa agc ccc aga ttt gag 240
Phe Glu Pro Gln Ser Pro Glu Phe Glu Pro Gln Ser Pro Arg Phe Glu
65 70 75 80

cct gaa agc ccg ggg ttt gag tcc cga agc cct ggg ctt gtg ccc cca 288
Pro Glu Ser Pro Gly Phe Glu Ser Arg Ser Pro Gly Leu Val Pro Pro
85 90 95

agc cct gag ttt gca ccc aga agc cct gaa tca gat tct cag agc cct 336
Ser Pro Glu Phe Ala Pro Arg Ser Pro Glu Ser Asp Ser Gln Ser Pro
100 105 110

gag ttt gaa tcc cag agc cct agg tat gaa ccc caa agc cct ggc tat 384

```
Glu Phe Glu Ser Gln Ser Pro Arg Tyr Glu Pro Gln Ser Pro Gly Tyr
        115                 120                 125

gaa cct cgg agc ccc ggg tat gaa ccc cgg agc cct ggc tat gaa tct      432
Glu Pro Arg Ser Pro Gly Tyr Glu Pro Arg Ser Pro Gly Tyr Glu Ser
    130                 135                 140

gag agc tct aga tat gaa tcc cag aac act gag ctc aaa acc caa agc      480
Glu Ser Ser Arg Tyr Glu Ser Gln Asn Thr Glu Leu Lys Thr Gln Ser
145                 150                 155                 160

cca gaa ttt gaa gct caa agt tcc aaa ttc cag gaa ggt gcg gag atg      528
Pro Glu Phe Glu Ala Gln Ser Ser Lys Phe Gln Glu Gly Ala Glu Met
                165                 170                 175

ctt ctg aac ccc gan gaa aag agt cct ttg aat atc tcc gta gga gtt      576
Leu Leu Asn Pro Xaa Glu Lys Ser Pro Leu Asn Ile Ser Val Gly Val
            180                 185                 190

cac ccc ctg gac tcc ttc act cag ggg ttt ggg gag cag ccc aca ggg      624
His Pro Leu Asp Ser Phe Thr Gln Gly Phe Gly Glu Gln Pro Thr Gly
        195                 200                 205

gac ctg ccc ata ggg cca cct ttt gag atg ccc aca ggg gcc ctg ctg      672
Asp Leu Pro Ile Gly Pro Pro Phe Glu Met Pro Thr Gly Ala Leu Leu
    210                 215                 220

tct aca ccg cag ttt gag atg ctt cag aat ccc ctg ggt ctc aca gga      720
Ser Thr Pro Gln Phe Glu Met Leu Gln Asn Pro Leu Gly Leu Thr Gly
225                 230                 235                 240

gcc ctt cga ggt cca ggt cgg cgg ggt ggc cgg gcc agg ggt ggg cag      768
Ala Leu Arg Gly Pro Gly Arg Arg Gly Gly Arg Ala Arg Gly Gly Gln
                245                 250                 255

ggc cct cgg cct aac atc tgt ggc atc tgc ggg aag agc ttc ggg cgg      816
Gly Pro Arg Pro Asn Ile Cys Gly Ile Cys Gly Lys Ser Phe Gly Arg
            260                 265                 270

ggc tcc acc ctg atc cag cac cag cgc atc cac acc ggt gag aag ccc      864
Gly Ser Thr Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro
        275                 280                 285

tac aaa tgt gag gtc tgc agc aag gcc ttc tcc cag agc tct gac ctc      912
```

```
Tyr Lys Cys Glu Val Cys Ser Lys Ala Phe Ser Gln Ser Ser Asp Leu
    290                 295                 300

atc aaa cac cag cgc acc cac act ggc gag cgg ccc tac aaa tgt ccc      960
Ile Lys His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Pro
305                 310                 315                 320

cgt tgc ggc aag gcc ttc gcc gac agc tct tac ctg ctt cgc cac cag     1008
Arg Cys Gly Lys Ala Phe Ala Asp Ser Ser Tyr Leu Leu Arg His Gln
                325                 330                 335

cgc act cac tct ggc cag aag ccc tac aag tgc cca cat tgt ggc aag     1056
Arg Thr His Ser Gly Gln Lys Pro Tyr Lys Cys Pro His Cys Gly Lys
            340                 345                 350

gcc ttc ggc gac agc tcc tac ctc ctg cga cac cag cgc acc cac agc     1104
Ala Phe Gly Asp Ser Ser Tyr Leu Leu Arg His Gln Arg Thr His Ser
        355                 360                 365

cac gag cgg ccc tac agc tgc acc gag tgc ggc aag tgc tat agc cag     1152
His Glu Arg Pro Tyr Ser Cys Thr Glu Cys Gly Lys Cys Tyr Ser Gln
    370                 375                 380

aac tcg tcc ctg cgc agc cat cag agg gtg cac acc ggt cag agg ccc     1200
Asn Ser Ser Leu Arg Ser His Gln Arg Val His Thr Gly Gln Arg Pro
385                 390                 395                 400

ttc agc tgt ggc atc tgc ggc aag agc ttc tcc cag cgg tcg gcc ctt     1248
Phe Ser Cys Gly Ile Cys Gly Lys Ser Phe Ser Gln Arg Ser Ala Leu
                405                 410                 415

atc ccc cat gcc cgc agc cac gcc cgg gag aag ccc ttc aag tgc cct     1296
Ile Pro His Ala Arg Ser His Ala Arg Glu Lys Pro Phe Lys Cys Pro
            420                 425                 430

gag tgc ggc aag cgc ttt ggc cag agc tcg gtg ctg gcc atc cac gcc     1344
Glu Cys Gly Lys Arg Phe Gly Gln Ser Ser Val Leu Ala Ile His Ala
        435                 440                 445

cgc acc cac ctg cca ggc cgc acc tac agc tgc ccc gac tgc ggc aag     1392
Arg Thr His Leu Pro Gly Arg Thr Tyr Ser Cys Pro Asp Cys Gly Lys
    450                 455                 460

acc ttc aat cgc tcc tcc act ctc atc cag cac cag cgc tcc cac acg     1440
```

Thr Phe Asn Arg Ser Ser Thr Leu Ile Gln His Gln Arg Ser His Thr
465 470 475 480

ggc gag cgg ccc tac agg tgc gcc gtg tgc ggc aag ggc ttc tgc cgc 1488
Gly Glu Arg Pro Tyr Arg Cys Ala Val Cys Gly Lys Gly Phe Cys Arg
485 490 495

tcc tcc acg ctt ctg cag cat cac cgg gtc cac agt ggc gag cgg cct 1536
Ser Ser Thr Leu Leu Gln His His Arg Val His Ser Gly Glu Arg Pro
500 505 510

tac aag tgc gat gac tgc gga aag gcc ttc tcc cag agc tcc gac ctc 1584
Tyr Lys Cys Asp Asp Cys Gly Lys Ala Phe Ser Gln Ser Ser Asp Leu
515 520 525

atc cgc cac cag cgg acc cac gcg gcg ggc cgg cgc tga 1623
Ile Arg His Gln Arg Thr His Ala Ala Gly Arg Arg *
530 535 540

<210> 22
<211> 540
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(540)
<223> Xaa = Any Amino Acid

<400> 22
Met Glu Arg Glu Ala Leu Pro Trp Gly Leu Glu Pro Gln Asp Val Gln
1 5 10 15
Ser Ser Asp Glu Met Arg Ser Pro Glu Gly Asn Leu Arg Gly Asn Met
20 25 30
Ser Glu Asn Glu Glu Glu Glu Ile Ser Gln Gln Glu Gly Ser Gly Asp
35 40 45
Tyr Glu Val Glu Glu Ile Pro Phe Gly Leu Glu Pro Gln Ser Pro Gly
50 55 60
Phe Glu Pro Gln Ser Pro Glu Phe Glu Pro Gln Ser Pro Arg Phe Glu
65 70 75 80
Pro Glu Ser Pro Gly Phe Glu Ser Arg Ser Pro Gly Leu Val Pro Pro
85 90 95
Ser Pro Glu Phe Ala Pro Arg Ser Pro Glu Ser Asp Ser Gln Ser Pro

100 105 110
Glu Phe Glu Ser Gln Ser Pro Arg Tyr Glu Pro Gln Ser Pro Gly Tyr
115 120 125
Glu Pro Arg Ser Pro Gly Tyr Glu Pro Arg Ser Pro Gly Tyr Glu Ser
130 135 140
Glu Ser Ser Arg Tyr Glu Ser Gln Asn Thr Glu Leu Lys Thr Gln Ser
145 150 155 160
Pro Glu Phe Glu Ala Gln Ser Ser Lys Phe Gln Glu Gly Ala Glu Met
165 170 175
Leu Leu Asn Pro Xaa Glu Lys Ser Pro Leu Asn Ile Ser Val Gly Val
180 185 190
His Pro Leu Asp Ser Phe Thr Gln Gly Phe Gly Glu Gln Pro Thr Gly
195 200 205
Asp Leu Pro Ile Gly Pro Pro Phe Glu Met Pro Thr Gly Ala Leu Leu
210 215 220
Ser Thr Pro Gln Phe Glu Met Leu Gln Asn Pro Leu Gly Leu Thr Gly
225 230 235 240
Ala Leu Arg Gly Pro Gly Arg Arg Gly Gly Arg Ala Arg Gly Gly Gln
245 250 255
Gly Pro Arg Pro Asn Ile Cys Gly Ile Cys Gly Lys Ser Phe Gly Arg
260 265 270
Gly Ser Thr Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro
275 280 285
Tyr Lys Cys Glu Val Cys Ser Lys Ala Phe Ser Gln Ser Ser Asp Leu
290 295 300
Ile Lys His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Pro
305 310 315 320
Arg Cys Gly Lys Ala Phe Ala Asp Ser Ser Tyr Leu Leu Arg His Gln
325 330 335
Arg Thr His Ser Gly Gln Lys Pro Tyr Lys Cys Pro His Cys Gly Lys
340 345 350
Ala Phe Gly Asp Ser Ser Tyr Leu Leu Arg His Gln Arg Thr His Ser
355 360 365
His Glu Arg Pro Tyr Ser Cys Thr Glu Cys Gly Lys Cys Tyr Ser Gln
370 375 380
Asn Ser Ser Leu Arg Ser His Gln Arg Val His Thr Gly Gln Arg Pro
385 390 395 400
Phe Ser Cys Gly Ile Cys Gly Lys Ser Phe Ser Gln Arg Ser Ala Leu
405 410 415
Ile Pro His Ala Arg Ser His Ala Arg Glu Lys Pro Phe Lys Cys Pro
420 425 430
Glu Cys Gly Lys Arg Phe Gly Gln Ser Ser Val Leu Ala Ile His Ala
435 440 445
Arg Thr His Leu Pro Gly Arg Thr Tyr Ser Cys Pro Asp Cys Gly Lys

```
    450                 455                 460
Thr Phe Asn Arg Ser Ser Thr Leu Ile Gln His Gln Arg Ser His Thr
465                 470                 475                 480
Gly Glu Arg Pro Tyr Arg Cys Ala Val Cys Gly Lys Gly Phe Cys Arg
                485                 490                 495
Ser Ser Thr Leu Leu Gln His His Arg Val His Ser Gly Glu Arg Pro
            500                 505                 510
Tyr Lys Cys Asp Asp Cys Gly Lys Ala Phe Ser Gln Ser Ser Asp Leu
        515                 520                 525
Ile Arg His Gln Arg Thr His Ala Ala Gly Arg Arg
    530                 535                 540

      <210> 23
      <211> 432
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(432)

      <400> 23
atg gag ccc gcg ctg cgc gct gtg tgc aaa gac gtg cgc atc ggc acc      48
Met Glu Pro Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr
 1               5                  10                  15

atc ctc atc cag acc aac cag ctt acc ggg gag ccc gag ctc cac tac      96
Ile Leu Ile Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr
            20                  25                  30

ctg agg ctg ccc aag gac atc agc gat gac cac gtg atc ctc atg gac     144
Leu Arg Leu Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp
        35                  40                  45

tgc acc gtg tcc acg ggc gcg gcg gcc atg atg gca gtg cgc gtg ctc     192
Cys Thr Val Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu
    50                  55                  60

ctg gac cac gac gtg cct gag gac aag atc ttt ttg ctg tcg ctg ctc     240
Leu Asp His Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu
65                  70                  75                  80

atg gca gag atg ggc gtg cac tca gtg gcc tat gca ttt ccg cga gtg     288
Met Ala Glu Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val
```

```
                 85                  90                  95

aga atc atc acc acg gcg gtg gac aag cgg gtc aat gac ctt ttc cgc      336
Arg Ile Ile Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg
            100                 105                 110

atc atc cca ggc att ggg aac ttt ggc gac cgc tac ttt ggg aca gac      384
Ile Ile Pro Gly Ile Gly Asn Phe Gly Asp Arg Tyr Phe Gly Thr Asp
        115                 120                 125

gcg gtc ccc gat ggc agt gac gag gag gaa gtg gcc tac acg ggt tag      432
Ala Val Pro Asp Gly Ser Asp Glu Glu Glu Val Ala Tyr Thr Gly  *
    130                 135                 140


      <210> 24
      <211> 143
      <212> PRT
      <213> Homo sapiens

      <400> 24
Met Glu Pro Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr
 1               5                  10                  15
Ile Leu Ile Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr
            20                  25                  30
Leu Arg Leu Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp
        35                  40                  45
Cys Thr Val Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu
    50                  55                  60
Leu Asp His Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu
65                  70                  75                  80
Met Ala Glu Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val
                85                  90                  95
Arg Ile Ile Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg
            100                 105                 110
Ile Ile Pro Gly Ile Gly Asn Phe Gly Asp Arg Tyr Phe Gly Thr Asp
        115                 120                 125
Ala Val Pro Asp Gly Ser Asp Glu Glu Glu Val Ala Tyr Thr Gly
    130                 135                 140

      <210> 25
      <211> 912
      <212> DNA
      <213> Homo sapiens
```

<220>
<221> CDS
<222> (1)...(912)

<400> 25
atg ctg gcc ggc cac ggc ggc gtc ttc gcg ctc acg ctg ctg ctc atc 48
Met Leu Ala Gly His Gly Gly Val Phe Ala Leu Thr Leu Leu Leu Ile
1 5 10 15

ctc acc acc acc ggc ctc ttc ttc gtc ttt gac tgt ccc tac ctg gct 96
Leu Thr Thr Thr Gly Leu Phe Phe Val Phe Asp Cys Pro Tyr Leu Ala
20 25 30

cgc aag ctg acc ctt gcc atc ccc atc atc gct gcc atc ctc ttc ttc 144
Arg Lys Leu Thr Leu Ala Ile Pro Ile Ile Ala Ala Ile Leu Phe Phe
35 40 45

ttc gtc atg agc tgc ctg ctg cag aca agc ttc acc gac cct ggg atc 192
Phe Val Met Ser Cys Leu Leu Gln Thr Ser Phe Thr Asp Pro Gly Ile
50 55 60

ctg ccc cgg gcc act gtc tgt gaa gca gcc gcc ctg gag aaa cag atc 240
Leu Pro Arg Ala Thr Val Cys Glu Ala Ala Ala Leu Glu Lys Gln Ile
65 70 75 80

gac aac aca ggc agt tct aca tac cgg cca ccc cct cgg acc cgg gag 288
Asp Asn Thr Gly Ser Ser Thr Tyr Arg Pro Pro Pro Arg Thr Arg Glu
85 90 95

gtg ctg atc aac ggg cag atg gtg aag ctg aag tac tgc ttc acc tgc 336
Val Leu Ile Asn Gly Gln Met Val Lys Leu Lys Tyr Cys Phe Thr Cys
100 105 110

aag atg ttc cgg cca ccc cga acc tca cac tgc agt gtc tgc gac aac 384
Lys Met Phe Arg Pro Pro Arg Thr Ser His Cys Ser Val Cys Asp Asn
115 120 125

tgt gtg gaa cga ttt gac cat cac tgc ccc tgg gtg ggc aac tgt gtg 432
Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
130 135 140

ggg aga cgg aac tat cgc ttc ttc tac gcg ttt att ctc tcc ctc tca 480
Gly Arg Arg Asn Tyr Arg Phe Phe Tyr Ala Phe Ile Leu Ser Leu Ser

```
145                 150                 155                 160

ttc ctg acg gcc ttc atc ttc gcc tgt gtg gtc acc cac ctg acg ttg      528
Phe Leu Thr Ala Phe Ile Phe Ala Cys Val Val Thr His Leu Thr Leu
                165                 170                 175

cgc gct cag gga agc aac ttc ctc tcc act ctg aag gag aca cca gca      576
Arg Ala Gln Gly Ser Asn Phe Leu Ser Thr Leu Lys Glu Thr Pro Ala
            180                 185                 190

agc gtg ctg gag ttg gtg atc tgc ttc ttc tcc atc tgg tcc att ctg      624
Ser Val Leu Glu Leu Val Ile Cys Phe Phe Ser Ile Trp Ser Ile Leu
        195                 200                 205

ggc ctc tca ggg ttt cac acg tac ctc gtc gcc tcc aac ctg act act      672
Gly Leu Ser Gly Phe His Thr Tyr Leu Val Ala Ser Asn Leu Thr Thr
    210                 215                 220

aat gaa gac atc aaa ggc tcg tgg tcc agc aag agg ggc ggt gag gcc      720
Asn Glu Asp Ile Lys Gly Ser Trp Ser Ser Lys Arg Gly Gly Glu Ala
225                 230                 235                 240

tct gtc aac ccc tac agc cat aaa agt att atc acc aac tgc tgt gct      768
Ser Val Asn Pro Tyr Ser His Lys Ser Ile Ile Thr Asn Cys Cys Ala
                245                 250                 255

gtg ctc tgt ggc ccc cta cct ccc agc cta att gac cgg agg gga ttt      816
Val Leu Cys Gly Pro Leu Pro Pro Ser Leu Ile Asp Arg Arg Gly Phe
            260                 265                 270

gtg cag tcc gac acc gtg ttg ccc tca ccc atc aga agc gat gag cca      864
Val Gln Ser Asp Thr Val Leu Pro Ser Pro Ile Arg Ser Asp Glu Pro
        275                 280                 285

gcc tgc aga gcc aag cct gat gcc agc atg gta gga ggc cac ccc tga      912
Ala Cys Arg Ala Lys Pro Asp Ala Ser Met Val Gly Gly His Pro  *
    290                 295                 300
```

<210> 26
<211> 303
<212> PRT
<213> Homo sapiens

<400> 26

```
Met Leu Ala Gly His Gly Gly Val Phe Ala Leu Thr Leu Leu Leu Ile
 1               5                  10                  15
Leu Thr Thr Thr Gly Leu Phe Phe Val Phe Asp Cys Pro Tyr Leu Ala
            20                  25                  30
Arg Lys Leu Thr Leu Ala Ile Pro Ile Ile Ala Ala Ile Leu Phe Phe
        35                  40                  45
Phe Val Met Ser Cys Leu Leu Gln Thr Ser Phe Thr Asp Pro Gly Ile
    50                  55                  60
Leu Pro Arg Ala Thr Val Cys Glu Ala Ala Ala Leu Glu Lys Gln Ile
65                  70                  75                  80
Asp Asn Thr Gly Ser Ser Thr Tyr Arg Pro Pro Pro Arg Thr Arg Glu
                85                  90                  95
Val Leu Ile Asn Gly Gln Met Val Lys Leu Lys Tyr Cys Phe Thr Cys
            100                 105                 110
Lys Met Phe Arg Pro Pro Arg Thr Ser His Cys Ser Val Cys Asp Asn
        115                 120                 125
Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
    130                 135                 140
Gly Arg Arg Asn Tyr Arg Phe Phe Tyr Ala Phe Ile Leu Ser Leu Ser
145                 150                 155                 160
Phe Leu Thr Ala Phe Ile Phe Ala Cys Val Val Thr His Leu Thr Leu
                165                 170                 175
Arg Ala Gln Gly Ser Asn Phe Leu Ser Thr Leu Lys Glu Thr Pro Ala
            180                 185                 190
Ser Val Leu Glu Leu Val Ile Cys Phe Phe Ser Ile Trp Ser Ile Leu
        195                 200                 205
Gly Leu Ser Gly Phe His Thr Tyr Leu Val Ala Ser Asn Leu Thr Thr
    210                 215                 220
Asn Glu Asp Ile Lys Gly Ser Trp Ser Ser Lys Arg Gly Gly Glu Ala
225                 230                 235                 240
Ser Val Asn Pro Tyr Ser His Lys Ser Ile Ile Thr Asn Cys Cys Ala
                245                 250                 255
Val Leu Cys Gly Pro Leu Pro Pro Ser Leu Ile Asp Arg Arg Gly Phe
            260                 265                 270
Val Gln Ser Asp Thr Val Leu Pro Ser Pro Ile Arg Ser Asp Glu Pro
        275                 280                 285
Ala Cys Arg Ala Lys Pro Asp Ala Ser Met Val Gly Gly His Pro
    290                 295                 300
```

<210> 27
<211> 795
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(795)

<221> misc_feature
<222> (1)...(795)
<223> n = A,T,C or G

<400> 27

```
atg aat tca aag cac act ttt ctg gcc ttg tgt gcc ctt cgc ttt atg       48
Met Asn Ser Lys His Thr Phe Leu Ala Leu Cys Ala Leu Arg Phe Met
 1               5                  10                  15

agg cgg ata att gga ctt aaa gat gaa ttt tat aat cgt tac atc acc       96
Arg Arg Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Thr
            20                  25                  30

aag gga aat ctt ttt gag cca gtt ata aat gca ctt ctg gat aat gga      144
Lys Gly Asn Leu Phe Glu Pro Val Ile Asn Ala Leu Leu Asp Asn Gly
        35                  40                  45

act cgg tat aat ctg ttg aat tca gct gtt att gag ttg ttt gaa ttt      192
Thr Arg Tyr Asn Leu Leu Asn Ser Ala Val Ile Glu Leu Phe Glu Phe
    50                  55                  60

ata aga gtg gaa gat atc aag tct ctt act gcc cat ata gtt gaa aac      240
Ile Arg Val Glu Asp Ile Lys Ser Leu Thr Ala His Ile Val Glu Asn
 65                  70                  75                  80

ttt tat aaa gca ctt gaa tcg att gaa tat gtt cag aca ttc aaa gga      288
Phe Tyr Lys Ala Leu Glu Ser Ile Glu Tyr Val Gln Thr Phe Lys Gly
                85                  90                  95

ttg aag act aaa tat gag cag aaa aag aac agt gta cca tct ata ttg      336
Leu Lys Thr Lys Tyr Glu Gln Lys Lys Asn Ser Val Pro Ser Ile Leu
            100                 105                 110

cgt agt aac aga ttt cgc aga gat gca aaa gcc ttg gaa gag gat gaa      384
Arg Ser Asn Arg Phe Arg Arg Asp Ala Lys Ala Leu Glu Glu Asp Glu
        115                 120                 125

gaa atg tgg ttt aat gaa gat gaa gaa gag gaa gga aaa gca gtt gtg      432
Glu Met Trp Phe Asn Glu Asp Glu Glu Glu Glu Gly Lys Ala Val Val
```

```
    130                 135                 140

gca cca gtg gaa aaa cct aag cca gaa gat gat ttt cca gat aat tat      480
Ala Pro Val Glu Lys Pro Lys Pro Glu Asp Asp Phe Pro Asp Asn Tyr
145                 150                 155                 160

gaa aag ttt atg gag act aaa aaa gca aaa gaa agt gaa gac aag gaa      528
Glu Lys Phe Met Glu Thr Lys Lys Ala Lys Glu Ser Glu Asp Lys Glu
                165                 170                 175

aac ctt ccc aaa agg aca tct cct ggt ggc ttc aaa ttt act ttc tcc      576
Asn Leu Pro Lys Arg Thr Ser Pro Gly Gly Phe Lys Phe Thr Phe Ser
            180                 185                 190

cac tct gcc agt gct gct aat gga aca aac agt aaa tct gta gtg gct      624
His Ser Ala Ser Ala Ala Asn Gly Thr Asn Ser Lys Ser Val Val Ala
        195                 200                 205

cag ata cca cca gca act tct aat gga tcc tct tcc aaa acc aca aac      672
Gln Ile Pro Pro Ala Thr Ser Asn Gly Ser Ser Ser Lys Thr Thr Asn
    210                 215                 220

ttg cct acg tca gta aca gcc acc aag gga agt ttg gtt ggc tta gtg      720
Leu Pro Thr Ser Val Thr Ala Thr Lys Gly Ser Leu Val Gly Leu Val
225                 230                 235                 240

gat tat cca gat gat gaa gag gaa gat gaa gaa gaa gnn tcg tcc ccc      768
Asp Tyr Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Xaa Ser Ser Pro
                245                 250                 255

agg aaa aga cct cgt ctt ggc tca taa                                  795
Arg Lys Arg Pro Arg Leu Gly Ser  *
            260
```

<210> 28
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(264)
<223> Xaa = Any Amino Acid

<400> 28

```
Met Asn Ser Lys His Thr Phe Leu Ala Leu Cys Ala Leu Arg Phe Met
 1               5                  10                  15
Arg Arg Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Thr
            20                  25                  30
Lys Gly Asn Leu Phe Glu Pro Val Ile Asn Ala Leu Leu Asp Asn Gly
        35                  40                  45
Thr Arg Tyr Asn Leu Leu Asn Ser Ala Val Ile Glu Leu Phe Glu Phe
    50                  55                  60
Ile Arg Val Glu Asp Ile Lys Ser Leu Thr Ala His Ile Val Glu Asn
65                  70                  75                  80
Phe Tyr Lys Ala Leu Glu Ser Ile Glu Tyr Val Gln Thr Phe Lys Gly
                85                  90                  95
Leu Lys Thr Lys Tyr Glu Gln Lys Lys Asn Ser Val Pro Ser Ile Leu
            100                 105                 110
Arg Ser Asn Arg Phe Arg Arg Asp Ala Lys Ala Leu Glu Glu Asp Glu
        115                 120                 125
Glu Met Trp Phe Asn Glu Asp Glu Glu Glu Glu Gly Lys Ala Val Val
    130                 135                 140
Ala Pro Val Glu Lys Pro Lys Pro Glu Asp Asp Phe Pro Asp Asn Tyr
145                 150                 155                 160
Glu Lys Phe Met Glu Thr Lys Lys Ala Lys Glu Ser Glu Asp Lys Glu
                165                 170                 175
Asn Leu Pro Lys Arg Thr Ser Pro Gly Gly Phe Lys Phe Thr Phe Ser
            180                 185                 190
His Ser Ala Ser Ala Ala Asn Gly Thr Asn Ser Lys Ser Val Val Ala
        195                 200                 205
Gln Ile Pro Pro Ala Thr Ser Asn Gly Ser Ser Ser Lys Thr Thr Asn
    210                 215                 220
Leu Pro Thr Ser Val Thr Ala Thr Lys Gly Ser Leu Val Gly Leu Val
225                 230                 235                 240
Asp Tyr Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Xaa Ser Ser Pro
                245                 250                 255
Arg Lys Arg Pro Arg Leu Gly Ser
            260
```

<210> 29
<211> 711
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1)...(711)

<400> 29

```
atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc      48
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1               5                  10                  15

ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg      96
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
            20                  25                  30

cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca gaa gac     144
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
        35                  40                  45

tta act gat ggt tca tat gat gat gtt cta aat gct gaa caa ctt cag     192
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
    50                  55                  60

aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta att att gaa     240
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
65                  70                  75                  80

aga gct ttg att act ttg ggt aac aat gca gcc ttt tca gtt aac caa     288
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
                85                  90                  95

gct att att cgt gaa ttg ggt ggt att cca att gtt gca aac aaa atc     336
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
            100                 105                 110

aac cat tcc aac cag agt att aaa gag aaa gct tta aat gca cta aat     384
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
        115                 120                 125

aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag ata tac atc     432
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Ile Tyr Ile
    130                 135                 140

agt caa gta tgt gag gat gtc ttc tct ggt cct ctg aac tct gct gtg     480
Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn Ser Ala Val
145                 150                 155                 160

cag ctg gct gga ctg aca ttg ttg aca aac atg act gtt acc aat gac     528
```

Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val Thr Asn Asp
165 170 175

cac cag cac atg ctt cac agt tac att aca gac ctg ttc cag gtg tta 576
His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe Gln Val Leu
180 185 190

ctt act gga aat gga aac acg aag gtg caa gtt ttg aaa ctg ctt ttg 624
Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys Leu Leu Leu
195 200 205

aat ttg tct gaa aat cca gcc atg aca gaa gga ctt ctc cgt gcc caa 672
Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu Arg Ala Gln
210 215 220

gtg gat tca tca ttc ctt tcc ctt atg aca gcc acg tag 711
Val Asp Ser Ser Phe Leu Ser Leu Met Thr Ala Thr *
225 230 235

<210> 30
<211> 236
<212> PRT
<213> Homo sapiens

<400> 30
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
1 5 10 15
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
20 25 30
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
35 40 45
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
50 55 60
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
65 70 75 80
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
85 90 95
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
100 105 110
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
115 120 125
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Ile Tyr Ile
130 135 140

Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn Ser Ala Val
145 150 155 160
Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val Thr Asn Asp
165 170 175
His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe Gln Val Leu
180 185 190
Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys Leu Leu Leu
195 200 205
Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu Arg Ala Gln
210 215 220
Val Asp Ser Ser Phe Leu Ser Leu Met Thr Ala Thr
225 230 235

<210> 31
<211> 1737
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1737)

<400> 31
atg cgc gct gcc cgc gcc gcg ccg ctg ctc cag ctg ctg ctc ctg ctg 48
Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu Leu
1 5 10 15

ggg ccg tgg ctg gag gct gcg ggc gtt gcg gag tcg ccg ctg ccc gcc 96
Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala
20 25 30

gtg gtc ctt gcc atc ctg gcc cgc aat gcc gaa cac tcg ctg ccc cac 144
Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His
35 40 45

tac ctg ggc gct ctg gag cgg ctg gac tac ccc cgg gcc agg atg gcc 192
Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala
50 55 60

ctc tgg tgt gcc acg gac cac aat gtg gac aac acc aca gag atg ctg 240
Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu
65 70 75 80

cag gag tgg ctg gcg gct gtg ggc gat gac tat gct gct-gtg gtc tgg 288

Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp
85 90 95

agg cct gag ggc gag ccc agg ttc tac cca gat gaa gag ggt ccc aag 336
Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys
100 105 110

cac tgg acc aaa gaa agg cac cag ttt ctg atg gag ctg aag cag gaa 384
His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu
115 120 125

gcc ctc acc ttt gcc agg aac tgg ggg gcc gac tat atc ctg ttt gca 432
Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala
130 135 140

gac aca gac aac att ctg acc aac aat cag act ctg cgg ctt ctc atg 480
Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met
145 150 155 160

ggg cag ggg ctt cca gtg gtg gcc cca atg ctg gac tcc cag acc tac 528
Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr
165 170 175

tac tcc aac ttc tgg tgt ggg atc acc ccc cag ggc tac tac cgc cgc 576
Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg
180 185 190

aca gcc gag tac ttc ccc acc aag aac cgc cag cgc cgg ggc tgc ttc 624
Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe
195 200 205

cgt gtc ccc atg gtc cac tcc acc ttc ctt gca tcc ctg cgg gct gaa 672
Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu
210 215 220

ggg gca gac cag ctt gct ttc tac ccg cca cat ccc aac tac act tgg 720
Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp
225 230 235 240

cct ttc gac gac atc atc gtc ttc gcc tat gcc tgc cag gct gct ggg 768
Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly
245 250 255

gtc tcc gtc cac gtg tgc aat gag cac cgt tat ggg tac atg aat gtg 816

Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val
260 265 270

ccg gtg aaa tcc cac cag ggg ctg gaa gac gag agg gtc aac ttc atc 864
Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile
275 280 285

cac ctg atc tta gaa gca cta gtg gac ggc ccc cgc atg cag gcc tca 912
His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser
290 295 300

gct cat gtg act cgg ccc tct aag agg ccc agc aag ata ggg ttt gac 960
Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp
305 310 315 320

gag gtc ttt gtc atc agc ctg gct cgc agg cct gac cgt cgg gaa cgc 1008
Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg
325 330 335

atg ctc gcc tcg ctc tgg gag atg gag atc tct ggg agg gtg gtg gac 1056
Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp
340 345 350

gct gtg gat ggc tgg atg ctc aac agc agt gcc atc agg aac ctc ggc 1104
Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly
355 360 365

gta gac ctg ctc ccg ggc tac cag gac cct tac tcg ggc cgc act ctg 1152
Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
370 375 380

acc aag ggc gag gtg ggc tgc ttc ctc agc cat tac tcc atc tgg gaa 1200
Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
385 390 395 400

gag gtg gtt gcc agg ggc ctg gcc cgg gtc ctg gtg ttt gag gat gac 1248
Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
405 410 415

gtg cgc ttt gag agc aac ttc agg ggg cgg ctg gag cgg ctg atg gag 1296
Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
420 425 430

gat gtg gag gca gag aaa ctg tct tgg gac ctg atc tac ctc gga cgg 1344

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Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
        435                 440                 445

aag cag gtg aac cct gag aag gag acg gcc gtg gag ggg ctg ccg ggc      1392
Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly
    450                 455                 460

ctg gtg gtg gct ggg tac tcc tac tgg acg ctg gcc tat gcc ctg cgt      1440
Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg
465                 470                 475                 480

ctg gcg ggt gcc cgc aag ctg ctg gcc tca cag cct ctg cgc cgc atg      1488
Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met
                485                 490                 495

ctg ccc gtg gac gag ttc ctg ccc atc atg ttc gac cag cac ccc aac      1536
Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn
            500                 505                 510

gag cag tac aag gca cac ttc tgg cca cgg gac ctg gtg gcc ttc tcc      1584
Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
        515                 520                 525

gcc cag ccc ctg ctc gct gcc cct acc cac tat gcc ggg gac gcc gag      1632
Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
    530                 535                 540

tgg ctc agt gac acg gag aca tcc tct cca tgg gat gat gac agc ggc      1680
Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
545                 550                 555                 560

cgc ctc atc agc tgg agc ggc tcc caa aag acc ctg cgc agc ccc gcc      1728
Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Ala
                565                 570                 575

tgg acc tga                                                          1737
Trp Thr  *
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<210> 32
<211> 578
<212> PRT
<213> Homo sapiens

<400> 32

Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu Leu
1 5 10 15

Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala
20 25 30

Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His
35 40 45

Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala
50 55 60

Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu
65 70 75 80

Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp
85 90 95

Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys
100 105 110

His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu
115 120 125

Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala
130 135 140

Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met
145 150 155 160

Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr
165 170 175

Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg
180 185 190

Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe
195 200 205

Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu
210 215 220

Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp
225 230 235 240

Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly
245 250 255

Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val
260 265 270

Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile
275 280 285

His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser
290 295 300

Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp
305 310 315 320

Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg
325 330 335

Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp
340 345 350
Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly
355 360 365
Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
370 375 380
Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
385 390 395 400
Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
405 410 415
Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
420 425 430
Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
435 440 445
Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly
450 455 460
Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg
465 470 475 480
Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met
485 490 495
Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn
500 505 510
Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
515 520 525
Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
530 535 540
Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
545 550 555 560
Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Ala
565 570 575
Trp Thr

<210> 33
<211> 1152
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1152)

<400> 33
atg tta ccc aac acc ggg agg ctg gca gga tgt aca gtt ttt atc aca 48

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Met Leu Pro Asn Thr Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr
 1               5                  10                  15

ggt gca agc cgt ggc att ggc aaa gct att gca ttg aaa gca gca aag      96
Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys
            20                  25                  30

gat gga gca aat att gtt att gct gca aag acc gcc cag cca cat cca     144
Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro
        35                  40                  45

aaa ctt cta ggc aca atc tat act gct gct gaa gaa att gaa gca gtt     192
Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val
    50                  55                  60

gga gga aag gcc ttg cca tgt att gtt gat gtg aga gat gaa cag cag     240
Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln
65                  70                  75                  80

atc agt gct gca gtg gag aaa gcc atc aag aaa ttt gga gga att gat     288
Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp
                85                  90                  95

att ctg gta aat aat gcc agt gcc att agt ttg acc aat aca ttg gac     336
Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp
            100                 105                 110

aca cct acc aag aga ttg gat ctg atg atg aac gtg aac acc aga ggc     384
Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly
        115                 120                 125

acc tac ctt gca tct aaa gca tgt att cct tat ttg aaa aag agc aaa     432
Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys
    130                 135                 140

gtt gct cat atc ctc aat atc agt cca cca ctg aac cta aat cca gtt     480
Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val
145                 150                 155                 160

tgg ttc aaa cag cac tgt gct tat acc att gct aag tat ggt atg tct     528
Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser
                165                 170                 175

atg tat gtg ctt gga atg gca gaa gaa ttt aaa ggt gaa att gca gtc     576
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Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val
180 185 190

aat gca tta tgg cct aaa aca gcc ata cac act gct gct atg gat atg 624
Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met
195 200 205

ctg gga gga cct ggt atc gaa agc cag tgt aga aaa gtt gat atc att 672
Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile
210 215 220

gca gat gca gca tat tcc att ttc caa aag cca aaa agt ttt act ggc 720
Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly
225 230 235 240

aac ttt gtc att gat gaa aat atc tta aaa gaa gaa gga ata gaa aat 768
Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn
245 250 255

ttt gac gtt tat gca att aaa cca ggt cat cct ttg caa cca gat ttc 816
Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe
260 265 270

ttc tta gat gaa tac cca gaa gca gtt agc aag aaa gtg gaa tca act 864
Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr
275 280 285

ggt gct gtt cca gaa ttc aaa gaa gag aaa ctg cag ctg caa cca aaa 912
Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys
290 295 300

cca cgt tct gga gct gtg gaa gaa aca ttt aga att gtt aag gac tct 960
Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser
305 310 315 320

ctc agt gat gat gtt gtt aaa gcc act caa gca atc tat ctg ttt gaa 1008
Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu
325 330 335

ctc tcc ggt gaa gat ggt ggc acg tgg ttt ctt gat ctg aaa agc aag 1056
Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys
340 345 350

ggt ggg aat gtc gga tat gga gag cct tct gat cag gca gat gtg gtg 1104

Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val
355 360 365

atg agt atg act act gat gac ttt gta aaa atg ttt tca ggg aac taa 1152
Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Asn *
370 375 380

<210> 34
<211> 383
<212> PRT
<213> Homo sapiens

<400> 34
Met Leu Pro Asn Thr Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr
1 5 10 15
Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys
20 25 30
Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro
35 40 45
Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val
50 55 60
Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln
65 70 75 80
Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp
85 90 95
Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp
100 105 110
Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly
115 120 125
Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys
130 135 140
Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val
145 150 155 160
Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser
165 170 175
Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val
180 185 190
Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met
195 200 205
Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile
210 215 220
Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly
225 230 235 240

Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn
245 250 255
Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe
260 265 270
Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr
275 280 285
Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys
290 295 300
Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser
305 310 315 320
Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu
325 330 335
Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys
340 345 350
Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val
355 360 365
Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Asn
370 375 380

<210> 35
<211> 1371
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1371)

<221> misc_feature
<222> (1)...(1371)
<223> n = A,T,C or G

<400> 35
atg ggg gcc tgc ctg gga gcc tgc tcc ctg ctc agc tgc gcg tcc tgc 48
Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser Cys
1 5 10 15

ctc tgc ggc tct gcc ccc tgc atc ctg tgc agc tgc tgc ccc gcc agc 96
Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro Ala Ser
20 25 30

cgc aac tcc acc gtg agc cgc ctc atc ttc acg ttc ttc ctc ttc ctg 144
Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe Leu Phe Leu
35 40 45

```
ggg gtg ctg gtg tcc atc att atg ctg agc ccg ggc gtg gag agt cag      192
Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu Ser Gln
     50                  55                  60

ctc tac aag ctg ccc tgg gtg tgt gag gag ggg gcc ggg atc ccc acc      240
Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile Pro Thr
 65                  70                  75                  80

gtc ctg cag ggc cac atc gac tgt ggc tcc ctg ctt ggc tac cgc gct      288
Val Leu Gln Gly His Ile Asp Cys Gly Ser Leu Leu Gly Tyr Arg Ala
                 85                  90                  95

gtc tac cgc atg tgc ttc gcc acg gcg gcc ttc ttc ttc ttt ttc acc      336
Val Tyr Arg Met Cys Phe Ala Thr Ala Ala Phe Phe Phe Phe Phe Thr
            100                 105                 110

ctg ctc atg ctc tgc gtg agc agc agc cgg gac ccc cgg gct gcc atc      384
Leu Leu Met Leu Cys Val Ser Ser Ser Arg Asp Pro Arg Ala Ala Ile
        115                 120                 125

cag aat ggg ttt tgg ttc ttt aag ttc ctg atc ctg gtg ggc ctc acc      432
Gln Asn Gly Phe Trp Phe Phe Lys Phe Leu Ile Leu Val Gly Leu Thr
    130                 135                 140

gtg ggt gcc ttc tac atc cct gac ggc tcc ttc acc aac atc tgg ttc      480
Val Gly Ala Phe Tyr Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe
145                 150                 155                 160

tac ttc ggc gtc gtg ggc tcc ttc ctc ttc atc ctc atc cag ctg gtg      528
Tyr Phe Gly Val Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val
                165                 170                 175

ctg ctc atc gac ttt gcg cac tcc tgg aac cag cgg tgg ctg ggc aag      576
Leu Leu Ile Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys
            180                 185                 190

gcc gag gag tgc gat tcc cgt gcc tgg tac gca ggc ctc ttc ttc ttc      624
Ala Glu Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe
        195                 200                 205

act ctc ctc ttc tac ttg ctg tcg atc gcg gcc gtg gcg ctg atg ttc      672
Thr Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe
    210                 215                 220
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atg tac tac act gag ccc agc ggc tgc cac gag ggc aag gtc ttc atc 720
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe Ile
225 230 235 240

agc ctc aac ctc acc ttc tgt gtc tgc gtg tcc atc gct gct gtc ctg 768
Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala Val Leu
245 250 255

ccc aag gtc cag gac gcc cag ccc aac tcg ggt ctg ctg cag gcc tcg 816
Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu Gln Ala Ser
260 265 270

gtc atc acc ctc tac acc atg ttt gtc acc tgg tca gcc cta tcc agt 864
Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser Ala Leu Ser Ser
275 280 285

atc cct gaa cag aaa tgc aac ccc cat ttg cca acc cag ctg ggc aac 912
Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro Thr Gln Leu Gly Asn
290 295 300

gag aca gtt gtg gca ggc ccc gag ggc tat gag acc cag tgg tgg gat 960
Glu Thr Val Val Ala Gly Pro Glu Gly Tyr Glu Thr Gln Trp Trp Asp
305 310 315 320

gcc ccg agc att gtg ggc ctc atc atc ttc ctc ctg tgc acc ctc ttc 1008
Ala Pro Ser Ile Val Gly Leu Ile Ile Phe Leu Leu Cys Thr Leu Phe
325 330 335

atc agt ctg cgc tcc tca gac cac cgg cag gtg aac agc ctg atg cag 1056
Ile Ser Leu Arg Ser Ser Asp His Arg Gln Val Asn Ser Leu Met Gln
340 345 350

acc gag gag tgc cca cct atg cta gac gcc aca cng cag cag cag cag 1104
Thr Glu Glu Cys Pro Pro Met Leu Asp Ala Thr Xaa Gln Gln Gln Gln
355 360 365

cag gtg gca gcc tgt gag ggc cgg gcc ttt gac aac gag cag gac ggc 1152
Gln Val Ala Ala Cys Glu Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly
370 375 380

gtc acc tac agc tac tcc ttc ttc cac ttc tgc ctg gtg ctg gcc tca 1200
Val Thr Tyr Ser Tyr Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser
385 390 395 400

```
ctg cac gtc atg atg acg ctc acc aac tgg tac aag ccc ggt gag acc      1248
Leu His Val Met Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr
                405                 410                 415

cgg aag atg atc agc acg tgg acc gcc gtg tgg gtg aag atc tgt gcc      1296
Arg Lys Met Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala
            420                 425                 430

agc tgg gca ggg ctg ctc ctc tac ctg tgg acc ctg gta gcc cca ctc      1344
Ser Trp Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu
        435                 440                 445

ctc ctg cgc aac cgc gac ttc agc tga                                  1371
Leu Leu Arg Asn Arg Asp Phe Ser  *
    450                 455
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<210> 36
<211> 456
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(456)
<223> Xaa = Any Amino Acid

<400> 36

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Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser Cys
 1               5                  10                  15
Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro Ala Ser
            20                  25                  30
Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe Leu Phe Leu
        35                  40                  45
Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu Ser Gln
    50                  55                  60
Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile Pro Thr
65                  70                  75                  80
Val Leu Gln Gly His Ile Asp Cys Gly Ser Leu Leu Gly Tyr Arg Ala
                85                  90                  95
Val Tyr Arg Met Cys Phe Ala Thr Ala Ala Phe Phe Phe Phe Phe Thr
            100                 105                 110
Leu Leu Met Leu Cys Val Ser Ser Ser Arg Asp Pro Arg Ala Ala Ile
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115 120 125
Gln Asn Gly Phe Trp Phe Phe Lys Phe Leu Ile Leu Val Gly Leu Thr
130 135 140
Val Gly Ala Phe Tyr Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe
145 150 155 160
Tyr Phe Gly Val Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val
165 170 175
Leu Leu Ile Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys
180 185 190
Ala Glu Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe
195 200 205
Thr Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe
210 215 220
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe Ile
225 230 235 240
Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala Val Leu
245 250 255
Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu Gln Ala Ser
260 265 270
Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser Ala Leu Ser Ser
275 280 285
Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro Thr Gln Leu Gly Asn
290 295 300
Glu Thr Val Val Ala Gly Pro Glu Gly Tyr Glu Thr Gln Trp Trp Asp
305 310 315 320
Ala Pro Ser Ile Val Gly Leu Ile Ile Phe Leu Leu Cys Thr Leu Phe
325 330 335
Ile Ser Leu Arg Ser Ser Asp His Arg Gln Val Asn Ser Leu Met Gln
340 345 350
Thr Glu Glu Cys Pro Pro Met Leu Asp Ala Thr Xaa Gln Gln Gln Gln
355 360 365
Gln Val Ala Ala Cys Glu Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly
370 375 380
Val Thr Tyr Ser Tyr Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser
385 390 395 400
Leu His Val Met Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr
405 410 415
Arg Lys Met Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala
420 425 430
Ser Trp Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu
435 440 445
Leu Leu Arg Asn Arg Asp Phe Ser
450 455

<210> 37
<211> 1257
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1257)

<400> 37
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atg tta ccc aac acc ggg agg ctg gca gga tgt aca gtt ttt atc aca        48
Met Leu Pro Asn Thr Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr
 1               5                  10                  15

ggt gca agc cgt ggc att ggc aaa gct att gca ttg aaa gca gca aag        96
Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys
            20                  25                  30

gat gga gca aat att gtt att gct gca aag acc gcc cag cca cat cca       144
Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro
        35                  40                  45

aaa ctt cta ggc aca atc tat act gct gct gaa gaa att gaa gca gtt       192
Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val
    50                  55                  60

gga gga aag gcc ttg cca tgt att gtt gat gtg aga gat gaa cag cag       240
Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln
65                  70                  75                  80

atc agt gct gca gtg gag aaa gcc atc aag aaa ttt gga gga att gat       288
Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp
                85                  90                  95

att ctg gta aat aat gcc agt gcc att agt ttg acc aat aca ttg gac       336
Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp
            100                 105                 110

aca cct acc aag aga ttg gat ctg atg atg aac gtg aac acc aga ggc       384
Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly
        115                 120                 125

acc tac ctt gca tct aaa gca tgt att cct tat ttg aaa aag agc aaa       432
Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys
```

130 135 140

gtt gct cat atc ctc aat atc agt cca cca ctg aac cta aat cca gtt 480
Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val
145 150 155 160

tgg ttc aaa cag cac tgt gct tat acc att gct aag tat ggt atg tct 528
Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser
165 170 175

atg tat gtg ctt gga atg gca gaa gaa ttt aaa ggt gaa att gca gtc 576
Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val
180 185 190

aat gca tta tgg cct aaa aca gcc ata cac act gct gct atg gat atg 624
Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met
195 200 205

ctg gga gga cct ggt atc gaa agc cag tgt aga aaa gtt gat atc att 672
Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile
210 215 220

gca gat gca gca tat tcc att ttc caa aag cca aaa agt ttt act ggc 720
Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly
225 230 235 240

aac ttt gtc att gat gaa aat atc tta aaa gaa gaa gga ata gaa aat 768
Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn
245 250 255

ttt gac gtt tat gca att aaa cca ggt cat cct ttg caa cca gat ttc 816
Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe
260 265 270

ttc tta gat gaa tac cca gaa gca gtt agc aag aaa gtg gaa tca act 864
Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr
275 280 285

ggt gct gtt cca gaa ttc aaa gaa gag aaa ctg cag ctg caa cca aaa 912
Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys
290 295 300

cca cgt tct gga gct gtg gaa gaa aca ttt aga att gtt aag gac tct 960
Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser

305 310 315 320

ctc agt gat gat gtt gtt aaa gcc act caa gca atc tat ctg ttt gaa 1008
Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu
325 330 335

ctc tcc ggt gaa gat ggt ggc acg tgg ttt ctt gat ctg aaa agc aag 1056
Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys
340 345 350

ggt ggg aat gtc gga tat gga gag cct tct gat cag gca gat gtg gtg 1104
Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val
355 360 365

atg agt atg act act gat gac ttt gta aaa atg ttt tca ggg aaa cta 1152
Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Lys Leu
370 375 380

aaa cca aca atg gca ttc atg tca ggg aaa ttg aag att aaa ggt aac 1200
Lys Pro Thr Met Ala Phe Met Ser Gly Lys Leu Lys Ile Lys Gly Asn
385 390 395 400

atg gcc cta gca atc aaa ttg gag aag cta atg aat cag atg aat gcc 1248
Met Ala Leu Ala Ile Lys Leu Glu Lys Leu Met Asn Gln Met Asn Ala
405 410 415

aga ctg tga 1257
Arg Leu *

<210> 38
<211> 418
<212> PRT
<213> Homo sapiens

<400> 38
Met Leu Pro Asn Thr Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr
1 5 10 15
Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys
20 25 30
Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro
35 40 45
Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val

50 55 60
Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln
65 70 75 80
Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp
85 90 95
Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp
100 105 110
Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly
115 120 125
Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys
130 135 140
Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val
145 150 155 160
Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser
165 170 175
Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val
180 185 190
Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met
195 200 205
Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile
210 215 220
Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly
225 230 235 240
Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn
245 250 255
Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe
260 265 270
Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr
275 280 285
Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys
290 295 300
Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser
305 310 315 320
Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu
325 330 335
Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys
340 345 350
Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val
355 360 365
Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Lys Leu
370 375 380
Lys Pro Thr Met Ala Phe Met Ser Gly Lys Leu Lys Ile Lys Gly Asn
385 390 395 400
Met Ala Leu Ala Ile Lys Leu Glu Lys Leu Met Asn Gln Met Asn Ala

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                405                 410                 415
Arg Leu


      <210> 39
      <211> 627
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(627)

      <400> 39
atg gtg ttc tac ttc acc agc agc agc gtt aat tca tct gcc tac act        48
Met Val Phe Tyr Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr
 1               5                  10                  15

att tac atg gga aaa gat aaa tat gaa aat gaa gat ctg atc aag cat        96
Ile Tyr Met Gly Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His
            20                  25                  30

ggc tgg cct gaa gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct       144
Gly Trp Pro Glu Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala
        35                  40                  45

cat gta tac ctt cga tta cat aag gga gag aat ata gaa gac atc cca       192
His Val Tyr Leu Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro
    50                  55                  60

aag gaa gtg ctg atg gac tgt gcc cac ctt gtg aag gcc aat agc att       240
Lys Glu Val Leu Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile
65                  70                  75                  80

caa ggc tgc aag atg aac aac gtt aat gtg gta tat acg ccg tgg tct       288
Gln Gly Cys Lys Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser
                85                  90                  95

aac ctg aag aaa aca gct gac atg gat gtg ggg cag ata ggc ttt cac       336
Asn Leu Lys Lys Thr Ala Asp Met Asp Val Gly Gln Ile Gly Phe His
            100                 105                 110

agg cag aag gat gta aaa att gtg aca gtg gag aag aaa gta aat gag       384
Arg Gln Lys Asp Val Lys Ile Val Thr Val Glu Lys Lys Val Asn Glu
```

115 120 125

atc ctg aac cga tta gaa aag acc aaa gtc gag cgg ttc cca gac cta 432
Ile Leu Asn Arg Leu Glu Lys Thr Lys Val Glu Arg Phe Pro Asp Leu
130 135 140

gca gca gag aaa gaa tgc aga gat cgt gaa gag agg aat gag aaa aaa 480
Ala Ala Glu Lys Glu Cys Arg Asp Arg Glu Glu Arg Asn Glu Lys Lys
145 150 155 160

gcc caa att cag gaa atg aaa aag aga gaa aaa gaa gaa atg aag aag 528
Ala Gln Ile Gln Glu Met Lys Lys Arg Glu Lys Glu Glu Met Lys Lys
165 170 175

aag agg gaa atg gat gaa ctt agg agc tat tca tca cta atg aaa gtt 576
Lys Arg Glu Met Asp Glu Leu Arg Ser Tyr Ser Ser Leu Met Lys Val
180 185 190

gaa aat atg tct tca aat cag gat ggc aat gat tca gat gaa ttc atg 624
Glu Asn Met Ser Ser Asn Gln Asp Gly Asn Asp Ser Asp Glu Phe Met
195 200 205

taa 627
*

<210> 40
<211> 208
<212> PRT
<213> Homo sapiens

<400> 40
Met Val Phe Tyr Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr
1 5 10 15
Ile Tyr Met Gly Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His
20 25 30
Gly Trp Pro Glu Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala
35 40 45
His Val Tyr Leu Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro
50 55 60
Lys Glu Val Leu Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile
65 70 75 80
Gln Gly Cys Lys Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser

```
                85                  90                  95
Asn Leu Lys Lys Thr Ala Asp Met Asp Val Gly Gln Ile Gly Phe His
            100                 105                 110
Arg Gln Lys Asp Val Lys Ile Val Thr Val Glu Lys Lys Val Asn Glu
        115                 120                 125
Ile Leu Asn Arg Leu Glu Lys Thr Lys Val Glu Arg Phe Pro Asp Leu
    130                 135                 140
Ala Ala Glu Lys Glu Cys Arg Asp Arg Glu Glu Arg Asn Glu Lys Lys
145                 150                 155                 160
Ala Gln Ile Gln Glu Met Lys Lys Arg Glu Lys Glu Glu Met Lys Lys
                165                 170                 175
Lys Arg Glu Met Asp Glu Leu Arg Ser Tyr Ser Ser Leu Met Lys Val
            180                 185                 190
Glu Asn Met Ser Ser Asn Gln Asp Gly Asn Asp Ser Asp Glu Phe Met
        195                 200                 205
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<210> 41
<211> 474
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(474)

<221> misc_feature
<222> (1)...(474)
<223> n = A,T,C or G

<400> 41

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atg agc ggg tcc ctc ggc cga gct gct gcg gct ctg ctc cgc tgg agg      48
Met Ser Gly Ser Leu Gly Arg Ala Ala Ala Ala Leu Leu Arg Trp Arg
 1               5                  10                  15

ctc tgc gcg ggc ggc ggt ggc ctt tgg ggt ccg gtc gtc cgg act gcg      96
Leu Cys Ala Gly Gly Gly Gly Leu Trp Gly Pro Val Val Arg Thr Ala
            20                  25                  30

gga tcg gcc ccg ggc ggc ggc ggc tcg gcg gan nag ttg gac gcg ctg     144
Gly Ser Ala Pro Gly Gly Gly Gly Ser Ala Xaa Xaa Leu Asp Ala Leu
        35                  40                  45

gtg aag aag gac aag gtg gtg gtc ttc ctc aag ggg acg ccg gag cag     192
Val Lys Lys Asp Lys Val Val Val Phe Leu Lys Gly Thr Pro Glu Gln
```

50 55 60

ccc cag tgc ggc ttc agc aac gcc gtg gtg cag atc ctg cgg ctg cac 240
Pro Gln Cys Gly Phe Ser Asn Ala Val Val Gln Ile Leu Arg Leu His
65 70 75 80

ggc gtc cgc gat tac gcg gcc tac aac gtg ctg gac gac ccg gag ctc 288
Gly Val Arg Asp Tyr Ala Ala Tyr Asn Val Leu Asp Asp Pro Glu Leu
85 90 95

cga caa ggc att aaa gac tat tcc aac tgg ccc acc atc ccg caa gtg 336
Arg Gln Gly Ile Lys Asp Tyr Ser Asn Trp Pro Thr Ile Pro Gln Val
100 105 110

tac ctc aat ggc gag ttt gta ggg ggc tgt gac att ctt ctg cag atg 384
Tyr Leu Asn Gly Glu Phe Val Gly Gly Cys Asp Ile Leu Leu Gln Met
115 120 125

cac cag aat ggg gac ttg gtg gaa gaa ctg aaa aag ctg ggg atc cac 432
His Gln Asn Gly Asp Leu Val Glu Glu Leu Lys Lys Leu Gly Ile His
130 135 140

tcc gcc ctt tta gat gaa aag aaa gac caa gac tcc aag tga 474
Ser Ala Leu Leu Asp Glu Lys Lys Asp Gln Asp Ser Lys *
145 150 155

<210> 42
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(157)
<223> Xaa = Any Amino Acid

<400> 42
Met Ser Gly Ser Leu Gly Arg Ala Ala Ala Ala Leu Leu Arg Trp Arg
1 5 10 15
Leu Cys Ala Gly Gly Gly Gly Leu Trp Gly Pro Val Val Arg Thr Ala
20 25 30
Gly Ser Ala Pro Gly Gly Gly Gly Ser Ala Xaa Xaa Leu Asp Ala Leu
35 40 45

Val Lys Lys Asp Lys Val Val Val Phe Leu Lys Gly Thr Pro Glu Gln
    50   55   60
Pro Gln Cys Gly Phe Ser Asn Ala Val Val Gln Ile Leu Arg Leu His
65   70   75   80
Gly Val Arg Asp Tyr Ala Ala Tyr Asn Val Leu Asp Asp Pro Glu Leu
                85   90   95
Arg Gln Gly Ile Lys Asp Tyr Ser Asn Trp Pro Thr Ile Pro Gln Val
            100   105   110
Tyr Leu Asn Gly Glu Phe Val Gly Gly Cys Asp Ile Leu Leu Gln Met
        115   120   125
His Gln Asn Gly Asp Leu Val Glu Glu Leu Lys Lys Leu Gly Ile His
    130   135   140
Ser Ala Leu Leu Asp Glu Lys Lys Asp Gln Asp Ser Lys
145   150   155

<210> 43
<211> 1032
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1032)

<400> 43
atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc 48
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1   5   10   15

ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg 96
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
            20   25   30

cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca ggt gcc 144
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Gly Ala
        35   40   45

ctg gaa gaa ggg acg tca gag ggt cag ttg tgc ggg cgc tcg gcc cgg 192
Leu Glu Glu Gly Thr Ser Glu Gly Gln Leu Cys Gly Arg Ser Ala Arg
    50   55   60

cct cag acg gga ggt acc tgg gag tca cag tgg tcc aag acc tcg cag 240
Pro Gln Thr Gly Gly Thr Trp Glu Ser Gln Trp Ser Lys Thr Ser Gln
65   70   75   80

```
cct gaa gac tta act gat ggt tca tat gat gat gtt cta aat gct gaa      288
Pro Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu
                 85                  90                  95

caa ctt cag aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta      336
Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val
            100                 105                 110

att att gaa aga gct ttg att act ttg ggt aac aat gca gcc ttt tca      384
Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser
        115                 120                 125

gtt aac caa gct att att cgt gaa ttg ggt ggt att cca att gtt gca      432
Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala
    130                 135                 140

aac aaa atc aac cat tcc aac cag agt att aaa gag aaa gct tta aat      480
Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn
145                 150                 155                 160

gca cta aat aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag      528
Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys
                165                 170                 175

ata tac atc agt caa gta tgt gag gat gtc ttc tct ggt cct ctg aac      576
Ile Tyr Ile Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn
            180                 185                 190

tct gct gtg cag ctg gct gga ctg aca ttg ttg aca aac atg act gtt      624
Ser Ala Val Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val
        195                 200                 205

acc aat gac cac cag cac atg ctt cac agt tac att aca gac ctg ttc      672
Thr Asn Asp His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe
    210                 215                 220

cag gtg tta ctt act gga aat gga aac acg aag gtg caa gtt ttg aaa      720
Gln Val Leu Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys
225                 230                 235                 240

ctg ctt ttg aat ttg tct gaa aat cca gcc atg aca gaa gga ctt ctc      768
Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu
                245                 250                 255
```

```
cgt gcc caa gtg gat tca tca ttc ctt tcc ctt tat gac agc cac gta      816
Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser His Val
            260                 265                 270

gca aag gag att ctt ctt cga gta ctt acg cta ttt cag aat ata aag      864
Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn Ile Lys
        275                 280                 285

aac tgc ctc aaa ata gaa ggc cat tta gct gtg cag cct act ttc act      912
Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr Phe Thr
    290                 295                 300

gaa ggt tca ttg ttt ttc ctg tta cat gga gaa gaa tgt gcc cag aaa      960
Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala Gln Lys
305                 310                 315                 320

ata aga gct tta gtt gat cac cat gat gca gag gtg aag gaa aag gtt     1008
Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu Lys Val
                325                 330                 335

gta aca ata ata ccc aaa atc tga                                     1032
Val Thr Ile Ile Pro Lys Ile  *
            340
```

<210> 44
<211> 343
<212> PRT
<213> Homo sapiens

<400> 44

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Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1               5                  10                  15
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
            20                  25                  30
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Gly Ala
        35                  40                  45
Leu Glu Glu Gly Thr Ser Glu Gly Gln Leu Cys Gly Arg Ser Ala Arg
    50                  55                  60
Pro Gln Thr Gly Gly Thr Trp Glu Ser Gln Trp Ser Lys Thr Ser Gln
65                  70                  75                  80
Pro Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu
                85                  90                  95
```

Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val
100 105 110
Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser
115 120 125
Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala
130 135 140
Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn
145 150 155 160
Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys
165 170 175
Ile Tyr Ile Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn
180 185 190
Ser Ala Val Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val
195 200 205
Thr Asn Asp His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe
210 215 220
Gln Val Leu Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys
225 230 235 240
Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu
245 250 255
Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser His Val
260 265 270
Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn Ile Lys
275 280 285
Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr Phe Thr
290 295 300
Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala Gln Lys
305 310 315 320
Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu Lys Val
325 330 335
Val Thr Ile Ile Pro Lys Ile
340

<210> 45
<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1335)

<221> misc_feature
<222> (1)...(1335)

<223> n = A,T,C or G

<400> 45

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atg tcg gga aga gat aca atc ctt ggc ctg tgt atc ctc gca tta gcc      48
Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu Ala
1               5                   10                  15

ttg tct ttg gcc atg atg ttt acc ttc aga ttc atc acc acc ctt ctg      96
Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr Leu Leu
            20                  25                  30

gtt cac att ttc att tca ttg gtt att ttg gga ttg ttg ttt gtc tgc     144
Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu Phe Val Cys
        35                  40                  45

ggt gtt tta tgg tgg ctg tat tat gac tat acc aac gac ctc agc ata     192
Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn Asp Leu Ser Ile
    50                  55                  60

gaa ttg gac aca gaa agg gaa aat atg aag tgc gtg ctg ggg ttt gct     240
Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys Val Leu Gly Phe Ala
65                  70                  75                  80

atc gta tcc aca ggc atc acg gca gtg ctg ctc gtc ttg att ttt gtt     288
Ile Val Ser Thr Gly Ile Thr Ala Val Leu Leu Val Leu Ile Phe Val
                85                  90                  95

ctc aga aag aga ata aaa ttg aca gtt gag ctt ttc caa atc aca aat     336
Leu Arg Lys Arg Ile Lys Leu Thr Val Glu Leu Phe Gln Ile Thr Asn
            100                 105                 110

aaa gcc atc agc agt gct ccc ttc ctg ctg ttc cag cca ctg tgg aca     384
Lys Ala Ile Ser Ser Ala Pro Phe Leu Leu Phe Gln Pro Leu Trp Thr
        115                 120                 125

ttt gcc atc ctc att ttc ttc tgg gtc ctc tgg gtg gct gtg ctg ctg     432
Phe Ala Ile Leu Ile Phe Phe Trp Val Leu Trp Val Ala Val Leu Leu
    130                 135                 140

agc ctg gga act gca gga gct gcc cag gtt atg gaa ggc ggc caa gtg     480
Ser Leu Gly Thr Ala Gly Ala Ala Gln Val Met Glu Gly Gly Gln Val
145                 150                 155                 160

gaa tat aag ccc ctt tcg ggc att cgg tac atg tgg tcg tac cat tta     528
```

```
Glu Tyr Lys Pro Leu Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu
                165                 170                 175

att ggc ctc atc tgg act agt gaa ttc atc ctt gcg tgc cag caa atg      576
Ile Gly Leu Ile Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met
            180                 185                 190

act ata gct ggg gca gtg gnt act tgt tat ttc aac aga agt aaa aat      624
Thr Ile Ala Gly Ala Val Xaa Thr Cys Tyr Phe Asn Arg Ser Lys Asn
        195                 200                 205

gat cct cct gat cat ccc atc ctt tcg tct ctc tcc att ctc ttc ttc      672
Asp Pro Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe
    210                 215                 220

tac cat caa gga acc att gtg aaa ggg tca ttt tta atc tct gtg gtg      720
Tyr His Gln Gly Thr Ile Val Lys Gly Ser Phe Leu Ile Ser Val Val
225                 230                 235                 240

agg att ccg aga atc att gtc atg tac atg caa aac gca ctg aaa gaa      768
Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys Glu
                245                 250                 255

cag cat ggt gca ttg tcc agg tac ctg ttc cga tgc tgc tac tgc tgt      816
Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys Tyr Cys Cys
            260                 265                 270

ttc tgg tgt ctt gac aaa tac ctg ctc cat ctc aac cag aat gca tat      864
Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn Gln Asn Ala Tyr
        275                 280                 285

act aca act gct att aat ggg aca gat ttc tgt aca tca gca aaa gat      912
Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys Thr Ser Ala Lys Asp
    290                 295                 300

gca ttc aaa atc ttg tcc aag aac tca agt cac ttt aca tct att aac      960
Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser His Phe Thr Ser Ile Asn
305                 310                 315                 320

tgc ttt gga gac ttc ata att ttt cta gga aag gtg tta gtg gtg tgt     1008
Cys Phe Gly Asp Phe Ile Ile Phe Leu Gly Lys Val Leu Val Val Cys
                325                 330                 335

ttc act gtt ttt gga gga ctc atg gct ttt aac tac aat cgg gca ttc     1056
```

Phe Thr Val Phe Gly Gly Leu Met Ala Phe Asn Tyr Asn Arg Ala Phe
340 345 350

cag gtg tgg gca gtc cct ctg tta ttg gta gct ttt ttt gcc tac tta 1104
Gln Val Trp Ala Val Pro Leu Leu Leu Val Ala Phe Phe Ala Tyr Leu
355 360 365

gta gcc cat agt ttt tta tct gtg ttt gaa act gtg ctg gat gca ctt 1152
Val Ala His Ser Phe Leu Ser Val Phe Glu Thr Val Leu Asp Ala Leu
370 375 380

ttc ctg tgt ttt gct gtt gat ctg gaa aca aat gat gga tcg tca gaa 1200
Phe Leu Cys Phe Ala Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu
385 390 395 400

aag ccc tac ttt atg gat caa gaa ttt ctg agt ttc gta aaa agg agc 1248
Lys Pro Tyr Phe Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser
405 410 415

aac aaa tta aac aat gca agg gca cag cag gac aag cac tca tta agg 1296
Asn Lys Leu Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg
420 425 430

aat gag gag gga aca gaa ctc cag gcc att gtg aga tag 1335
Asn Glu Glu Gly Thr Glu Leu Gln Ala Ile Val Arg *
435 440

<210> 46
<211> 444
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(444)
<223> Xaa = Any Amino Acid

<400> 46
Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu Ala
1 5 10 15
Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr Leu Leu
20 25 30
Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu Phe Val Cys

35 40 45
Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn Asp Leu Ser Ile
50 55 60
Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys Val Leu Gly Phe Ala
65 70 75 80
Ile Val Ser Thr Gly Ile Thr Ala Val Leu Leu Val Leu Ile Phe Val
85 90 95
Leu Arg Lys Arg Ile Lys Leu Thr Val Glu Leu Phe Gln Ile Thr Asn
100 105 110
Lys Ala Ile Ser Ser Ala Pro Phe Leu Leu Phe Gln Pro Leu Trp Thr
115 120 125
Phe Ala Ile Leu Ile Phe Phe Trp Val Leu Trp Val Ala Val Leu Leu
130 135 140
Ser Leu Gly Thr Ala Gly Ala Ala Gln Val Met Glu Gly Gly Gln Val
145 150 155 160
Glu Tyr Lys Pro Leu Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu
165 170 175
Ile Gly Leu Ile Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met
180 185 190
Thr Ile Ala Gly Ala Val Xaa Thr Cys Tyr Phe Asn Arg Ser Lys Asn
195 200 205
Asp Pro Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe
210 215 220
Tyr His Gln Gly Thr Ile Val Lys Gly Ser Phe Leu Ile Ser Val Val
225 230 235 240
Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys Glu
245 250 255
Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys Tyr Cys Cys
260 265 270
Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn Gln Asn Ala Tyr
275 280 285
Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys Thr Ser Ala Lys Asp
290 295 300
Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser His Phe Thr Ser Ile Asn
305 310 315 320
Cys Phe Gly Asp Phe Ile Ile Phe Leu Gly Lys Val Leu Val Val Cys
325 330 335
Phe Thr Val Phe Gly Gly Leu Met Ala Phe Asn Tyr Asn Arg Ala Phe
340 345 350
Gln Val Trp Ala Val Pro Leu Leu Leu Val Ala Phe Phe Ala Tyr Leu
355 360 365
Val Ala His Ser Phe Leu Ser Val Phe Glu Thr Val Leu Asp Ala Leu
370 375 380
Phe Leu Cys Phe Ala Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu

385 390 395 400
Lys Pro Tyr Phe Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser
405 410 415
Asn Lys Leu Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg
420 425 430
Asn Glu Glu Gly Thr Glu Leu Gln Ala Ile Val Arg
435 440

<210> 47
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(351)

<400> 47
atg gcg gat gag gcg ttg ttt ttg ctt ctc cat aac gag atg gtg tct 48
Met Ala Asp Glu Ala Leu Phe Leu Leu Leu His Asn Glu Met Val Ser
1 5 10 15

gga gtg tac aag tcc gcg gag cag ggg gag gtg gaa aac gga cga tgt 96
Gly Val Tyr Lys Ser Ala Glu Gln Gly Glu Val Glu Asn Gly Arg Cys
20 25 30

att act aag ctg gaa aac atg ggg ttt cga gtg gga caa gga ttg ata 144
Ile Thr Lys Leu Glu Asn Met Gly Phe Arg Val Gly Gln Gly Leu Ile
35 40 45

gaa agg ttt aca aaa gat act gca agg ttc aag gat gag tta gat atc 192
Glu Arg Phe Thr Lys Asp Thr Ala Arg Phe Lys Asp Glu Leu Asp Ile
50 55 60

atg aag ttc att tgt aaa gat ttt tgg act acg gta ttc aag aaa caa 240
Met Lys Phe Ile Cys Lys Asp Phe Trp Thr Thr Val Phe Lys Lys Gln
65 70 75 80

atc gac aat cta agg aca aat cat cag ggc atc tat gta ctt cag gac 288
Ile Asp Asn Leu Arg Thr Asn His Gln Gly Ile Tyr Val Leu Gln Asp
85 90 95

aac aaa ttt cgc ctg ctt act cag atg tct gca gga aaa cag tat tta 336
Asn Lys Phe Arg Leu Leu Thr Gln Met Ser Ala Gly Lys Gln Tyr Leu

100 105 110

gaa cat gca tcc taa 351
Glu His Ala Ser *
115

<210> 48
<211> 116
<212> PRT
<213> Homo sapiens

<400> 48
Met Ala Asp Glu Ala Leu Phe Leu Leu Leu His Asn Glu Met Val Ser
1 5 10 15
Gly Val Tyr Lys Ser Ala Glu Gln Gly Glu Val Glu Asn Gly Arg Cys
20 25 30
Ile Thr Lys Leu Glu Asn Met Gly Phe Arg Val Gly Gln Gly Leu Ile
35 40 45
Glu Arg Phe Thr Lys Asp Thr Ala Arg Phe Lys Asp Glu Leu Asp Ile
50 55 60
Met Lys Phe Ile Cys Lys Asp Phe Trp Thr Thr Val Phe Lys Lys Gln
65 70 75 80
Ile Asp Asn Leu Arg Thr Asn His Gln Gly Ile Tyr Val Leu Gln Asp
85 90 95
Asn Lys Phe Arg Leu Leu Thr Gln Met Ser Ala Gly Lys Gln Tyr Leu
100 105 110
Glu His Ala Ser
115

<210> 49
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(516)

<400> 49
atg aag aaa tgt ctt ttg ccc gtt ttg att acg tgc atg caa aca gcg 48
Met Lys Lys Cys Leu Leu Pro Val Leu Ile Thr Cys Met Gln Thr Ala
1 5 10 15

```
att tgc aaa gac cgt atg atg atg atc atg atc tta ctg gtg aat tac       96
Ile Cys Lys Asp Arg Met Met Met Ile Met Ile Leu Leu Val Asn Tyr
            20                  25                  30

cta cct gat gaa ttt ata gaa tgt gaa gac cca gtg gat cat gtt gga      144
Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro Val Asp His Val Gly
        35                  40                  45

aat gca act gca tcc cag gaa ctt ggt tat ggt tgt ctc aag ttc ggc      192
Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly
    50                  55                  60

ggt cag gcc tac agc gac gtg gaa cac act tca gtc cag tgc cat gcc      240
Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser Val Gln Cys His Ala
65                  70                  75                  80

tta gat gga att gag tgt gcc agt cct agg acc ttt cta cga gaa aat      288
Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr Phe Leu Arg Glu Asn
                85                  90                  95

aaa cct tgt ata aag tat acc gga cac tac ttc ata acc act tta ctc      336
Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe Ile Thr Thr Leu Leu
            100                 105                 110

tac tcc ttc ttc ctg gga tgt ttt ggt gtg gat cga ttc tgt ttg gga      384
Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp Arg Phe Cys Leu Gly
        115                 120                 125

cac act ggc act gca gta ggg aag ctg ttg acg ctt gga gga ctt ggg      432
His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly
    130                 135                 140

att tgg tgg ttt gtt gac ctt att ttg cta att act gga ggg ctg atg      480
Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile Thr Gly Gly Leu Met
145                 150                 155                 160

cca agt gat ggc agc aac tgg tgc act gtt tac taa                       516
Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr  *
                165                 170
```

<210> 50
<211> 171
<212> PRT

<213> Homo sapiens

<400> 50

```
Met Lys Lys Cys Leu Leu Pro Val Leu Ile Thr Cys Met Gln Thr Ala
 1               5                  10                  15
Ile Cys Lys Asp Arg Met Met Met Ile Met Ile Leu Leu Val Asn Tyr
            20                  25                  30
Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro Val Asp His Val Gly
        35                  40                  45
Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly
    50                  55                  60
Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser Val Gln Cys His Ala
65                  70                  75                  80
Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr Phe Leu Arg Glu Asn
                85                  90                  95
Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe Ile Thr Thr Leu Leu
            100                 105                 110
Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp Arg Phe Cys Leu Gly
        115                 120                 125
His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly
    130                 135                 140
Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile Thr Gly Gly Leu Met
145                 150                 155                 160
Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr
                165                 170
```

<210> 51
<211> 870
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(870)

<400> 51

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atg ccc cta tta aaa ctt gta cat ggc tcc cca ttg gtt ttt gga gaa      48
Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1               5                  10                  15

aag ttc aag ctt ttt acc ttg gtg tct gcc tgt atc cca gtg ttc agg      96
Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
            20                  25                  30
```

```
ctg gct aga cgg cgg aag aag atc cta ttt tac tgt cac ttc cca gat      144
Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
        35                  40                  45

ctg ctt ctc acc aag aga gat tct ttt ctt aaa cga cta tac agg gcc      192
Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
    50                  55                  60

cca att gac tgg ata gag gaa tac acc aca ggc atg gca gac tgc atc      240
Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
65                  70                  75                  80

tta gtc aac agc cag ttc aca gct gct gtt ttt aag gaa aca ttc aag      288
Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
                85                  90                  95

tcc ctg tct cac ata gac cct gat gtc ctc tat cca tct cta aat gtc      336
Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
            100                 105                 110

acc agc ttt gac tca gtt gtt cct gaa aag ctg gat gac cta gtc ccc      384
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
        115                 120                 125

aag ggg aaa aaa ttc ctg ctg ctc tcc atc aac aga tac gaa agg aag      432
Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
    130                 135                 140

aaa aat ctg act ttg gca ctg gaa gcc cta gta cag ctg cgt gga aga      480
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
145                 150                 155                 160

ttg aca tcc caa gat tgg gag agg gtt cat ctg atc gtg gca ggt ggt      528
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
                165                 170                 175

tat gac gag aga gtc ctg gag aat gtg gaa cat tat cag gaa ttg aag      576
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
            180                 185                 190

aaa atg gtc caa cag tcc gac ctt ggc cag tat gtg acc ttc ttg agg      624
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
        195                 200                 205
```

```
tct ttc tca gac aaa cag aaa atc tcc ctc ctc cac agc tgc acg tgt      672
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
    210                 215                 220

gtg ctt tac aca cca agc aat gag cac ttt ggc att gtc cct ctg gaa      720
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
225                 230                 235                 240

gcc atg tac atg cag tgc cca gtc att gct gtt aat tcg ggt gga ccc      768
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
                245                 250                 255

ttg gag tcc att gac cac agt gtc aca ggg ttt ctg tgt gag cct gac      816
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
            260                 265                 270

ccg gtg cac ttc tca gaa gca ata gaa aag ttc atc cag aaa agt cat      864
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Gln Lys Ser His
        275                 280                 285

ccg tga                                                              870
Pro  *
```

<210> 52
<211> 289
<212> PRT
<213> Homo sapiens

<400> 52

```
Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1               5                  10                  15
Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
            20                  25                  30
Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
        35                  40                  45
Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
    50                  55                  60
Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
65                  70                  75                  80
Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
                85                  90                  95
Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
```

```
            100                 105                 110
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
        115                 120                 125
Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
    130                 135                 140
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
145                 150                 155                 160
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
                165                 170                 175
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
            180                 185                 190
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
        195                 200                 205
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
    210                 215                 220
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
225                 230                 235                 240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
                245                 250                 255
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
            260                 265                 270
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Gln Lys Ser His
        275                 280                 285
Pro
```

<210> 53
<211> 1041
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1041)

<221> misc_feature
<222> (1)...(1041)
<223> n = A,T,C or G

<400> 53

```
atg cca cgg gtg ttt gtg ttt cgt gcc ctt ttg ttg gtc ctc atc ttt      48
Met Pro Arg Val Phe Val Phe Arg Ala Leu Leu Leu Val Leu Ile Phe
 1               5                  10                  15
```

ctc tnt gtg gtt tcc tat tgg ctt ttt tac ggg gtc cgc att ttg gac 96
Leu Xaa Val Val Ser Tyr Trp Leu Phe Tyr Gly Val Arg Ile Leu Asp
20 25 30

tct cgg gac cgg aat tac cag ggc att gtg caa tat gca gtc tcc ctt 144
Ser Arg Asp Arg Asn Tyr Gln Gly Ile Val Gln Tyr Ala Val Ser Leu
35 40 45

gtg gat gcc ctc ctc ttc atc cat tac ctg gcc atc gtc ctg ctg gag 192
Val Asp Ala Leu Leu Phe Ile His Tyr Leu Ala Ile Val Leu Leu Glu
50 55 60

ctc agg cag ctg cag ccc atg ttc acg ctg cag gtg gtc cgc tcc acc 240
Leu Arg Gln Leu Gln Pro Met Phe Thr Leu Gln Val Val Arg Ser Thr
65 70 75 80

gat ggc gag tcc cgc ttc tac agc ctg gga cac ctg agt atc cag cga 288
Asp Gly Glu Ser Arg Phe Tyr Ser Leu Gly His Leu Ser Ile Gln Arg
85 90 95

gca gca ttg gtg gtc cta gaa aat tac tac aaa gat ttc acc atc tat 336
Ala Ala Leu Val Val Leu Glu Asn Tyr Tyr Lys Asp Phe Thr Ile Tyr
100 105 110

aac cca aac ctc cta aca gcc tcc aaa ttc cga gca gcc aag cat atg 384
Asn Pro Asn Leu Leu Thr Ala Ser Lys Phe Arg Ala Ala Lys His Met
115 120 125

gcc ggg ctg aaa gtc tac aat gta gat ggc ccc agt aac aat gcc act 432
Ala Gly Leu Lys Val Tyr Asn Val Asp Gly Pro Ser Asn Asn Ala Thr
130 135 140

ggc cag tcc cgg gcc atg att gct gca gct gct cgg cgc agg gac tca 480
Gly Gln Ser Arg Ala Met Ile Ala Ala Ala Ala Arg Arg Arg Asp Ser
145 150 155 160

agc cac aac gag ttg tat tat gaa gag gcc gaa cat gaa cgg cga gta 528
Ser His Asn Glu Leu Tyr Tyr Glu Glu Ala Glu His Glu Arg Arg Val
165 170 175

aag aag cgg aaa gca agg ctg gtg gtt gca gtg gaa gag gcc ttc atc 576
Lys Lys Arg Lys Ala Arg Leu Val Val Ala Val Glu Glu Ala Phe Ile
180 185 190

```
cac att cag cgt ctc cag gct gag gag cag cag aaa gcc cca ggg gag      624
His Ile Gln Arg Leu Gln Ala Glu Glu Gln Gln Lys Ala Pro Gly Glu
        195                 200                 205

gtg atg gac cct agg gag gcc gcc cag gcn att ttc ccc tcc atg gcc      672
Val Met Asp Pro Arg Glu Ala Ala Gln Xaa Ile Phe Pro Ser Met Ala
    210                 215                 220

agg gct ctc cag aag tac ctg cgc atc acc cgg cag cag aac tac cac      720
Arg Ala Leu Gln Lys Tyr Leu Arg Ile Thr Arg Gln Gln Asn Tyr His
225                 230                 235                 240

agc atg gag agc atc ctg cag cac ctg gcc ttc tgc atc acc aac ggc      768
Ser Met Glu Ser Ile Leu Gln His Leu Ala Phe Cys Ile Thr Asn Gly
                245                 250                 255

atg acc ccc aag gcc ttc cta gaa cgg tac ctc agt gcg ggc ccc acc      816
Met Thr Pro Lys Ala Phe Leu Glu Arg Tyr Leu Ser Ala Gly Pro Thr
            260                 265                 270

ctg caa tat gac aag gac cgc tgg ctc tct aca cag tgg agg ctt gtc      864
Leu Gln Tyr Asp Lys Asp Arg Trp Leu Ser Thr Gln Trp Arg Leu Val
        275                 280                 285

agt gat gag gct gtg act aat gga tta cgg gat gga att gtg ttc gtc      912
Ser Asp Glu Ala Val Thr Asn Gly Leu Arg Asp Gly Ile Val Phe Val
    290                 295                 300

ctt aag tgc ttg gac ttc agc ctc gta gtc aat gtg aag aaa att cca      960
Leu Lys Cys Leu Asp Phe Ser Leu Val Val Asn Val Lys Lys Ile Pro
305                 310                 315                 320

ttc atc ata ctc tct gaa gag ttc ata gac ccc aaa tct cac aaa ttt     1008
Phe Ile Ile Leu Ser Glu Glu Phe Ile Asp Pro Lys Ser His Lys Phe
                325                 330                 335

gtc ctt cgc tta cag tct gag aca tcc gtt taa                         1041
Val Leu Arg Leu Gln Ser Glu Thr Ser Val  *
            340                 345
```

<210> 54
<211> 346
<212> PRT

<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(346)
<223> Xaa = Any Amino Acid

<400> 54
Met Pro Arg Val Phe Val Phe Arg Ala Leu Leu Leu Val Leu Ile Phe
1 5 10 15
Leu Xaa Val Val Ser Tyr Trp Leu Phe Tyr Gly Val Arg Ile Leu Asp
20 25 30
Ser Arg Asp Arg Asn Tyr Gln Gly Ile Val Gln Tyr Ala Val Ser Leu
35 40 45
Val Asp Ala Leu Leu Phe Ile His Tyr Leu Ala Ile Val Leu Leu Glu
50 55 60
Leu Arg Gln Leu Gln Pro Met Phe Thr Leu Gln Val Val Arg Ser Thr
65 70 75 80
Asp Gly Glu Ser Arg Phe Tyr Ser Leu Gly His Leu Ser Ile Gln Arg
85 90 95
Ala Ala Leu Val Val Leu Glu Asn Tyr Tyr Lys Asp Phe Thr Ile Tyr
100 105 110
Asn Pro Asn Leu Leu Thr Ala Ser Lys Phe Arg Ala Ala Lys His Met
115 120 125
Ala Gly Leu Lys Val Tyr Asn Val Asp Gly Pro Ser Asn Asn Ala Thr
130 135 140
Gly Gln Ser Arg Ala Met Ile Ala Ala Ala Ala Arg Arg Arg Asp Ser
145 150 155 160
Ser His Asn Glu Leu Tyr Tyr Glu Glu Ala Glu His Glu Arg Arg Val
165 170 175
Lys Lys Arg Lys Ala Arg Leu Val Val Ala Val Glu Glu Ala Phe Ile
180 185 190
His Ile Gln Arg Leu Gln Ala Glu Glu Gln Gln Lys Ala Pro Gly Glu
195 200 205
Val Met Asp Pro Arg Glu Ala Ala Gln Xaa Ile Phe Pro Ser Met Ala
210 215 220
Arg Ala Leu Gln Lys Tyr Leu Arg Ile Thr Arg Gln Gln Asn Tyr His
225 230 235 240
Ser Met Glu Ser Ile Leu Gln His Leu Ala Phe Cys Ile Thr Asn Gly
245 250 255
Met Thr Pro Lys Ala Phe Leu Glu Arg Tyr Leu Ser Ala Gly Pro Thr
260 265 270
Leu Gln Tyr Asp Lys Asp Arg Trp Leu Ser Thr Gln Trp Arg Leu Val
275 280 285

```
Ser Asp Glu Ala Val Thr Asn Gly Leu Arg Asp Gly Ile Val Phe Val
    290                 295                 300
Leu Lys Cys Leu Asp Phe Ser Leu Val Val Asn Val Lys Lys Ile Pro
305                 310                 315                 320
Phe Ile Ile Leu Ser Glu Glu Phe Ile Asp Pro Lys Ser His Lys Phe
                325                 330                 335
Val Leu Arg Leu Gln Ser Glu Thr Ser Val
            340                 345
```

<210> 55
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(195)

<400> 55

```
atg gcc ttt ctc gcc aag aaa ggg tac cgg cat gac agc tca aca gca      48
Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His Asp Ser Ser Thr Ala
 1               5                  10                  15

gtg gcc ggc agc ccc cga ggc cat ggg cag agc cgc gag aca acc cag      96
Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser Arg Glu Thr Thr Gln
            20                  25                  30

gaa cgc agg aag aag gaa gcc aac aag gcg aca aga gcc aac cac aac     144
Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr Arg Ala Asn His Asn
        35                  40                  45

cgg aga acc atg gcc gac cgc aag agg agc aaa ggc atg atc cca tcc     192
Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys Gly Met Ile Pro Ser
    50                  55                  60

tga                                                                 195
 *
```

<210> 56
<211> 64
<212> PRT
<213> Homo sapiens

<400> 56
Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His Asp Ser Ser Thr Ala
1   5   10   15
Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser Arg Glu Thr Thr Gln
            20   25   30
Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr Arg Ala Asn His Asn
        35   40   45
Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys Gly Met Ile Pro Ser
    50   55   60

<210> 57
<211> 1011
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1011)

<400> 57
atg ggt aca tct gat tcc cac cac gcg ggg ctc agc tta gtt agc agg 48
Met Gly Thr Ser Asp Ser His His Ala Gly Leu Ser Leu Val Ser Arg
1   5   10   15

aga cct tca ggt ggt gct gct ggg gaa cgg gag ctg gat gag gtt gat 96
Arg Pro Ser Gly Gly Ala Ala Gly Glu Arg Glu Leu Asp Glu Val Asp
            20   25   30

atg tca gat ctc tct cca gaa gag caa tgg agg gtc gag cac gca cgc 144
Met Ser Asp Leu Ser Pro Glu Glu Gln Trp Arg Val Glu His Ala Arg
        35   40   45

atg cat gcc aag cac cgt ggc cat gaa gct atg cat gct gaa atg gtc 192
Met His Ala Lys His Arg Gly His Glu Ala Met His Ala Glu Met Val
    50   55   60

ctc atc ctc atc gca acc ttg gtg gtg gcc cag ctg ctc ctg gtg cag 240
Leu Ile Leu Ile Ala Thr Leu Val Val Ala Gln Leu Leu Leu Val Gln
65   70   75   80

tgg aag cag agg cac cca cgc tcc tac aat atg gtg acc ctc ttt cag 288
Trp Lys Gln Arg His Pro Arg Ser Tyr Asn Met Val Thr Leu Phe Gln
                85   90   95

atg tgg gtt gtt ccc ctc tat ttc aca gtg aag ctg cac tgg tgg agg 336
Met Trp Val Val Pro Leu Tyr Phe Thr Val Lys Leu His Trp Trp Arg
100 105 110

ttc cta gtg atc tgg atc ttg ttc tct gct gtc aca gcc ttt gtt acc 384
Phe Leu Val Ile Trp Ile Leu Phe Ser Ala Val Thr Ala Phe Val Thr
115 120 125

ttc cga gcc acc cga aaa cct cta gta cag aca acc cca agg ttg gtt 432
Phe Arg Ala Thr Arg Lys Pro Leu Val Gln Thr Thr Pro Arg Leu Val
130 135 140

tat aag tgg ttc ctg cta atc tat aaa atc agc tat gcc act ggc att 480
Tyr Lys Trp Phe Leu Leu Ile Tyr Lys Ile Ser Tyr Ala Thr Gly Ile
145 150 155 160

gtt ggc tac atg gct gtc atg ttt acc ctc ttt ggt ctt aac tta tta 528
Val Gly Tyr Met Ala Val Met Phe Thr Leu Phe Gly Leu Asn Leu Leu
165 170 175

ttc aag atc aaa cca gaa gat gcc atg gac ttt ggc atc tcc ctt ctc 576
Phe Lys Ile Lys Pro Glu Asp Ala Met Asp Phe Gly Ile Ser Leu Leu
180 185 190

ttc tat ggc ctc tac tat gga gtt ctg gaa cgg gac ttt gca gaa atg 624
Phe Tyr Gly Leu Tyr Tyr Gly Val Leu Glu Arg Asp Phe Ala Glu Met
195 200 205

tgt gca gac tac atg gca tct acc ata ggg ttc tac agc gag tcg ggc 672
Cys Ala Asp Tyr Met Ala Ser Thr Ile Gly Phe Tyr Ser Glu Ser Gly
210 215 220

atg cct acc aaa cat ctt tca gac agt gtg tgt gct gtg tgt ggg cag 720
Met Pro Thr Lys His Leu Ser Asp Ser Val Cys Ala Val Cys Gly Gln
225 230 235 240

cag atc ttt gtg gac gtc agt gaa gag ggg atc att gag aac acg tat 768
Gln Ile Phe Val Asp Val Ser Glu Glu Gly Ile Ile Glu Asn Thr Tyr
245 250 255

agg ctg tcc tgc aat cat gtc ttc cac gag ttc tgc atc cgt ggc tgg 816
Arg Leu Ser Cys Asn His Val Phe His Glu Phe Cys Ile Arg Gly Trp
260 265 270

```
tgc atc gtg gga aag aag caa acg tgt ccc tac tgc aaa gag aag gta      864
Cys Ile Val Gly Lys Lys Gln Thr Cys Pro Tyr Cys Lys Glu Lys Val
        275                 280                 285

gac ctc aag agg atg ttc agc aat ccc tgg gag agg cct cac gtc atg      912
Asp Leu Lys Arg Met Phe Ser Asn Pro Trp Glu Arg Pro His Val Met
    290                 295                 300

tat ggg caa ctg ctg gac tgg ctt cga tac ttg gta gcc tgg cag cct      960
Tyr Gly Gln Leu Leu Asp Trp Leu Arg Tyr Leu Val Ala Trp Gln Pro
305                 310                 315                 320

gtc atc att ggt gta gtc caa ggc atc aac tac atc ctg ggc ctg gaa     1008
Val Ile Ile Gly Val Val Gln Gly Ile Asn Tyr Ile Leu Gly Leu Glu
                325                 330                 335

tag                                                                 1011
 *
```

<210> 58
<211> 336
<212> PRT
<213> Homo sapiens

<400> 58

```
Met Gly Thr Ser Asp Ser His His Ala Gly Leu Ser Leu Val Ser Arg
 1               5                  10                  15
Arg Pro Ser Gly Gly Ala Ala Gly Glu Arg Glu Leu Asp Glu Val Asp
            20                  25                  30
Met Ser Asp Leu Ser Pro Glu Glu Gln Trp Arg Val Glu His Ala Arg
        35                  40                  45
Met His Ala Lys His Arg Gly His Glu Ala Met His Ala Glu Met Val
    50                  55                  60
Leu Ile Leu Ile Ala Thr Leu Val Val Ala Gln Leu Leu Leu Val Gln
65                  70                  75                  80
Trp Lys Gln Arg His Pro Arg Ser Tyr Asn Met Val Thr Leu Phe Gln
                85                  90                  95
Met Trp Val Val Pro Leu Tyr Phe Thr Val Lys Leu His Trp Trp Arg
            100                 105                 110
Phe Leu Val Ile Trp Ile Leu Phe Ser Ala Val Thr Ala Phe Val Thr
        115                 120                 125
```

```
Phe Arg Ala Thr Arg Lys Pro Leu Val Gln Thr Thr Pro Arg Leu Val
    130                 135                 140
Tyr Lys Trp Phe Leu Leu Ile Tyr Lys Ile Ser Tyr Ala Thr Gly Ile
145                 150                 155                 160
Val Gly Tyr Met Ala Val Met Phe Thr Leu Phe Gly Leu Asn Leu Leu
                165                 170                 175
Phe Lys Ile Lys Pro Glu Asp Ala Met Asp Phe Gly Ile Ser Leu Leu
            180                 185                 190
Phe Tyr Gly Leu Tyr Tyr Gly Val Leu Glu Arg Asp Phe Ala Glu Met
        195                 200                 205
Cys Ala Asp Tyr Met Ala Ser Thr Ile Gly Phe Tyr Ser Glu Ser Gly
    210                 215                 220
Met Pro Thr Lys His Leu Ser Asp Ser Val Cys Ala Val Cys Gly Gln
225                 230                 235                 240
Gln Ile Phe Val Asp Val Ser Glu Glu Gly Ile Ile Glu Asn Thr Tyr
                245                 250                 255
Arg Leu Ser Cys Asn His Val Phe His Glu Phe Cys Ile Arg Gly Trp
            260                 265                 270
Cys Ile Val Gly Lys Lys Gln Thr Cys Pro Tyr Cys Lys Glu Lys Val
        275                 280                 285
Asp Leu Lys Arg Met Phe Ser Asn Pro Trp Glu Arg Pro His Val Met
    290                 295                 300
Tyr Gly Gln Leu Leu Asp Trp Leu Arg Tyr Leu Val Ala Trp Gln Pro
305                 310                 315                 320
Val Ile Ile Gly Val Val Gln Gly Ile Asn Tyr Ile Leu Gly Leu Glu
                325                 330                 335

      <210> 59
      <211> 393
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(393)

      <221> misc_feature
      <222> (1)...(393)
      <223> n = A,T,C or G

      <400> 59
atg ctg gac ttg cag aag cag ctg ggc aga tnc cag ggn gcc ana ttt      48
Met Leu Asp Leu Gln Lys Gln Leu Gly Arg Xaa Gln Xaa Ala Xaa Phe
 1               5                  10                  15
```

```
ccc ggc acc ttc gtg ggc acc aca gag ccc gcc tcc cca ccc ctg agc       96
Pro Gly Thr Phe Val Gly Thr Thr Glu Pro Ala Ser Pro Pro Leu Ser
            20                  25                  30

agc acc tca ccc acc act gct gcg gcc act atg cct gtg gtg ccc tct      144
Ser Thr Ser Pro Thr Thr Ala Ala Ala Thr Met Pro Val Val Pro Ser
        35                  40                  45

gtg gcc agc ctg gcc cct ccg ggg gag gcc tcg ctc tgc ctg gaa gag      192
Val Ala Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu
    50                  55                  60

gtg gcc ccc cct gcc agt ggg acc cgc aaa gct cgg gtg ctc tat gac      240
Val Ala Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp
65                  70                  75                  80

tac gag gca gcc gac agc agt gag ctg gcc ctg ctg gct gat gag ctc      288
Tyr Glu Ala Ala Asp Ser Ser Glu Leu Ala Leu Leu Ala Asp Glu Leu
                85                  90                  95

atc act gtc tac agc ctg cct ggc atg gac cct gac tgg ctc att ggc      336
Ile Thr Val Tyr Ser Leu Pro Gly Met Asp Pro Asp Trp Leu Ile Gly
            100                 105                 110

gag aga ggc aac aag aag ggc aag gtc cct gtc acc tac ttg gaa ctg      384
Glu Arg Gly Asn Lys Lys Gly Lys Val Pro Val Thr Tyr Leu Glu Leu
        115                 120                 125

ctc agc tag                                                          393
Leu Ser  *
    130
```

```
<210> 60
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(130)
<223> Xaa = Any Amino Acid
```

<400> 60
Met Leu Asp Leu Gln Lys Gln Leu Gly Arg Xaa Gln Xaa Ala Xaa Phe
1 5 10 15
Pro Gly Thr Phe Val Gly Thr Thr Glu Pro Ala Ser Pro Pro Leu Ser
20 25 30
Ser Thr Ser Pro Thr Thr Ala Ala Ala Thr Met Pro Val Val Pro Ser
35 40 45
Val Ala Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu
50 55 60
Val Ala Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp
65 70 75 80
Tyr Glu Ala Ala Asp Ser Ser Glu Leu Ala Leu Leu Ala Asp Glu Leu
85 90 95
Ile Thr Val Tyr Ser Leu Pro Gly Met Asp Pro Asp Trp Leu Ile Gly
100 105 110
Glu Arg Gly Asn Lys Lys Gly Lys Val Pro Val Thr Tyr Leu Glu Leu
115 120 125
Leu Ser
130

<210> 61
<211> 1383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1383)

<221> misc_feature
<222> (1)...(1383)
<223> n = A,T,C or G

<400> 61
atg gcc ccg ggt cgc gcg gtg gcc ggg ctc ctg ttg ctg gcg gcc gcc 48
Met Ala Pro Gly Arg Ala Val Ala Gly Leu Leu Leu Leu Ala Ala Ala
1 5 10 15

gnc ctc gga gga gtg gcg gag ggg cca ggg cta gcc ttc agc gag gat 96
Xaa Leu Gly Gly Val Ala Glu Gly Pro Gly Leu Ala Phe Ser Glu Asp
20 25 30

gtg ctg agc gtg ttc ggc gcg aat ctg agc ctg tcg gcg gcg cag ctc 144
Val Leu Ser Val Phe Gly Ala Asn Leu Ser Leu Ser Ala Ala Gln Leu

```
        35                  40                  45

cag cac ttg ctg gag cag atg gga gcc gcc tcc cgc gtg ggc gtc ccg      192
Gln His Leu Leu Glu Gln Met Gly Ala Ala Ser Arg Val Gly Val Pro
    50                  55                  60

gag cct ggc cag ctg cac ttc aac cag tgt tta act gct gaa gag atc      240
Glu Pro Gly Gln Leu His Phe Asn Gln Cys Leu Thr Ala Glu Glu Ile
65                  70                  75                  80

ttt tcc ctt cat ggc ttt tca aat gct acc caa ata acc agc tcc aaa      288
Phe Ser Leu His Gly Phe Ser Asn Ala Thr Gln Ile Thr Ser Ser Lys
                85                  90                  95

ttc tct gtc atc tgt cca gca gtc tta cag caa ttg aac ttt cac cca      336
Phe Ser Val Ile Cys Pro Ala Val Leu Gln Gln Leu Asn Phe His Pro
            100                 105                 110

tgt gag gat cgg ccc aag cac aaa aca aga cca agt cat tca gaa gtt      384
Cys Glu Asp Arg Pro Lys His Lys Thr Arg Pro Ser His Ser Glu Val
        115                 120                 125

tgg gga tat gga ttc ctg tca gtg acg att att aat ctg gca tct ctc      432
Trp Gly Tyr Gly Phe Leu Ser Val Thr Ile Ile Asn Leu Ala Ser Leu
    130                 135                 140

ctc gga ttg att ttg act cca ctg ata aag aaa tct tat ttc cca aag      480
Leu Gly Leu Ile Leu Thr Pro Leu Ile Lys Lys Ser Tyr Phe Pro Lys
145                 150                 155                 160

att ttg acc ttt ttt gtg ggg ctg gct att ggg act ctt ttt tca aat      528
Ile Leu Thr Phe Phe Val Gly Leu Ala Ile Gly Thr Leu Phe Ser Asn
                165                 170                 175

gca att ttc caa ctt att cca gag gca ttt gga ttt gat ccc aaa gtc      576
Ala Ile Phe Gln Leu Ile Pro Glu Ala Phe Gly Phe Asp Pro Lys Val
            180                 185                 190

gac agt tat gtt gag aag gca gtt gct gtg ttt ggt gga ttt tac cta      624
Asp Ser Tyr Val Glu Lys Ala Val Ala Val Phe Gly Gly Phe Tyr Leu
        195                 200                 205

ctt ttc ttt ttt gaa aga atg cta aag atg tta tta aag aca tat ggt      672
Leu Phe Phe Phe Glu Arg Met Leu Lys Met Leu Leu Lys Thr Tyr Gly
```

```
    210                 215                 220

cag aat ggt cat acc cac ttt gga aat gat aac ttt ggt cct caa gaa       720
Gln Asn Gly His Thr His Phe Gly Asn Asp Asn Phe Gly Pro Gln Glu
225                 230                 235                 240

aaa act cat caa cct aaa gca tta cct gcc atc aat ggt gtg aca tgc       768
Lys Thr His Gln Pro Lys Ala Leu Pro Ala Ile Asn Gly Val Thr Cys
                245                 250                 255

tat gca aat cct gct gtc aca gaa gct aat gga cat atc cat ttt gat       816
Tyr Ala Asn Pro Ala Val Thr Glu Ala Asn Gly His Ile His Phe Asp
            260                 265                 270

aat gtc agt gtg gta tct cta cag gat gga aaa aaa gag cca agt tca       864
Asn Val Ser Val Val Ser Leu Gln Asp Gly Lys Lys Glu Pro Ser Ser
        275                 280                 285

tgt acc tgt ttg aag ggg ccc aaa ctg tca gaa ata ggg acg att gcc       912
Cys Thr Cys Leu Lys Gly Pro Lys Leu Ser Glu Ile Gly Thr Ile Ala
    290                 295                 300

tgg atg ata acg ctc tgc gat gcc ctc cac aat ttc atc gat ggc ctg       960
Trp Met Ile Thr Leu Cys Asp Ala Leu His Asn Phe Ile Asp Gly Leu
305                 310                 315                 320

gcg att ggg gct tcc tgc acc ttg tct ctc ctt cag gga ctc agt act      1008
Ala Ile Gly Ala Ser Cys Thr Leu Ser Leu Leu Gln Gly Leu Ser Thr
                325                 330                 335

tcc ata gca atc cta tgt gag gag ttt ccc cac gag tta gga gac ttt      1056
Ser Ile Ala Ile Leu Cys Glu Glu Phe Pro His Glu Leu Gly Asp Phe
            340                 345                 350

gtg atc cta ctc aat gca ggg atg agc act cga caa gcc ttg cta ttc      1104
Val Ile Leu Leu Asn Ala Gly Met Ser Thr Arg Gln Ala Leu Leu Phe
        355                 360                 365

aac ttc ctt tct gca tgt tcc tgc tat gtt ggg cta gct ttt ggc att      1152
Asn Phe Leu Ser Ala Cys Ser Cys Tyr Val Gly Leu Ala Phe Gly Ile
    370                 375                 380

ttg gtg ggc aac aat ttc gct cca aat att ata ttt gca ctt gct gga      1200
Leu Val Gly Asn Asn Phe Ala Pro Asn Ile Ile Phe Ala Leu Ala Gly
```

385 390 395 400

ggc atg ttc ctc tat att tct ctg gca gat atg ttt cca gag atg aat 1248
Gly Met Phe Leu Tyr Ile Ser Leu Ala Asp Met Phe Pro Glu Met Asn
405 410 415

gat atg ctg aga gaa aag gta act gga aga aaa acc gat ttc acc ttc 1296
Asp Met Leu Arg Glu Lys Val Thr Gly Arg Lys Thr Asp Phe Thr Phe
420 425 430

ttc atg att cag aat gct gga atg tta act gga ttc aca gcc att cta 1344
Phe Met Ile Gln Asn Ala Gly Met Leu Thr Gly Phe Thr Ala Ile Leu
435 440 445

ctc att acc ttg tat gca gga gaa atc gaa ttg gag taa 1383
Leu Ile Thr Leu Tyr Ala Gly Glu Ile Glu Leu Glu *
450 455 460

<210> 62
<211> 460
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(460)
<223> Xaa = Any Amino Acid

<400> 62
Met Ala Pro Gly Arg Ala Val Ala Gly Leu Leu Leu Leu Ala Ala Ala
1 5 10 15
Xaa Leu Gly Gly Val Ala Glu Gly Pro Gly Leu Ala Phe Ser Glu Asp
20 25 30
Val Leu Ser Val Phe Gly Ala Asn Leu Ser Leu Ser Ala Ala Gln Leu
35 40 45
Gln His Leu Leu Glu Gln Met Gly Ala Ala Ser Arg Val Gly Val Pro
50 55 60
Glu Pro Gly Gln Leu His Phe Asn Gln Cys Leu Thr Ala Glu Glu Ile
65 70 75 80
Phe Ser Leu His Gly Phe Ser Asn Ala Thr Gln Ile Thr Ser Ser Lys
85 90 95
Phe Ser Val Ile Cys Pro Ala Val Leu Gln Gln Leu Asn Phe His Pro
100 105 110

Cys Glu Asp Arg Pro Lys His Lys Thr Arg Pro Ser His Ser Glu Val
115 120 125
Trp Gly Tyr Gly Phe Leu Ser Val Thr Ile Ile Asn Leu Ala Ser Leu
130 135 140
Leu Gly Leu Ile Leu Thr Pro Leu Ile Lys Lys Ser Tyr Phe Pro Lys
145 150 155 160
Ile Leu Thr Phe Phe Val Gly Leu Ala Ile Gly Thr Leu Phe Ser Asn
165 170 175
Ala Ile Phe Gln Leu Ile Pro Glu Ala Phe Gly Phe Asp Pro Lys Val
180 185 190
Asp Ser Tyr Val Glu Lys Ala Val Ala Val Phe Gly Gly Phe Tyr Leu
195 200 205
Leu Phe Phe Phe Glu Arg Met Leu Lys Met Leu Leu Lys Thr Tyr Gly
210 215 220
Gln Asn Gly His Thr His Phe Gly Asn Asp Asn Phe Gly Pro Gln Glu
225 230 235 240
Lys Thr His Gln Pro Lys Ala Leu Pro Ala Ile Asn Gly Val Thr Cys
245 250 255
Tyr Ala Asn Pro Ala Val Thr Glu Ala Asn Gly His Ile His Phe Asp
260 265 270
Asn Val Ser Val Val Ser Leu Gln Asp Gly Lys Lys Glu Pro Ser Ser
275 280 285
Cys Thr Cys Leu Lys Gly Pro Lys Leu Ser Glu Ile Gly Thr Ile Ala
290 295 300
Trp Met Ile Thr Leu Cys Asp Ala Leu His Asn Phe Ile Asp Gly Leu
305 310 315 320
Ala Ile Gly Ala Ser Cys Thr Leu Ser Leu Leu Gln Gly Leu Ser Thr
325 330 335
Ser Ile Ala Ile Leu Cys Glu Glu Phe Pro His Glu Leu Gly Asp Phe
340 345 350
Val Ile Leu Leu Asn Ala Gly Met Ser Thr Arg Gln Ala Leu Leu Phe
355 360 365
Asn Phe Leu Ser Ala Cys Ser Cys Tyr Val Gly Leu Ala Phe Gly Ile
370 375 380
Leu Val Gly Asn Asn Phe Ala Pro Asn Ile Ile Phe Ala Leu Ala Gly
385 390 395 400
Gly Met Phe Leu Tyr Ile Ser Leu Ala Asp Met Phe Pro Glu Met Asn
405 410 415
Asp Met Leu Arg Glu Lys Val Thr Gly Arg Lys Thr Asp Phe Thr Phe
420 425 430
Phe Met Ile Gln Asn Ala Gly Met Leu Thr Gly Phe Thr Ala Ile Leu
435 440 445
Leu Ile Thr Leu Tyr Ala Gly Glu Ile Glu Leu Glu
450 455 460

<210> 63
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(378)

<400> 63
```
atg ctg aca gaa gtc atg gag gtc tgg cat ggc tta gtg atc gcg gtg        48
Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1               5                  10                  15

gtg tcc ctc ttc ctg cag gcc tgc ttc ctc acc gcc atc aac tac ctg        96
Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
            20                  25                  30

ctc agc agg cac atg gcc cac aag agt gaa cag ata ctg aaa gcg gcc       144
Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
        35                  40                  45

agt ctc cag gtt ccc agg ccc agc cct ggc cac cat cat cca cct gct       192
Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
    50                  55                  60

gtc aaa gag atg aag gag act cag aca gag aga gac atc cca atg tct       240
Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
 65                  70                  75                  80

gat tcc ctt tac agg cat gac agc gac aca ccc tca gat agc ttg gat       288
Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
                85                  90                  95

agc tcc tgc agt tcg cct cct gcc tgc cag gcc aca gag gat gtg gat       336
Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
            100                 105                 110

tac aca caa gtc gtc ttt tct gac cct gga gaa cta aaa tga               378
Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys  *
        115                 120                 125
```

<210> 64
<211> 125
<212> PRT
<213> Homo sapiens

<400> 64
Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
1 5 10 15
Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
20 25 30
Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
35 40 45
Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
50 55 60
Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
65 70 75 80
Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
85 90 95
Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
100 105 110
Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys
115 120 125

<210> 65
<211> 519
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(519)

<400> 65
atg ctg aca gaa gtc atg gag gtc tgg cat ggc tta gtg atc gcg gtg 48
Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
1 5 10 15

gtg tcc ctc ttc ctg cag gcc tgc ttc ctc acc gcc atc aac tac ctg 96
Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
20 25 30

ctc agc agg cac atg gcc cac aag agt gaa cag ata ctg aaa gcg gcc 144
Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
35 40 45

```
agt ctc cag gtt ccc agg ccc agc cct ggc cac cat cat cca cct gct      192
Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
     50                  55                  60

gtc aaa gag atg aag gag act cag aca gag aga gac atc cca atg tct      240
Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
 65                  70                  75                  80

gat tcc ctt tac agg cat gac agc gac aca ccc tca gat agc ttg gat      288
Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
                 85                  90                  95

agc tcc tgc agt tcg cct cct gcc tgc cag gcc aca gag gat gtg gat      336
Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
            100                 105                 110

tac aca caa gtc gtc ttt tct gac cct gga gaa cta aaa aat gac tcc      384
Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys Asn Asp Ser
        115                 120                 125

ccg ctg gac tat gag aac ata aag gaa atc aca gat tat gtc aat gtc      432
Pro Leu Asp Tyr Glu Asn Ile Lys Glu Ile Thr Asp Tyr Val Asn Val
    130                 135                 140

aat cca gaa aga cac aag ccc agt ttc tgg tat ttt gtc aac cct gct      480
Asn Pro Glu Arg His Lys Pro Ser Phe Trp Tyr Phe Val Asn Pro Ala
145                 150                 155                 160

ctg tct gag cca gcg gaa tat gat caa gtg gcc atg tga                  519
Leu Ser Glu Pro Ala Glu Tyr Asp Gln Val Ala Met  *
                165                 170
```

<210> 66
<211> 172
<212> PRT
<213> Homo sapiens

<400> 66

```
Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1               5                  10                  15
Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
            20                  25                  30
```

Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
35 40 45
Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
50 55 60
Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
65 70 75 80
Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
85 90 95
Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
100 105 110
Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys Asn Asp Ser
115 120 125
Pro Leu Asp Tyr Glu Asn Ile Lys Glu Ile Thr Asp Tyr Val Asn Val
130 135 140
Asn Pro Glu Arg His Lys Pro Ser Phe Trp Tyr Phe Val Asn Pro Ala
145 150 155 160
Leu Ser Glu Pro Ala Glu Tyr Asp Gln Val Ala Met
165 170

<210> 67
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(393)

<400> 67
atg caa gca gag gct ggg gac ctc agc aca gcc ctg gag agg ttt ggc 48
Met Gln Ala Glu Ala Gly Asp Leu Ser Thr Ala Leu Glu Arg Phe Gly
1 5 10 15

caa gcc atc tgc ctg ctg cct gag agg gct tca gcc tac aac aac cgt 96
Gln Ala Ile Cys Leu Leu Pro Glu Arg Ala Ser Ala Tyr Asn Asn Arg
20 25 30

gcc cag gcc cgg cga ctc cag gga gac gtg gca ggc gcc ctg gag gat 144
Ala Gln Ala Arg Arg Leu Gln Gly Asp Val Ala Gly Ala Leu Glu Asp
35 40 45

ctg gaa cgc gcg gtg gag ctg agc ggc ggc cgg ggc cgc gcc gcc cgc 192
Leu Glu Arg Ala Val Glu Leu Ser Gly Gly Arg Gly Arg Ala Ala Arg
50 55 60

```
cag agc ttt gtg cag cgc gga ctc ctg gcg cgg ctg cag ggc cga gac        240
Gln Ser Phe Val Gln Arg Gly Leu Leu Ala Arg Leu Gln Gly Arg Asp
 65                 70                  75                  80

gac gac gcc cgc agg gac ttc gag agg gcg gca cgg ctg ggc agc ccc        288
Asp Asp Ala Arg Arg Asp Phe Glu Arg Ala Ala Arg Leu Gly Ser Pro
                85                  90                  95

ttc gcg cgg cgc cag ctg gtg ctg ctc aac ccc tac gcc gcg ctg tgc        336
Phe Ala Arg Arg Gln Leu Val Leu Leu Asn Pro Tyr Ala Ala Leu Cys
            100                 105                 110

aac cgc atg ctg gcc gac atg atg ggg cag ctg cgc cgc ccc cgt gac        384
Asn Arg Met Leu Ala Asp Met Met Gly Gln Leu Arg Arg Pro Arg Asp
        115                 120                 125

agc cgc tga                                                            393
Ser Arg  *
    130


      <210> 68
      <211> 130
      <212> PRT
      <213> Homo sapiens

      <400> 68
Met Gln Ala Glu Ala Gly Asp Leu Ser Thr Ala Leu Glu Arg Phe Gly
1               5                   10                  15
Gln Ala Ile Cys Leu Leu Pro Glu Arg Ala Ser Ala Tyr Asn Asn Arg
            20                  25                  30
Ala Gln Ala Arg Arg Leu Gln Gly Asp Val Ala Gly Ala Leu Glu Asp
        35                  40                  45
Leu Glu Arg Ala Val Glu Leu Ser Gly Gly Arg Gly Arg Ala Ala Arg
    50                  55                  60
Gln Ser Phe Val Gln Arg Gly Leu Leu Ala Arg Leu Gln Gly Arg Asp
65                  70                  75                  80
Asp Asp Ala Arg Arg Asp Phe Glu Arg Ala Ala Arg Leu Gly Ser Pro
                85                  90                  95
Phe Ala Arg Arg Gln Leu Val Leu Leu Asn Pro Tyr Ala Ala Leu Cys
            100                 105                 110
Asn Arg Met Leu Ala Asp Met Met Gly Gln Leu Arg Arg Pro Arg Asp
        115                 120                 125
```

Ser Arg
130

<210> 69
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(378)

<400> 69
atg agg cca cga tgc tgc atc ttg gct ctt gtc tgc tgg ata aca gtc 48
Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr Val
1 5 10 15

ttc ctc ctc cag tgt tca aaa gga act aca gac gct cct gtt ggc tca 96
Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val Gly Ser
20 25 30

gga ctg tgg ctg tgc cag ccg aca ccc agg tgt ggg aac aag atc tac 144
Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn Lys Ile Tyr
35 40 45

aac cct tca gag cag tgc tgt tat gat gat gcc atc tta tcc tta aag 192
Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile Leu Ser Leu Lys
50 55 60

gag acc cgc cgc tgt ggc tcc acc tgc acc ttc tgg ccc tgc ttt gag 240
Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe Trp Pro Cys Phe Glu
65 70 75 80

ctc tgc tgt ccc gag tct ttt ggc ccc cag cag aag ttt ctt gtg aag 288
Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln Gln Lys Phe Leu Val Lys
85 90 95

ttg agg gtt ctg ggt atg aag tct cag tgt cac tta tct ccc atc tcc 336
Leu Arg Val Leu Gly Met Lys Ser Gln Cys His Leu Ser Pro Ile Ser
100 105 110

cgg agc tgt acc agg aac agg agg cac gtc ctg tac cca taa 378
Arg Ser Cys Thr Arg Asn Arg Arg His Val Leu Tyr Pro *
115 120 125

<210> 70
<211> 125
<212> PRT
<213> Homo sapiens

<400> 70
Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr Val
1 5 10 15
Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val Gly Ser
20 25 30
Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn Lys Ile Tyr
35 40 45
Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile Leu Ser Leu Lys
50 55 60
Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe Trp Pro Cys Phe Glu
65 70 75 80
Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln Gln Lys Phe Leu Val Lys
85 90 95
Leu Arg Val Leu Gly Met Lys Ser Gln Cys His Leu Ser Pro Ile Ser
100 105 110
Arg Ser Cys Thr Arg Asn Arg Arg His Val Leu Tyr Pro
115 120 125

<210> 71
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(657)

<400> 71
atg gct caa gag aaa gat tgc caa gga atc atc gag gac gtc atc ctg 48
Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu
1 5 10 15

ctg ggt gcg cct gtg gag gga gaa gcc aag cat tgg gag cct ttc cgg 96
Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg
20 25 30

aag gtg gtg tcc ggg agg atc atc aac ggc tac tgc agg gga gac tgg 144

```
Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp Trp
        35                  40                  45

ctg ctg agt ttc gtg tac cgc aca tcc tcg gtg cag ctc cac gtc gcc      192
Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val Ala
    50                  55                  60

ggc cta cag ccc gtg ctg ctg cag gac agg agg gtg gag aac gtg gac      240
Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val Asp
65                  70                  75                  80

ctg acc tct gtg gtc agc ggc cac ctg gac tat gcc aag cag atg gat      288
Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met Asp
                85                  90                  95

gcc atc ctg aag gcc gtg ggc atc cgc acc aag cca ggc tgg gac gag      336
Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp Glu
            100                 105                 110

aag ggg ctc ttg ctg gcc cca ggc tgc ctg ccc tcc gag gag cct cgc      384
Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro Arg
        115                 120                 125

cag gca gca gct gcc gcc tca tca ggc gag acc ccc cac cag gtt ggg      432
Gln Ala Ala Ala Ala Ala Ser Ser Gly Glu Thr Pro His Gln Val Gly
    130                 135                 140

caa acc cag ggt ccc ata tcc gga gac acc tcc aaa ttg gcc atg tcc      480
Gln Thr Gln Gly Pro Ile Ser Gly Asp Thr Ser Lys Leu Ala Met Ser
145                 150                 155                 160

aca gac ccc agc caa gcc cag gtg cca gta ggg ctg gac cag tct gaa      528
Thr Asp Pro Ser Gln Ala Gln Val Pro Val Gly Leu Asp Gln Ser Glu
                165                 170                 175

ggg gcc tcc ctt cct gct gct gcc agc cct gaa agg ccc ccc atc tgc      576
Gly Ala Ser Leu Pro Ala Ala Ala Ser Pro Glu Arg Pro Pro Ile Cys
            180                 185                 190

agc cat ggc atg gac ccc aac cca ctg ggc tgc ccc gat tgt gcc tgc      624
Ser His Gly Met Asp Pro Asn Pro Leu Gly Cys Pro Asp Cys Ala Cys
        195                 200                 205

aag acc cag ggc ccc agc acg ggg ctg gac tga                          657
```

Lys Thr Gln Gly Pro Ser Thr Gly Leu Asp *
210 215

<210> 72
<211> 218
<212> PRT
<213> Homo sapiens

<400> 72
Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu
1 5 10 15
Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg
20 25 30
Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp Trp
35 40 45
Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val Ala
50 55 60
Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val Asp
65 70 75 80
Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met Asp
85 90 95
Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp Glu
100 105 110
Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro Arg
115 120 125
Gln Ala Ala Ala Ala Ala Ser Ser Gly Glu Thr Pro His Gln Val Gly
130 135 140
Gln Thr Gln Gly Pro Ile Ser Gly Asp Thr Ser Lys Leu Ala Met Ser
145 150 155 160
Thr Asp Pro Ser Gln Ala Gln Val Pro Val Gly Leu Asp Gln Ser Glu
165 170 175
Gly Ala Ser Leu Pro Ala Ala Ala Ser Pro Glu Arg Pro Pro Ile Cys
180 185 190
Ser His Gly Met Asp Pro Asn Pro Leu Gly Cys Pro Asp Cys Ala Cys
195 200 205
Lys Thr Gln Gly Pro Ser Thr Gly Leu Asp
210 215

<210> 73
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(441)

<400> 73

```
atg ttg ttg gcc ctg gtc tgt ctg ctc agc tgc ctg cta ccc tcc agt      48
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser Ser
 1               5                  10                  15

gag gcc aag ctc tac ggt cgt tgt gaa ctg gcc aga gtg cta cat gac      96
Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu His Asp
            20                  25                  30

ttc ggg ctg gac gga tac cgg gga tac agc ctg gct gac tgg gtc tgc     144
Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp Trp Val Cys
        35                  40                  45

ctt gct tat ttc aca agc ggt ttc aac gca gct gct ttg gac tac gag     192
Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala Leu Asp Tyr Glu
    50                  55                  60

gct gat ggg agc acc aac aac ggg atc ttc cag atc aac agc cgg agg     240
Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln Ile Asn Ser Arg Arg
 65                  70                  75                  80

tgg tgc agc aac ctc acc ccg aac gtc ccc aac gtg tgc cgg atg tac     288
Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn Val Cys Arg Met Tyr
                 85                  90                  95

tgc tca gat ttg ttg aat cct aat ctc aag gat acc gtt atc tgt gcc     336
Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp Thr Val Ile Cys Ala
            100                 105                 110

atg aag ata acc caa gag cct cag ggt ctg ggt tac tgg gag gcc tgg     384
Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly Tyr Trp Glu Ala Trp
        115                 120                 125

agg cat cac tgc cag gga aaa gac ctc act gaa tgg gtg gat ggc tgt     432
Arg His His Cys Gln Gly Lys Asp Leu Thr Glu Trp Val Asp Gly Cys
    130                 135                 140

gac ttc tag                                                         441
Asp Phe  *
145
```

<210> 74
<211> 146
<212> PRT
<213> Homo sapiens

<400> 74
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser Ser
1 5 10 15
Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu His Asp
20 25 30
Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp Trp Val Cys
35 40 45
Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala Leu Asp Tyr Glu
50 55 60
Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln Ile Asn Ser Arg Arg
65 70 75 80
Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn Val Cys Arg Met Tyr
85 90 95
Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp Thr Val Ile Cys Ala
100 105 110
Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly Tyr Trp Glu Ala Trp
115 120 125
Arg His His Cys Gln Gly Lys Asp Leu Thr Glu Trp Val Asp Gly Cys
130 135 140
Asp Phe
145

<210> 75
<211> 345
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(345)

<400> 75
atg ctg tgc ttc ctg agg gga atg gct ttc gtc ccc ttc ctc ttg gtg 48
Met Leu Cys Phe Leu Arg Gly Met Ala Phe Val Pro Phe Leu Leu Val
1 5 10 15

acc tgg tcg tca gcc gcc ttc att atc tcc tac gtg gtc gcc gtg ctc 96

Thr Trp Ser Ser Ala Ala Phe Ile Ile Ser Tyr Val Val Ala Val Leu
20 25 30

tcc ggg cac gtc aac ccc ttc ctc ccg tat atc agt gat acg gga aca 144
Ser Gly His Val Asn Pro Phe Leu Pro Tyr Ile Ser Asp Thr Gly Thr
35 40 45

aca cct cca gag agt ggt att ttt gga ttt atg ata aac ttc tct gca 192
Thr Pro Pro Glu Ser Gly Ile Phe Gly Phe Met Ile Asn Phe Ser Ala
50 55 60

ttt ctt ggt gca gcc acg atg tat aca aga tac aaa ata gta cag aag 240
Phe Leu Gly Ala Ala Thr Met Tyr Thr Arg Tyr Lys Ile Val Gln Lys
65 70 75 80

caa aat caa acc tgc tat ttc agc act cct gtt ttt aac ttg gtg tct 288
Gln Asn Gln Thr Cys Tyr Phe Ser Thr Pro Val Phe Asn Leu Val Ser
85 90 95

tta gtg ctt gga ttg gtg gga tgt ttc gga atg ggc att gtc gcc aat 336
Leu Val Leu Gly Leu Val Gly Cys Phe Gly Met Gly Ile Val Ala Asn
100 105 110

ttt cag tga 345
Phe Gln *

<210> 76
<211> 114
<212> PRT
<213> Homo sapiens

<400> 76
Met Leu Cys Phe Leu Arg Gly Met Ala Phe Val Pro Phe Leu Leu Val
1 5 10 15
Thr Trp Ser Ser Ala Ala Phe Ile Ile Ser Tyr Val Val Ala Val Leu
20 25 30
Ser Gly His Val Asn Pro Phe Leu Pro Tyr Ile Ser Asp Thr Gly Thr
35 40 45
Thr Pro Pro Glu Ser Gly Ile Phe Gly Phe Met Ile Asn Phe Ser Ala
50 55 60
Phe Leu Gly Ala Ala Thr Met Tyr Thr Arg Tyr Lys Ile Val Gln Lys
65 70 75 80

Gln Asn Gln Thr Cys Tyr Phe Ser Thr Pro Val Phe Asn Leu Val Ser
85 90 95
Leu Val Leu Gly Leu Val Gly Cys Phe Gly Met Gly Ile Val Ala Asn
100 105 110
Phe Gln

<210> 77
<211> 972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(972)

<400> 77
atg ccc cta tta aaa ctt gta cat ggc tcc cca ttg gtt ttt gga gaa 48
Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
1 5 10 15

aag ttc aag ctt ttt acc ttg gtg tct gcc tgt atc cca gtg ttc agg 96
Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
20 25 30

ctg gct aga cgg cgg aag aag atc cta ttt tac tgt cac ttc cca gat 144
Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
35 40 45

ctg ctt ctc acc aag aga gat tct ttt ctt aaa cga cta tac agg gcc 192
Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
50 55 60

cca att gac tgg ata gag gaa tac acc aca ggc atg gca gac tgc atc 240
Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
65 70 75 80

tta gtc aac agc cag ttc aca gct gct gtt ttt aag gaa aca ttc aag 288
Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
85 90 95

tcc ctg tct cac ata gac cct gat gtc ctc tat cca tct cta aat gtc 336
Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
100 105 110

```
acc agc ttt gac tca gtt gtt cct gaa aag ctg gat gac cta gtc ccc      384
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
        115                 120                 125

aag ggg aaa aaa ttc ctg ctg ctc tcc atc aac aga tac gaa agg aag      432
Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
    130                 135                 140

aaa aat ctg act ttg gca ctg gaa gcc cta gta cag ctg cgt gga aga      480
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
145                 150                 155                 160

ttg aca tcc caa gat tgg gag agg gtt cat ctg atc gtg gca ggt ggt      528
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
                165                 170                 175

tat gac gag aga gtc ctg gag aat gtg gaa cat tat cag gaa ttg aag      576
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
            180                 185                 190

aaa atg gtc caa cag tcc gac ctt ggc cag tat gtg acc ttc ttg agg      624
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
        195                 200                 205

tct ttc tca gac aaa cag aaa atc tcc ctc ctc cac agc tgc acg tgt      672
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
    210                 215                 220

gtg ctt tac aca cca agc aat gag cac ttt ggc att gtc cct ctg gaa      720
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
225                 230                 235                 240

gcc atg tac atg cag tgc cca gtc att gct gtt aat tcg ggt gga ccc      768
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
                245                 250                 255

ttg gag tcc att gac cac agt gtc aca ggg ttt ctg tgt gag cct gac      816
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
            260                 265                 270

ccg gtg cac ttc tca gaa gca ata gaa aag ttc atc cgt gaa cct tcc      864
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg Glu Pro Ser
        275                 280                 285
```

tta aaa gcc acc atg ggc ctg gct gga aga gcc aga gtg aag gaa aaa 912
Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg Val Lys Glu Lys
290 295 300

ttt tcc cct gaa gca ttt aca gaa cag ctc tac cga tat gtt acc aaa 960
Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr Arg Tyr Val Thr Lys
305 310 315 320

ctg ctg gta taa 972
Leu Leu Val *

<210> 78
<211> 323
<212> PRT
<213> Homo sapiens

<400> 78
Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
1 5 10 15
Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
20 25 30
Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
35 40 45
Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
50 55 60
Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
65 70 75 80
Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
85 90 95
Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
100 105 110
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
115 120 125
Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
130 135 140
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
145 150 155 160
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
165 170 175
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
180 185 190

```
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
        195                 200                 205
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
    210                 215                 220
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
225                 230                 235                 240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
                245                 250                 255
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
            260                 265                 270
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg Glu Pro Ser
        275                 280                 285
Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg Val Lys Glu Lys
    290                 295                 300
Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr Arg Tyr Val Thr Lys
305                 310                 315                 320
Leu Leu Val
```

<210> 79
<211> 891
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(891)
<223>

<221> misc_feature
<222> (1)...(891)
<223> n = A,T,C or G

<400> 79

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atg cac ggg aag act gtg ctg atc acc ggg gcg aac agc ggc ctg ggc      48
Met His Gly Lys Thr Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly
 1               5                  10                  15

cgn tcc acg gcc gcc gag cta ctg cgc ctg gga gcg cgg gtg atc atg      96
Xaa Ser Thr Ala Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met
```

20 25 30

ggc tgc cgg gac cgc gcg cgc gcc gag gag gcg gcg ggt cag ctc cgc 144
Gly Cys Arg Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg
35 40 45

cgc gag ctc cgc cag gcc gcg gag tgc ggc cca gag cct ggc gtc agc 192
Arg Glu Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser
50 55 60

ggg gtg ggc gag ctc ata gtc cgg gag ctg gac ctc gcc tcg ctg cgc 240
Gly Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg
65 70 75 80

tcg gtg cgc gcc ttc tgc cag gaa atg ctc cag gaa gag cct agg ctg 288
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg Leu
85 90 95

gat gtc ttg atc aat aac gca ggg atc ttc cag tgc cct tac atg aag 336
Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr Met Lys
100 105 110

act gaa gat ggg ttt gag atg cag ttc gga gtg aac cat ctg ggg cac 384
Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
115 120 125

ttt cta ctc acc aat ctt ctc ctt gga ctc ctc aaa agt tca gct ccc 432
Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys Ser Ser Ala Pro
130 135 140

agc agg att gtg gta gtt tct tcc aaa ctt tat aaa tac gga gac atc 480
Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr Lys Tyr Gly Asp Ile
145 150 155 160

aat ttt gat gac ttg aac agt gaa caa agc tat aat aaa agc ttt tgt 528
Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser Tyr Asn Lys Ser Phe Cys
165 170 175

tat agc cgg agc aaa ctg gct aac att ctt ttt acc agg gaa cta gcc 576
Tyr Ser Arg Ser Lys Leu Ala Asn Ile Leu Phe Thr Arg Glu Leu Ala
180 185 190

cgc cgc tta gaa ggc aca aat gtc acc gtc aat gtg ttg cat cct ggt 624
Arg Arg Leu Glu Gly Thr Asn Val Thr Val Asn Val Leu His Pro Gly

```
        195                 200                 205

att gta cgg aca aat ctg ggg agg cac ata cac att cca ctg ttg gtc      672
Ile Val Arg Thr Asn Leu Gly Arg His Ile His Ile Pro Leu Leu Val
    210                 215                 220

aaa cca ctc ttc aat ttg gtg tca tgg gct ttt ttc aaa act cca gta      720
Lys Pro Leu Phe Asn Leu Val Ser Trp Ala Phe Phe Lys Thr Pro Val
225                 230                 235                 240

gaa ggt gcc cag act tcc att tat ttg gcc tct tca cct gag gta gaa      768
Glu Gly Ala Gln Thr Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu
                245                 250                 255

gga gtg tca gga aga tac ttt ggg gat tgt aaa gag gaa gaa ctg ttg      816
Gly Val Ser Gly Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu
            260                 265                 270

ccc aaa gct atg gat gaa tct gtt gca aga aaa ctc tgg gat atc agt      864
Pro Lys Ala Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser
        275                 280                 285

gaa gtg atg gtt ggc ctg cta aaa tag                                  891
Glu Val Met Val Gly Leu Leu Lys  *
    290                 295


<210> 80
<211> 296
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(296)
<223> Xaa = Any Amino Acid

<400> 80
Met His Gly Lys Thr Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly
 1               5                  10                  15
Xaa Ser Thr Ala Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met
            20                  25                  30
Gly Cys Arg Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg
        35                  40                  45
```

Arg Glu Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser
    50   55   60
Gly Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg
65   70   75   80
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg Leu
                85   90   95
Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr Met Lys
            100   105   110
Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
        115   120   125
Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys Ser Ser Ala Pro
    130   135   140
Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr Lys Tyr Gly Asp Ile
145   150   155   160
Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser Tyr Asn Lys Ser Phe Cys
                165   170   175
Tyr Ser Arg Ser Lys Leu Ala Asn Ile Leu Phe Thr Arg Glu Leu Ala
            180   185   190
Arg Arg Leu Glu Gly Thr Asn Val Thr Val Asn Val Leu His Pro Gly
        195   200   205
Ile Val Arg Thr Asn Leu Gly Arg His Ile His Ile Pro Leu Leu Val
    210   215   220
Lys Pro Leu Phe Asn Leu Val Ser Trp Ala Phe Phe Lys Thr Pro Val
225   230   235   240
Glu Gly Ala Gln Thr Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu
                245   250   255
Gly Val Ser Gly Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu
            260   265   270
Pro Lys Ala Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser
        275   280   285
Glu Val Met Val Gly Leu Leu Lys
    290   295

<210> 81
<211> 1716
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1716)

<400> 81
atg gta gaa tca att aaa cac tgc att gtg ttg ctg cag att gcc aaa 48

Met Val Glu Ser Ile Lys His Cys Ile Val Leu Leu Gln Ile Ala Lys
1 5 10 15

gac cag agt aat gcg gag aag cac gca gat gga atg ata agt act att 96
Asp Gln Ser Asn Ala Glu Lys His Ala Asp Gly Met Ile Ser Thr Ile
20 25 30

aat ccc gta gat gca ata tat caa cct agt cct ttg gaa cct gtg atc 144
Asn Pro Val Asp Ala Ile Tyr Gln Pro Ser Pro Leu Glu Pro Val Ile
35 40 45

agc aca atg cct tcc cag act gtg tta cct cca gaa cct gtt cag ttg 192
Ser Thr Met Pro Ser Gln Thr Val Leu Pro Pro Glu Pro Val Gln Leu
50 55 60

tgt aag tca gag cag cgt cca tct tcc cta cca gtt gga cct gtg ttg 240
Cys Lys Ser Glu Gln Arg Pro Ser Ser Leu Pro Val Gly Pro Val Leu
65 70 75 80

gct acc ttg gga cat cat cag act cct aca cca aat agt aca ggc agt 288
Ala Thr Leu Gly His His Gln Thr Pro Thr Pro Asn Ser Thr Gly Ser
85 90 95

ggc cat tca cca ccg agt agc agt ctc act tct cca agc cac gtg aac 336
Gly His Ser Pro Pro Ser Ser Ser Leu Thr Ser Pro Ser His Val Asn
100 105 110

ttg tct cca aat aca gtc cca gag ttc tct tac tcc agc agt gaa gat 384
Leu Ser Pro Asn Thr Val Pro Glu Phe Ser Tyr Ser Ser Ser Glu Asp
115 120 125

gaa ttt tat gat gct gat gaa ttc cat caa agt ggc tca tcc cca aag 432
Glu Phe Tyr Asp Ala Asp Glu Phe His Gln Ser Gly Ser Ser Pro Lys
130 135 140

cgc tta ata gat tct tct gga tct gcc tca gtc ctg aca cac agc agc 480
Arg Leu Ile Asp Ser Ser Gly Ser Ala Ser Val Leu Thr His Ser Ser
145 150 155 160

tcg gga aat agt cta aaa cgc cca gat acc aca gaa tca ctt aat tct 528
Ser Gly Asn Ser Leu Lys Arg Pro Asp Thr Thr Glu Ser Leu Asn Ser
165 170 175

tcc ttg tcc aat gga aca agt gat gct gac ctg ttt gat tca cat gat 576

Ser Leu Ser Asn Gly Thr Ser Asp Ala Asp Leu Phe Asp Ser His Asp
180 185 190

gac aga gat gat gat gcg gag gca ggg tct gtg gag gag cac aag agc 624
Asp Arg Asp Asp Asp Ala Glu Ala Gly Ser Val Glu Glu His Lys Ser
195 200 205

gtt atc atg cat ctc ttg tcg cag gtt aga ctt gga atg gat ctt act 672
Val Ile Met His Leu Leu Ser Gln Val Arg Leu Gly Met Asp Leu Thr
210 215 220

aag gta gtt ctt cca acg ttt att ctt gaa aga aga tct ctt tta gaa 720
Lys Val Val Leu Pro Thr Phe Ile Leu Glu Arg Arg Ser Leu Leu Glu
225 230 235 240

atg tat gca gac ttt ttt gca cat ccg gac ctg ttt gtg agc att agt 768
Met Tyr Ala Asp Phe Phe Ala His Pro Asp Leu Phe Val Ser Ile Ser
245 250 255

gac cag aag gat ccc aag gat cga atg gtt cag gtt gtg aaa tgg tac 816
Asp Gln Lys Asp Pro Lys Asp Arg Met Val Gln Val Val Lys Trp Tyr
260 265 270

ctc tca gcc ttt cat gcg gga agg aaa gga tca gtt gcc aaa aag cca 864
Leu Ser Ala Phe His Ala Gly Arg Lys Gly Ser Val Ala Lys Lys Pro
275 280 285

tac aat ccc att ttg ggc gag att ttt cag tgt cat tgg aca tta cca 912
Tyr Asn Pro Ile Leu Gly Glu Ile Phe Gln Cys His Trp Thr Leu Pro
290 295 300

aat gat act gaa gag aac aca gaa cta gtt tca gaa gga cca gtt ccc 960
Asn Asp Thr Glu Glu Asn Thr Glu Leu Val Ser Glu Gly Pro Val Pro
305 310 315 320

tgg gtt tcc aaa aac agt gta aca ttt gtg gct gag cag gtt tcc cat 1008
Trp Val Ser Lys Asn Ser Val Thr Phe Val Ala Glu Gln Val Ser His
325 330 335

cat cca ccc att tca gcc ttt tat gct gag tgt ttt aac aag aag ata 1056
His Pro Pro Ile Ser Ala Phe Tyr Ala Glu Cys Phe Asn Lys Lys Ile
340 345 350

caa ttc aat gct cat atc tgg acc aaa tca aaa ttc ctt ggg atg tca 1104

Gln Phe Asn Ala His Ile Trp Thr Lys Ser Lys Phe Leu Gly Met Ser
355 360 365

att ggg gtg cac aac ata ggg cag ggc tgt gtc tca tgt cta gac tat 1152
Ile Gly Val His Asn Ile Gly Gln Gly Cys Val Ser Cys Leu Asp Tyr
370 375 380

gat gaa cat tac att ctc aca ttc ccc aat ggc tat gga agg tct atc 1200
Asp Glu His Tyr Ile Leu Thr Phe Pro Asn Gly Tyr Gly Arg Ser Ile
385 390 395 400

ctc aca gtg ccc tgg gtg gaa tta gga gga gaa tgc aat att aat tgt 1248
Leu Thr Val Pro Trp Val Glu Leu Gly Gly Glu Cys Asn Ile Asn Cys
405 410 415

tcc aaa aca ggc tat agt gca aat atc atc ttc cac act aaa ccc ttc 1296
Ser Lys Thr Gly Tyr Ser Ala Asn Ile Ile Phe His Thr Lys Pro Phe
420 425 430

tat ggg ggc aag aag cac aga att act gcc gag att ttt tct cca aat 1344
Tyr Gly Gly Lys Lys His Arg Ile Thr Ala Glu Ile Phe Ser Pro Asn
435 440 445

gac aag aag tct ttt tgc tca att gaa ggg gaa tgg aat ggt gtg atg 1392
Asp Lys Lys Ser Phe Cys Ser Ile Glu Gly Glu Trp Asn Gly Val Met
450 455 460

tat gca aaa tat gca aca ggg gaa aat aca gtc ttt gta gat acc aag 1440
Tyr Ala Lys Tyr Ala Thr Gly Glu Asn Thr Val Phe Val Asp Thr Lys
465 470 475 480

aag ttg cct ata atc aag aag aaa gtg agg aag ttg gaa gat cag aac 1488
Lys Leu Pro Ile Ile Lys Lys Lys Val Arg Lys Leu Glu Asp Gln Asn
485 490 495

gag tat gaa tcc cgc agc ctt tgg aag gat gtc act ttc aac tta aaa 1536
Glu Tyr Glu Ser Arg Ser Leu Trp Lys Asp Val Thr Phe Asn Leu Lys
500 505 510

atc aga gac att gat gca gca act gaa gca aag cac agg ctt gaa gaa 1584
Ile Arg Asp Ile Asp Ala Ala Thr Glu Ala Lys His Arg Leu Glu Glu
515 520 525

aga caa aga gca gaa gcc cga gaa agg aag gag aag gaa att cag tgg 1632

Arg Gln Arg Ala Glu Ala Arg Glu Arg Lys Glu Lys Glu Ile Gln Trp
    530   535   540

gag aca agg tta ttt cat gaa gat gga gaa tgc tgg gtt tat gat gaa   1680
Glu Thr Arg Leu Phe His Glu Asp Gly Glu Cys Trp Val Tyr Asp Glu
545   550   555   560

cca tta ctg aaa cgt ctt ggt gct gcc aag cat tag   1716
Pro Leu Leu Lys Arg Leu Gly Ala Ala Lys His *
                565   570

<210> 82
<211> 571
<212> PRT
<213> Homo sapiens

<400> 82
Met Val Glu Ser Ile Lys His Cys Ile Val Leu Leu Gln Ile Ala Lys
1   5   10   15
Asp Gln Ser Asn Ala Glu Lys His Ala Asp Gly Met Ile Ser Thr Ile
            20   25   30
Asn Pro Val Asp Ala Ile Tyr Gln Pro Ser Pro Leu Glu Pro Val Ile
        35   40   45
Ser Thr Met Pro Ser Gln Thr Val Leu Pro Pro Glu Pro Val Gln Leu
    50   55   60
Cys Lys Ser Glu Gln Arg Pro Ser Ser Leu Pro Val Gly Pro Val Leu
65   70   75   80
Ala Thr Leu Gly His His Gln Thr Pro Thr Pro Asn Ser Thr Gly Ser
                85   90   95
Gly His Ser Pro Pro Ser Ser Ser Leu Thr Ser Pro Ser His Val Asn
            100   105   110
Leu Ser Pro Asn Thr Val Pro Glu Phe Ser Tyr Ser Ser Ser Glu Asp
        115   120   125
Glu Phe Tyr Asp Ala Asp Glu Phe His Gln Ser Gly Ser Ser Pro Lys
    130   135   140
Arg Leu Ile Asp Ser Ser Gly Ser Ala Ser Val Leu Thr His Ser Ser
145   150   155   160
Ser Gly Asn Ser Leu Lys Arg Pro Asp Thr Thr Glu Ser Leu Asn Ser
                165   170   175
Ser Leu Ser Asn Gly Thr Ser Asp Ala Asp Leu Phe Asp Ser His Asp
            180   185   190
Asp Arg Asp Asp Asp Ala Glu Ala Gly Ser Val Glu Glu His Lys Ser
        195   200   205

Val Ile Met His Leu Leu Ser Gln Val Arg Leu Gly Met Asp Leu Thr
210 215 220
Lys Val Val Leu Pro Thr Phe Ile Leu Glu Arg Arg Ser Leu Leu Glu
225 230 235 240
Met Tyr Ala Asp Phe Phe Ala His Pro Asp Leu Phe Val Ser Ile Ser
245 250 255
Asp Gln Lys Asp Pro Lys Asp Arg Met Val Gln Val Val Lys Trp Tyr
260 265 270
Leu Ser Ala Phe His Ala Gly Arg Lys Gly Ser Val Ala Lys Lys Pro
275 280 285
Tyr Asn Pro Ile Leu Gly Glu Ile Phe Gln Cys His Trp Thr Leu Pro
290 295 300
Asn Asp Thr Glu Glu Asn Thr Glu Leu Val Ser Glu Gly Pro Val Pro
305 310 315 320
Trp Val Ser Lys Asn Ser Val Thr Phe Val Ala Glu Gln Val Ser His
325 330 335
His Pro Pro Ile Ser Ala Phe Tyr Ala Glu Cys Phe Asn Lys Lys Ile
340 345 350
Gln Phe Asn Ala His Ile Trp Thr Lys Ser Lys Phe Leu Gly Met Ser
355 360 365
Ile Gly Val His Asn Ile Gly Gln Gly Cys Val Ser Cys Leu Asp Tyr
370 375 380
Asp Glu His Tyr Ile Leu Thr Phe Pro Asn Gly Tyr Gly Arg Ser Ile
385 390 395 400
Leu Thr Val Pro Trp Val Glu Leu Gly Gly Glu Cys Asn Ile Asn Cys
405 410 415
Ser Lys Thr Gly Tyr Ser Ala Asn Ile Ile Phe His Thr Lys Pro Phe
420 425 430
Tyr Gly Gly Lys Lys His Arg Ile Thr Ala Glu Ile Phe Ser Pro Asn
435 440 445
Asp Lys Lys Ser Phe Cys Ser Ile Glu Gly Glu Trp Asn Gly Val Met
450 455 460
Tyr Ala Lys Tyr Ala Thr Gly Glu Asn Thr Val Phe Val Asp Thr Lys
465 470 475 480
Lys Leu Pro Ile Ile Lys Lys Lys Val Arg Lys Leu Glu Asp Gln Asn
485 490 495
Glu Tyr Glu Ser Arg Ser Leu Trp Lys Asp Val Thr Phe Asn Leu Lys
500 505 510
Ile Arg Asp Ile Asp Ala Ala Thr Glu Ala Lys His Arg Leu Glu Glu
515 520 525
Arg Gln Arg Ala Glu Ala Arg Glu Arg Lys Glu Lys Glu Ile Gln Trp
530 535 540
Glu Thr Arg Leu Phe His Glu Asp Gly Glu Cys Trp Val Tyr Asp Glu
545 550 555 560

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Pro Leu Leu Lys Arg Leu Gly Ala Ala Lys His
                565                 570

      <210> 83
      <211> 648
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(648)

      <400> 83
atg ctt ttg caa gtt gta cga gaa ggg aag ttc tcg ggg ttt ctg acc        48
Met Leu Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr
 1               5                  10                  15

tcc tgc agc ctc ctc ttg cct cgg gct gcc cag atc ttg gcg gct gag        96
Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu
            20                  25                  30

gct ggc tta cct tcg agc cgt tcc ttc atg gga ttt gct gct ccc ttc       144
Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe
        35                  40                  45

acc aac aag cga aag gct tac tcg gag cgt aga atc atg ggg tac tca       192
Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser
    50                  55                  60

atg cag gag atg tat gag gtg gtg tcc aac gtc cag gag tat cgt gag       240
Met Gln Glu Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu
65                  70                  75                  80

ttt gtg ccc tgg tgt aag aag tct ctg gtg gta tcc agc cgt aag ggt       288
Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly
                85                  90                  95

cat ttg aaa gcc cag ctg gag gtt ggc ttt cca cct gtc atg gaa cgt       336
His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg
            100                 105                 110

tac acc tct gca gtt tcc atg gtc aaa cct cac atg gtc aag gct gtt       384
Tyr Thr Ser Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val
        115                 120                 125
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tgt act gat ggc aag ctc ttc aac cac tta gag act att tgg cga ttc      432
Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe
    130                 135                 140

agc cct ggt att cct gcc tat cct cga acc tgc act gtg gac ttt tcg      480
Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser
145                 150                 155                 160

att tcc ttt gaa ttt cgt tct ctg ctg cac tcc cag ctg gcc acc atg      528
Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met
                165                 170                 175

ttt ttt gat gag gtt gtc aaa cag aat gtt gct gcc ttt gag cgt cgg      576
Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg
            180                 185                 190

gca gcc acc aag ttt ggt cca gaa aca gcc atc ccc cgt gaa ctg atg      624
Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met
        195                 200                 205

ttc cat gag gtg cac cag act tga                                      648
Phe His Glu Val His Gln Thr  *
    210                 215


      <210> 84
      <211> 215
      <212> PRT
      <213> Homo sapiens

      <400> 84
Met Leu Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr
 1               5                  10                  15
Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu
            20                  25                  30
Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe
        35                  40                  45
Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser
    50                  55                  60
Met Gln Glu Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu
65                  70                  75                  80
Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly
                85                  90                  95
```

His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg
100 105 110
Tyr Thr Ser Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val
115 120 125
Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe
130 135 140
Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser
145 150 155 160
Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met
165 170 175
Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg
180 185 190
Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met
195 200 205
Phe His Glu Val His Gln Thr
210 215

<210> 85
<211> 615
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(615)

<400> 85
atg ggg ttt ctg acc tcc tgc agc ctc ctc ttg cct cgg gct gcc cag 48
Met Gly Phe Leu Thr Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln
1 5 10 15

atc ttg gcg gct gag gct ggc tta cct tcg agc cgt tcc ttc atg gga 96
Ile Leu Ala Ala Glu Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly
20 25 30

ttt gct gct ccc ttc acc aac aag cga aag gct tac tcg gag cgt aga 144
Phe Ala Ala Pro Phe Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg
35 40 45

atc atg ggg tac tca atg cag gag atg tat gag gtg gtg tcc aac gtc 192
Ile Met Gly Tyr Ser Met Gln Glu Met Tyr Glu Val Val Ser Asn Val
50 55 60

cag gag tat cgt gag ttt gtg ccc tgg tgt aag aag tct ctg gtg gta 240

Gln Glu Tyr Arg Glu Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val
65 70 75 80

tcc agc cgt aag ggt cat ttg aaa gcc cag ctg gag gtt ggc ttt cca 288
Ser Ser Arg Lys Gly His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro
85 90 95

cct gtc atg gaa cgt tac acc tct gca gtt tcc atg gtc aaa cct cac 336
Pro Val Met Glu Arg Tyr Thr Ser Ala Val Ser Met Val Lys Pro His
100 105 110

atg gtc aag gct gtt tgt act gat ggc aag ctc ttc aac cac tta gag 384
Met Val Lys Ala Val Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu
115 120 125

act att tgg cga ttc agc cct ggt att cct gcc tat cct cga acc tgc 432
Thr Ile Trp Arg Phe Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys
130 135 140

act gtg gac ttt tcg att tcc ttt gaa ttt cgt tct ctg ctg cac tcc 480
Thr Val Asp Phe Ser Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser
145 150 155 160

cag ctg gcc acc atg ttt ttt gat gag gtt gtc aaa cag aat gtt gct 528
Gln Leu Ala Thr Met Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala
165 170 175

gcc ttt gag cgt cgg gca gcc acc aag ttt ggt cca gaa aca gcc atc 576
Ala Phe Glu Arg Arg Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile
180 185 190

ccc cgt gaa ctg atg ttc cat gag gtg cac cag act tga 615
Pro Arg Glu Leu Met Phe His Glu Val His Gln Thr *
195 200

<210> 86
<211> 204
<212> PRT
<213> Homo sapiens

<400> 86
Met Gly Phe Leu Thr Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln
1 5 10 15

Ile Leu Ala Ala Glu Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly
20 25 30
Phe Ala Ala Pro Phe Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg
35 40 45
Ile Met Gly Tyr Ser Met Gln Glu Met Tyr Glu Val Val Ser Asn Val
50 55 60
Gln Glu Tyr Arg Glu Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val
65 70 75 80
Ser Ser Arg Lys Gly His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro
85 90 95
Pro Val Met Glu Arg Tyr Thr Ser Ala Val Ser Met Val Lys Pro His
100 105 110
Met Val Lys Ala Val Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu
115 120 125
Thr Ile Trp Arg Phe Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys
130 135 140
Thr Val Asp Phe Ser Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser
145 150 155 160
Gln Leu Ala Thr Met Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala
165 170 175
Ala Phe Glu Arg Arg Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile
180 185 190
Pro Arg Glu Leu Met Phe His Glu Val His Gln Thr
195 200

<210> 87
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(570)

<400> 87
atg gcc ctg ctc tcg cgc ccc gcg ctc acc ctc ctg ctc ctc ctc atg 48
Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Leu Met
1 5 10 15

gcc gct gtt gtc agg tgc cag gag cag gcc cag acc acc gac tgg aga 96
Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg
20 25 30

gcc acc ctg aag acc atc cgg aac ggc gtt cat aag ata gac acg tac 144

```
Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr
        35                  40                  45

ctg aac gcc gcc ttg gac ctc ctg gga ggc gag gac ggt ctc tgc cag       192
Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln
    50                  55                  60

tat aaa tgc agt gac gga tct aag cct ttc cca cgt tat ggt tat aaa       240
Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys
65                  70                  75                  80

ccc tcc cca ccg aat gga tgt ggc tct cca ctg ttt ggt gtt cat ctt       288
Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu
                85                  90                  95

aac att ggt atc cct tcc ctg aca aag tgt tgc aac caa cac gac agg       336
Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg
            100                 105                 110

tgc tat gaa acc tgt ggc aaa agc aag aat gac tgt gat gaa gaa ttc       384
Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe
        115                 120                 125

cag tat tgc ctc tcc aag atc tgc cga gat gta cag aaa aca cta gga       432
Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly
    130                 135                 140

cta act cag cat gtt cag gca tgt gaa aca aca gtg gag ctc ttg ttt       480
Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe
145                 150                 155                 160

gac agt gtt ata cat tta ggt tgt aaa cca tat ctg gac agc caa cga       528
Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg
                165                 170                 175

gcc gca tgc agg tgt cat tat gaa gaa aaa act gat ctt taa               570
Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu  *
            180                 185
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<210> 88
<211> 189
<212> PRT
<213> Homo sapiens

<400> 88

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Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Leu Met
 1               5                  10                  15
Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg
            20                  25                  30
Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr
        35                  40                  45
Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln
    50                  55                  60
Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys
65                  70                  75                  80
Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu
                85                  90                  95
Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg
            100                 105                 110
Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe
        115                 120                 125
Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly
    130                 135                 140
Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe
145                 150                 155                 160
Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg
                165                 170                 175
Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu
            180                 185
```

<210> 89
<211> 696
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(696)

<400> 89

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atg ttt ctg gtg ggc ctg aca ggg ggc att gcc tca ggc aag agc tca       48
Met Phe Leu Val Gly Leu Thr Gly Gly Ile Ala Ser Gly Lys Ser Ser
 1               5                  10                  15

gtg atc cag gtg ttc cag cag ctg ggc tgt gcg gtg att gac gtg gac       96
Val Ile Gln Val Phe Gln Gln Leu Gly Cys Ala Val Ile Asp Val Asp
            20                  25                  30
```

```
gtg atg gcc cgg cac gtc gtg cag cca gga tac cct gcc cac cgg cgc      144
Val Met Ala Arg His Val Val Gln Pro Gly Tyr Pro Ala His Arg Arg
         35                  40                  45

atc gta gag gtc ttc ggc act gag gtc ttg ctg gag aac ggc gac ata      192
Ile Val Glu Val Phe Gly Thr Glu Val Leu Leu Glu Asn Gly Asp Ile
     50                  55                  60

aat cgc aag gtc ctg ggg gac ctg atc ttt aac cag cct gac cgg cgg      240
Asn Arg Lys Val Leu Gly Asp Leu Ile Phe Asn Gln Pro Asp Arg Arg
 65                  70                  75                  80

cag ctg ctc aac gcc atc acc cac ccc gag att cgc aag gag atg atg      288
Gln Leu Leu Asn Ala Ile Thr His Pro Glu Ile Arg Lys Glu Met Met
                 85                  90                  95

aag gag acg ttc aag tac ttc ctc cgg gga tac cgc tac gtg att ctg      336
Lys Glu Thr Phe Lys Tyr Phe Leu Arg Gly Tyr Arg Tyr Val Ile Leu
            100                 105                 110

gat atc ccc ctg ctg ttt gag acc aag aag ttg ctc aag tac atg aag      384
Asp Ile Pro Leu Leu Phe Glu Thr Lys Lys Leu Leu Lys Tyr Met Lys
        115                 120                 125

cac acc gtg gta gta tac tgc gac cgg gac aca cag ctg gca cgg ctg      432
His Thr Val Val Val Tyr Cys Asp Arg Asp Thr Gln Leu Ala Arg Leu
    130                 135                 140

atg cgg cgg aac agc ctg aac cgc aag gac gca gag gcc cgc atc aat      480
Met Arg Arg Asn Ser Leu Asn Arg Lys Asp Ala Glu Ala Arg Ile Asn
145                 150                 155                 160

gcc cag ctg ccc ctg aca gac aag gcc cgc atg gcc cgc cat gtc cta      528
Ala Gln Leu Pro Leu Thr Asp Lys Ala Arg Met Ala Arg His Val Leu
                165                 170                 175

gac aac tcg ggc gag tgg agt gtc acc aaa cgc cag gtc atc ctc ttg      576
Asp Asn Ser Gly Glu Trp Ser Val Thr Lys Arg Gln Val Ile Leu Leu
            180                 185                 190

cac act gag ctg gag cgc tcc ctg gag tac ctg ccg ctg agg ttt ggg      624
His Thr Glu Leu Glu Arg Ser Leu Glu Tyr Leu Pro Leu Arg Phe Gly
        195                 200                 205
```

```
gtc ctc aca ggg ctc gct gcc att gcc agc ctc ctc tac ctg ctc acc      672
Val Leu Thr Gly Leu Ala Ala Ile Ala Ser Leu Leu Tyr Leu Leu Thr
    210                 215                 220

cac tac ctt ctg cct tac gcc tag                                      696
His Tyr Leu Leu Pro Tyr Ala  *
225                 230


      <210> 90
      <211> 231
      <212> PRT
      <213> Homo sapiens

      <400> 90
Met Phe Leu Val Gly Leu Thr Gly Gly Ile Ala Ser Gly Lys Ser Ser
 1               5                  10                  15
Val Ile Gln Val Phe Gln Gln Leu Gly Cys Ala Val Ile Asp Val Asp
            20                  25                  30
Val Met Ala Arg His Val Val Gln Pro Gly Tyr Pro Ala His Arg Arg
        35                  40                  45
Ile Val Glu Val Phe Gly Thr Glu Val Leu Leu Glu Asn Gly Asp Ile
    50                  55                  60
Asn Arg Lys Val Leu Gly Asp Leu Ile Phe Asn Gln Pro Asp Arg Arg
65                  70                  75                  80
Gln Leu Leu Asn Ala Ile Thr His Pro Glu Ile Arg Lys Glu Met Met
                85                  90                  95
Lys Glu Thr Phe Lys Tyr Phe Leu Arg Gly Tyr Arg Tyr Val Ile Leu
            100                 105                 110
Asp Ile Pro Leu Leu Phe Glu Thr Lys Lys Leu Leu Lys Tyr Met Lys
        115                 120                 125
His Thr Val Val Val Tyr Cys Asp Arg Asp Thr Gln Leu Ala Arg Leu
    130                 135                 140
Met Arg Arg Asn Ser Leu Asn Arg Lys Asp Ala Glu Ala Arg Ile Asn
145                 150                 155                 160
Ala Gln Leu Pro Leu Thr Asp Lys Ala Arg Met Ala Arg His Val Leu
                165                 170                 175
Asp Asn Ser Gly Glu Trp Ser Val Thr Lys Arg Gln Val Ile Leu Leu
            180                 185                 190
His Thr Glu Leu Glu Arg Ser Leu Glu Tyr Leu Pro Leu Arg Phe Gly
        195                 200                 205
Val Leu Thr Gly Leu Ala Ala Ile Ala Ser Leu Leu Tyr Leu Leu Thr
    210                 215                 220
```

His Tyr Leu Leu Pro Tyr Ala
225 230

<210> 91
<211> 198
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(198)

<221> misc_feature
<222> (1)...(198)
<223> n = A,T,C or G

<400> 91
atg gac gca ctg gcg ctg ctt ggg gga ctg gta aat nta gcc cgt ctg 48
Met Asp Ala Leu Ala Leu Leu Gly Gly Leu Val Asn Xaa Ala Arg Leu
1 5 10 15

ccc gag cgc tgg gga cct ggc cgc ttt gac tac tgg ggc aac tcc cac 96
Pro Glu Arg Trp Gly Pro Gly Arg Phe Asp Tyr Trp Gly Asn Ser His
20 25 30

cag atc atg cac ctg ctg agc gtg ggc tcc atc ctg cag ctg cac gcc 144
Gln Ile Met His Leu Leu Ser Val Gly Ser Ile Leu Gln Leu His Ala
35 40 45

ggc gtc gtg ccc gac ctg ctc tgg gct gcc cac cac gcc tgt ccc cgg 192
Gly Val Val Pro Asp Leu Leu Trp Ala Ala His His Ala Cys Pro Arg
50 55 60

gac tga 198
Asp *
65

<210> 92
<211> 65
<212> PRT
<213> Homo sapiens

<220>

<221> VARIANT
<222> (1)...(65)
<223> Xaa = Any Amino Acid

<400> 92
Met Asp Ala Leu Ala Leu Leu Gly Gly Leu Val Asn Xaa Ala Arg Leu
1 5 10 15
Pro Glu Arg Trp Gly Pro Gly Arg Phe Asp Tyr Trp Gly Asn Ser His
20 25 30
Gln Ile Met His Leu Leu Ser Val Gly Ser Ile Leu Gln Leu His Ala
35 40 45
Gly Val Val Pro Asp Leu Leu Trp Ala Ala His His Ala Cys Pro Arg
50 55 60
Asp
65

<210> 93
<211> 498
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(498)

<400> 93
atg gtg tct aca gtg ttc tcg act tcg tcg ctg atg ctt gct ctg tca 48
Met Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu Ser
1 5 10 15

agg cac agc cta ttg tct cct ttg ctc agt gtg aca tca ttc aga cgc 96
Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg Arg
20 25 30

ttc tac aga ggt gac agc cca aca gat tcc caa aag gac atg att gaa 144
Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile Glu
35 40 45

atc cct ttg cct cca tgg cag gag aga act gat gaa tcc ata gaa acc 192
Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu Thr
50 55 60

aaa aga gcc cgc ctg ctc tat gag agc aga aag agg gga atg ttg gaa 240
Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu Glu

65 70 75 80

aac tgc att ctt ctt agt ctt ttt gct aaa gaa cat ctg cag cac atg 288
Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His Met
85 90 95

aca gaa aag cag ctg aac ctc tat gac cgc ctg att aac gag cct agt 336
Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro Ser
100 105 110

aat gac tgg gat att tac tac tgg gcc aca gaa gct aaa cca gcc cca 384
Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala Pro
115 120 125

gaa ata ttt gaa aat gaa gtc atg gcc ctg ctg aga gac ttt gct aaa 432
Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala Lys
130 135 140

aac aaa aac aaa gag cag aga ctg cgt gcc cca gat ctt gag tac ctc 480
Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr Leu
145 150 155 160

ttt gaa aag cca cgt tga 498
Phe Glu Lys Pro Arg *
165

<210> 94
<211> 165
<212> PRT
<213> Homo sapiens

<400> 94
Met Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu Ser
1 5 10 15
Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg Arg
20 25 30
Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile Glu
35 40 45
Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu Thr
50 55 60
Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu Glu
65 70 75 80
Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His Met

```
                85                  90                  95
Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro Ser
            100                 105                 110
Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala Pro
        115                 120                 125
Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala Lys
    130                 135                 140
Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr Leu
145                 150                 155                 160
Phe Glu Lys Pro Arg
                165

      &lt;210&gt; 95
      &lt;211&gt; 501
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapiens

      &lt;220&gt;
      &lt;221&gt; CDS
      &lt;222&gt; (1)...(501)

      &lt;400&gt; 95
atg gcg gtg tct aca gtg ttc tcg act tcg tcg ctg atg ctt gct ctg      48
Met Ala Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu
 1               5                  10                  15

tca agg cac agc cta ttg tct cct ttg ctc agt gtg aca tca ttc aga      96
Ser Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg
            20                  25                  30

cgc ttc tac aga ggt gac agc cca aca gat tcc caa aag gac atg att     144
Arg Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile
        35                  40                  45

gaa atc cct ttg cct cca tgg cag gag aga act gat gaa tcc ata gaa     192
Glu Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu
    50                  55                  60

acc aaa aga gcc cgc ctg ctc tat gag agc aga aag agg gga atg ttg     240
Thr Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu
65                  70                  75                  80

gaa aac tgc att ctt ctt agt ctt ttt gct aaa gaa cat ctg cag cac     288
Glu Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His
```

85 90 95

atg aca gaa aag cag ctg aac ctc tat gac cgc ctg att aac gag cct 336
Met Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro
100 105 110

agt aat gac tgg gat att tac tac tgg gcc aca gaa gct aaa cca gcc 384
Ser Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala
115 120 125

cca gaa ata ttt gaa aat gaa gtc atg gcc ctg ctg aga gac ttt gct 432
Pro Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala
130 135 140

aaa aac aaa aac aaa gag cag aga ctg cgt gcc cca gat ctt gag tac 480
Lys Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr
145 150 155 160

ctc ttt gaa aag cca cgt tga 501
Leu Phe Glu Lys Pro Arg *
165

<210> 96
<211> 166
<212> PRT
<213> Homo sapiens

<400> 96
Met Ala Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu
1 5 10 15
Ser Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg
20 25 30
Arg Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile
35 40 45
Glu Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu
50 55 60
Thr Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu
65 70 75 80
Glu Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His
85 90 95
Met Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro
100 105 110
Ser Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala

115 120 125
Pro Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala
130 135 140
Lys Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr
145 150 155 160
Leu Phe Glu Lys Pro Arg
165

<210> 97
<211> 492
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(492)

<400> 97
atg gct ggc ttc tat gga ttg tat acc tgg ctg act cat act atg ttt 48
Met Ala Gly Phe Tyr Gly Leu Tyr Thr Trp Leu Thr His Thr Met Phe
1 5 10 15

ggc atc aat att gtc ttc ata cca tca gca tta gca gca atc ctt gga 96
Gly Ile Asn Ile Val Phe Ile Pro Ser Ala Leu Ala Ala Ile Leu Gly
20 25 30

gca gtg cca ttc ctg ggg aca tac tgg gca gca gta cct gca gtt ctt 144
Ala Val Pro Phe Leu Gly Thr Tyr Trp Ala Ala Val Pro Ala Val Leu
35 40 45

gac ctg tgg ctg aca caa ggg tta gga tgc aag gcc att tta ctg ttg 192
Asp Leu Trp Leu Thr Gln Gly Leu Gly Cys Lys Ala Ile Leu Leu Leu
50 55 60

att ttt cat ctc ttg cca aca tac ttt gta gat act gca atc tac tct 240
Ile Phe His Leu Leu Pro Thr Tyr Phe Val Asp Thr Ala Ile Tyr Ser
65 70 75 80

gac ata tca gga ggt ggc cat cct tac ctg aca ggc ttg gca gtg gcc 288
Asp Ile Ser Gly Gly Gly His Pro Tyr Leu Thr Gly Leu Ala Val Ala
85 90 95

ggt gga gca tac tac cta ggc ctg gaa gga gca atc atc ggt cct att 336
Gly Gly Ala Tyr Tyr Leu Gly Leu Glu Gly Ala Ile Ile Gly Pro Ile

```
            100                 105                 110

ctt ctc tgc ata ctt gtg gtt gct tcc aat atc tat agt gcc atg cta      384
Leu Leu Cys Ile Leu Val Val Ala Ser Asn Ile Tyr Ser Ala Met Leu
        115                 120                 125

gtg agt ccc acg aat tca gtt ccc acg cca aac cag acc cca tgg cct      432
Val Ser Pro Thr Asn Ser Val Pro Thr Pro Asn Gln Thr Pro Trp Pro
    130                 135                 140

gct cag cct cag cgg act ttc cgt gac att tct gaa gat ctg aaa tct      480
Ala Gln Pro Gln Arg Thr Phe Arg Asp Ile Ser Glu Asp Leu Lys Ser
145                 150                 155                 160

tca gta ggt tga                                                      492
Ser Val Gly  *


      <210> 98
      <211> 163
      <212> PRT
      <213> Homo sapiens

      <400> 98
Met Ala Gly Phe Tyr Gly Leu Tyr Thr Trp Leu Thr His Thr Met Phe
 1               5                  10                  15
Gly Ile Asn Ile Val Phe Ile Pro Ser Ala Leu Ala Ala Ile Leu Gly
            20                  25                  30
Ala Val Pro Phe Leu Gly Thr Tyr Trp Ala Ala Val Pro Ala Val Leu
        35                  40                  45
Asp Leu Trp Leu Thr Gln Gly Leu Gly Cys Lys Ala Ile Leu Leu Leu
    50                  55                  60
Ile Phe His Leu Leu Pro Thr Tyr Phe Val Asp Thr Ala Ile Tyr Ser
65                  70                  75                  80
Asp Ile Ser Gly Gly Gly His Pro Tyr Leu Thr Gly Leu Ala Val Ala
                85                  90                  95
Gly Gly Ala Tyr Tyr Leu Gly Leu Glu Gly Ala Ile Ile Gly Pro Ile
            100                 105                 110
Leu Leu Cys Ile Leu Val Val Ala Ser Asn Ile Tyr Ser Ala Met Leu
        115                 120                 125
Val Ser Pro Thr Asn Ser Val Pro Thr Pro Asn Gln Thr Pro Trp Pro
    130                 135                 140
Ala Gln Pro Gln Arg Thr Phe Arg Asp Ile Ser Glu Asp Leu Lys Ser
```

```
145                 150                 155                 160
Ser Val Gly


      <210> 99
      <211> 1464
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(1464)

      <221> misc_feature
      <222> (1)...(1464)
      <223> n = A,T,C or G

      <400> 99
atg tgg gga cct aac tcc tat gca tgg gtg ctc atg cag ttg gcc acc         48
Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
 1               5                  10                  15

gcc cag gcg ggc atc att ctg gtg tct gtg aac cca gcc tac cag gct         96
Ala Gln Ala Gly Ile Ile Leu Val Ser Val Asn Pro Ala Tyr Gln Ala
            20                  25                  30

atg gaa ctg gag tac gtc ctc aag aag gtg ggc tgc aag gcc ctt gtg        144
Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val
        35                  40                  45

ttc ccc aag caa ttc aag acc cag caa tac tac aac gtc ctg aag cag        192
Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln
    50                  55                  60

atc tgt cca gaa gtg gag aat gcc cag cca ggg gcc ttg aag agt cag        240
Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln
 65                  70                  75                  80

agg ctc cca gat ctg acc aca gtc atc tcg gtg gat gcc cct ttg ccg        288
Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro
                 85                  90                  95

ggg acc ctg ctc ctg gat gaa gtg gtg gcg gct ggc agc aca cgg cag        336
Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
```

```
            100                 105                 110

cat ctg gac cag ctc caa tac aac cag cag ttc ctg tcc tgc cat gac      384
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His Asp
        115                 120                 125

ccc atc aac atc cag ttc acc tcg ggg aca aca ggc agc ccc aag ggg      432
Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro Lys Gly
    130                 135                 140

gcc acc ctc tcc cac tac aac att gtc aac aac tcc aac att tta gga      480
Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn Ile Leu Gly
145                 150                 155                 160

gag cgc ctg aaa ctg cat gag aag aca cca gag cag ttg cgg atg atc      528
Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu Arg Met Ile
                165                 170                 175

ctg ccc aac ccc ctg tac cat tgc ctg ggt tcc gtg gca ggc aca atg      576
Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala Gly Thr Met
            180                 185                 190

atg tgt ctg atg tac ggt gcc acc ctc atc ctg gcc tct ccc atc ttc      624
Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser Pro Ile Phe
        195                 200                 205

aat ggc aag aag gca ctg gag gcc atc agc aga gag aga ggc acc ttc      672
Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe
    210                 215                 220

ctg tat ggt acc ccc acg atg ttc gtg gac att ctg aac cag cca gac      720
Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp
225                 230                 235                 240

ttc tcc agt tat gac atc tcg acc atg tgt gga ggt gtc att gct ggg      768
Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly
                245                 250                 255

tcc cct gca cct cca gag ttg atc cga gcc atc atc aac aag ata aat      816
Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn
            260                 265                 270

atg aag gac ctg gtg gtt gct tat gga acc aca gag aac agt ccc gtg      864
Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val
```

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        275                 280                 285

aca ttc gcg cac ttc cct gag gac act gtg gag cag aag gca gaa agc      912
Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser
    290                 295                 300

gtg ggc aga att atg cct cac acg gag gcc cgg atc atg aac atg gag      960
Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu
305                 310                 315                 320

gca ggg acg ctg gca aag ctg aac acg ccc ggg gag ctg tgc atc cga     1008
Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg
                325                 330                 335

ggg tac tgc gtc atg ctg ggc tac tgg ggt gag cct cag aag aca gag     1056
Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
            340                 345                 350

gaa gca gtg gat cag gac aag tgg tat tgg aca gga gat gtc gcc aca     1104
Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala Thr
        355                 360                 365

atg aat gag cag ggc ttc tgc aag atc gtg ggc cgc tct aag gat atg     1152
Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys Asp Met
    370                 375                 380

atc atc cgg ggt ggt gag aac atc tac ccc gca gag ctc gag gac ttc     1200
Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu Glu Asp Phe
385                 390                 395                 400

ttt cac aca cac ccg aag ntg cag gaa gtg cag gtg gtg gga gtg aag     1248
Phe His Thr His Pro Lys Xaa Gln Glu Val Gln Val Val Gly Val Lys
                405                 410                 415

gac gat cgg atg ggg gaa gag att tgt gcc tgc att cgg ctg aag gac     1296
Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg Leu Lys Asp
            420                 425                 430

ggg gag gag acc acg gtg gag gag ata aaa gct ttc tgc aaa ggg aag     1344
Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys Lys Gly Lys
        435                 440                 445

atc tct cac ttc aag att ccg aag tac atc gtg ttt gtc aca aac tac     1392
Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val Thr Asn Tyr
```

450 455 460

ccc ctc acc att tca gga aag atc cag aaa ttc aaa ctt cga gag cag 1440
Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu Arg Glu Gln
465 470 475 480

atg gaa cga cat cta aat ctg tga 1464
Met Glu Arg His Leu Asn Leu *
485

<210> 100
<211> 487
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(487)
<223> Xaa = Any Amino Acid

<400> 100
Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
1 5 10 15
Ala Gln Ala Gly Ile Ile Leu Val Ser Val Asn Pro Ala Tyr Gln Ala
20 25 30
Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val
35 40 45
Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln
50 55 60
Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln
65 70 75 80
Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro
85 90 95
Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
100 105 110
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His Asp
115 120 125
Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro Lys Gly
130 135 140
Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn Ile Leu Gly
145 150 155 160
Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu Arg Met Ile
165 170 175

Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala Gly Thr Met
180 185 190
Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser Pro Ile Phe
195 200 205
Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe
210 215 220
Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp
225 230 235 240
Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly
245 250 255
Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn
260 265 270
Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val
275 280 285
Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser
290 295 300
Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu
305 310 315 320
Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg
325 330 335
Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
340 345 350
Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala Thr
355 360 365
Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys Asp Met
370 375 380
Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu Glu Asp Phe
385 390 395 400
Phe His Thr His Pro Lys Xaa Gln Glu Val Gln Val Val Gly Val Lys
405 410 415
Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg Leu Lys Asp
420 425 430
Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys Lys Gly Lys
435 440 445
Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val Thr Asn Tyr
450 455 460
Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu Arg Glu Gln
465 470 475 480
Met Glu Arg His Leu Asn Leu
485

<210> 101
<211> 348
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(348)

<400> 101
atg ggg atc acc ttc ctg gct gct ggg acc agc gtg cct gac tgc atg 48
Met Gly Ile Thr Phe Leu Ala Ala Gly Thr Ser Val Pro Asp Cys Met
1 5 10 15

gcc agc ctc att gtg gcc aga caa ggg atg ggg gac atg gct gtg tcc 96
Ala Ser Leu Ile Val Ala Arg Gln Gly Met Gly Asp Met Ala Val Ser
20 25 30

aac tcc att ggg agc aac gtg ttt gac atc ctg att ggc ctc ggt ctc 144
Asn Ser Ile Gly Ser Asn Val Phe Asp Ile Leu Ile Gly Leu Gly Leu
35 40 45

ccc tgg gct ctg cag acc ctg gct gtg gat tac gga tcc tac atc cgg 192
Pro Trp Ala Leu Gln Thr Leu Ala Val Asp Tyr Gly Ser Tyr Ile Arg
50 55 60

ctg aat agc agg ggg ctg atc tac tcc gta ggc ttg ctc ctg gcc tct 240
Leu Asn Ser Arg Gly Leu Ile Tyr Ser Val Gly Leu Leu Leu Ala Ser
65 70 75 80

gtt ttt gtc acg gtg ttc ggc gtc cac ctg aac aag tgg cag ctg gac 288
Val Phe Val Thr Val Phe Gly Val His Leu Asn Lys Trp Gln Leu Asp
85 90 95

aag aag ctg ggc tgt ggg tgc ctc ctc ctg tat ggg tgt tcc tgt gct 336
Lys Lys Leu Gly Cys Gly Cys Leu Leu Leu Tyr Gly Cys Ser Cys Ala
100 105 110

tct cca tca tga 348
Ser Pro Ser *
115

<210> 102
<211> 115
<212> PRT
<213> Homo sapiens

<400> 102
Met Gly Ile Thr Phe Leu Ala Ala Gly Thr Ser Val Pro Asp Cys Met
1 5 10 15
Ala Ser Leu Ile Val Ala Arg Gln Gly Met Gly Asp Met Ala Val Ser
20 25 30
Asn Ser Ile Gly Ser Asn Val Phe Asp Ile Leu Ile Gly Leu Gly Leu
35 40 45
Pro Trp Ala Leu Gln Thr Leu Ala Val Asp Tyr Gly Ser Tyr Ile Arg
50 55 60
Leu Asn Ser Arg Gly Leu Ile Tyr Ser Val Gly Leu Leu Leu Ala Ser
65 70 75 80
Val Phe Val Thr Val Phe Gly Val His Leu Asn Lys Trp Gln Leu Asp
85 90 95
Lys Lys Leu Gly Cys Gly Cys Leu Leu Leu Tyr Gly Cys Ser Cys Ala
100 105 110
Ser Pro Ser
115

<210> 103
<211> 1239
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1239)

<400> 103
atg gcg ggc tct gtg gga ctg gcg ttg tgc ggg cag acg ttg gtg gtg 48
Met Ala Gly Ser Val Gly Leu Ala Leu Cys Gly Gln Thr Leu Val Val
1 5 10 15

cgg ggc ggc agc cga ttc ctg gcc acc tcc ata gca agc agt gat gat 96
Arg Gly Gly Ser Arg Phe Leu Ala Thr Ser Ile Ala Ser Ser Asp Asp
20 25 30

gac agc ctc ttc atc tat gac tgc agt gct gca gaa aag aag tca caa 144
Asp Ser Leu Phe Ile Tyr Asp Cys Ser Ala Ala Glu Lys Lys Ser Gln
35 40 45

gaa aat aaa ggg gag gac gcg ccc ttg gac cag ggg agc ggt gcg att 192
Glu Asn Lys Gly Glu Asp Ala Pro Leu Asp Gln Gly Ser Gly Ala Ile
50 55 60

ctg gcg tcc acc ttc tcc aag tct ggc agc tat ttt gct tta acc gat 240
Leu Ala Ser Thr Phe Ser Lys Ser Gly Ser Tyr Phe Ala Leu Thr Asp
65 70 75 80

gac agt aag cgt ctg att ctt ttc cgt aca aaa cca tgg caa tgt ctg 288
Asp Ser Lys Arg Leu Ile Leu Phe Arg Thr Lys Pro Trp Gln Cys Leu
85 90 95

agt gtc agg acc gtg gca agg agg tgt aca gcc ctg act ttc ata gcc 336
Ser Val Arg Thr Val Ala Arg Arg Cys Thr Ala Leu Thr Phe Ile Ala
100 105 110

tcg gag gag aag gtc ttg gtg gcc gac aag tct gga gac gtc tac tcc 384
Ser Glu Glu Lys Val Leu Val Ala Asp Lys Ser Gly Asp Val Tyr Ser
115 120 125

ttt tcg gtg ctg gag cca cac ggg tgt ggc cgt cta gag ctg ggg cac 432
Phe Ser Val Leu Glu Pro His Gly Cys Gly Arg Leu Glu Leu Gly His
130 135 140

ctg tct atg ctg tta gat gtg gct gtg agt cct gat gac cgc ttc atc 480
Leu Ser Met Leu Leu Asp Val Ala Val Ser Pro Asp Asp Arg Phe Ile
145 150 155 160

ctc act gcc gac cgg gac gag aag atc cga gtc agc tgg gcc gcg gcg 528
Leu Thr Ala Asp Arg Asp Glu Lys Ile Arg Val Ser Trp Ala Ala Ala
165 170 175

ccc cat agc atc gag tcc ttc tgc ttg ggg cac aca gag ttt gtg agc 576
Pro His Ser Ile Glu Ser Phe Cys Leu Gly His Thr Glu Phe Val Ser
180 185 190

cgt atc tcc gtg gtg cca act cag ccc ggg ctg ctt ctg tcc tcc tct 624
Arg Ile Ser Val Val Pro Thr Gln Pro Gly Leu Leu Leu Ser Ser Ser
195 200 205

ggg gac ggc acc ctg agg ctc tgg gag tac agg agc ggc cgc cag ctg 672
Gly Asp Gly Thr Leu Arg Leu Trp Glu Tyr Arg Ser Gly Arg Gln Leu
210 215 220

cac tgc tgt cac ctg gcc agt ctg cag gag ctg gtg gac ccc cag gcc 720
His Cys Cys His Leu Ala Ser Leu Gln Glu Leu Val Asp Pro Gln Ala
225 230 235 240

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ccc cag aag ttt gcc gcg tcc agg att gca ttc tgg tgc cag gag aac      768
Pro Gln Lys Phe Ala Ala Ser Arg Ile Ala Phe Trp Cys Gln Glu Asn
                245                 250                 255

tgc gtg gcg ctc ctg tgc gac ggc act cct gtg gtc tac atc ttc cag      816
Cys Val Ala Leu Leu Cys Asp Gly Thr Pro Val Val Tyr Ile Phe Gln
            260                 265                 270

ctg gac gcc cgc aga cag cag ttg gtg tac agg cag cag ctg gcg ttc      864
Leu Asp Ala Arg Arg Gln Gln Leu Val Tyr Arg Gln Gln Leu Ala Phe
        275                 280                 285

cag cac caa gtg tgg gac gtg gct ttc gag gag acc cag ggg ctg tgg      912
Gln His Gln Val Trp Asp Val Ala Phe Glu Glu Thr Gln Gly Leu Trp
    290                 295                 300

gtg ctc cag gac tgc cag gaa gcc ccc ctg gtg ctc tac agg cct gtg      960
Val Leu Gln Asp Cys Gln Glu Ala Pro Leu Val Leu Tyr Arg Pro Val
305                 310                 315                 320

ggc gac cag tgg cag tct gtt cct gag agc acc gtg tta aag aaa gtc     1008
Gly Asp Gln Trp Gln Ser Val Pro Glu Ser Thr Val Leu Lys Lys Val
                325                 330                 335

tct ggt gtt ctt cgt ggg aac tgg gcc atg ctg gaa ggc tct gcc ggc     1056
Ser Gly Val Leu Arg Gly Asn Trp Ala Met Leu Glu Gly Ser Ala Gly
            340                 345                 350

gca gac gcc agc ttc agc agt ctc tac aag gcc acg ttc gac aac gtg     1104
Ala Asp Ala Ser Phe Ser Ser Leu Tyr Lys Ala Thr Phe Asp Asn Val
        355                 360                 365

acc tcc tac ctg aag aag aaa gag gag aga ctg cag cag cag cta gag     1152
Thr Ser Tyr Leu Lys Lys Lys Glu Glu Arg Leu Gln Gln Gln Leu Glu
    370                 375                 380

aag aag cag cgg cgc cgg agt ccc ccg cct ggg ccc gac ggg cat gcc     1200
Lys Lys Gln Arg Arg Arg Ser Pro Pro Pro Gly Pro Asp Gly His Ala
385                 390                 395                 400

aag aag atg aga ccg ggg gag gcg acg cta agt tgc tga                 1239
Lys Lys Met Arg Pro Gly Glu Ala Thr Leu Ser Cys  *
                405                 410
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<210> 104
<211> 412
<212> PRT
<213> Homo sapiens

<400> 104
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Met Ala Gly Ser Val Gly Leu Ala Leu Cys Gly Gln Thr Leu Val Val
 1               5                  10                  15
Arg Gly Gly Ser Arg Phe Leu Ala Thr Ser Ile Ala Ser Ser Asp Asp
            20                  25                  30
Asp Ser Leu Phe Ile Tyr Asp Cys Ser Ala Ala Glu Lys Lys Ser Gln
        35                  40                  45
Glu Asn Lys Gly Glu Asp Ala Pro Leu Asp Gln Gly Ser Gly Ala Ile
    50                  55                  60
Leu Ala Ser Thr Phe Ser Lys Ser Gly Ser Tyr Phe Ala Leu Thr Asp
65                  70                  75                  80
Asp Ser Lys Arg Leu Ile Leu Phe Arg Thr Lys Pro Trp Gln Cys Leu
                85                  90                  95
Ser Val Arg Thr Val Ala Arg Arg Cys Thr Ala Leu Thr Phe Ile Ala
            100                 105                 110
Ser Glu Glu Lys Val Leu Val Ala Asp Lys Ser Gly Asp Val Tyr Ser
        115                 120                 125
Phe Ser Val Leu Glu Pro His Gly Cys Gly Arg Leu Glu Leu Gly His
    130                 135                 140
Leu Ser Met Leu Leu Asp Val Ala Val Ser Pro Asp Asp Arg Phe Ile
145                 150                 155                 160
Leu Thr Ala Asp Arg Asp Glu Lys Ile Arg Val Ser Trp Ala Ala Ala
                165                 170                 175
Pro His Ser Ile Glu Ser Phe Cys Leu Gly His Thr Glu Phe Val Ser
            180                 185                 190
Arg Ile Ser Val Val Pro Thr Gln Pro Gly Leu Leu Leu Ser Ser Ser
        195                 200                 205
Gly Asp Gly Thr Leu Arg Leu Trp Glu Tyr Arg Ser Gly Arg Gln Leu
    210                 215                 220
His Cys Cys His Leu Ala Ser Leu Gln Glu Leu Val Asp Pro Gln Ala
225                 230                 235                 240
Pro Gln Lys Phe Ala Ala Ser Arg Ile Ala Phe Trp Cys Gln Glu Asn
                245                 250                 255
Cys Val Ala Leu Leu Cys Asp Gly Thr Pro Val Val Tyr Ile Phe Gln
            260                 265                 270
Leu Asp Ala Arg Arg Gln Gln Leu Val Tyr Arg Gln Gln Leu Ala Phe
        275                 280                 285
```

Gln His Gln Val Trp Asp Val Ala Phe Glu Glu Thr Gln Gly Leu Trp
290 295 300
Val Leu Gln Asp Cys Gln Glu Ala Pro Leu Val Leu Tyr Arg Pro Val
305 310 315 320
Gly Asp Gln Trp Gln Ser Val Pro Glu Ser Thr Val Leu Lys Lys Val
325 330 335
Ser Gly Val Leu Arg Gly Asn Trp Ala Met Leu Glu Gly Ser Ala Gly
340 345 350
Ala Asp Ala Ser Phe Ser Ser Leu Tyr Lys Ala Thr Phe Asp Asn Val
355 360 365
Thr Ser Tyr Leu Lys Lys Lys Glu Glu Arg Leu Gln Gln Gln Leu Glu
370 375 380
Lys Lys Gln Arg Arg Arg Ser Pro Pro Pro Gly Pro Asp Gly His Ala
385 390 395 400
Lys Lys Met Arg Pro Gly Glu Ala Thr Leu Ser Cys
405 410

<210> 105
<211> 645
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(645)

<400> 105
atg agt gat ttg gaa gat gat gag aca ccc cag ctt tct gcc cat gcc 48
Met Ser Asp Leu Glu Asp Asp Glu Thr Pro Gln Leu Ser Ala His Ala
1 5 10 15

tta gca gct ctc cag gaa ttt tat gct gag caa aag caa caa att gag 96
Leu Ala Ala Leu Gln Glu Phe Tyr Ala Glu Gln Lys Gln Gln Ile Glu
20 25 30

cca ggc gag gat gat aaa tat aac att gga ata ata gaa gag aat tgg 144
Pro Gly Glu Asp Asp Lys Tyr Asn Ile Gly Ile Ile Glu Glu Asn Trp
35 40 45

caa ctg agc cag ttt tgg tat agt cag gaa act gct ctg cag ctg gca 192
Gln Leu Ser Gln Phe Trp Tyr Ser Gln Glu Thr Ala Leu Gln Leu Ala
50 55 60

cag gag gca att gca gct gta gga gaa ggt ggc aga atc gca tgt gtg 240

```
Gln Glu Ala Ile Ala Ala Val Gly Glu Gly Gly Arg Ile Ala Cys Val
65                  70                  75                  80

agt gcc cct agt gtt tac cag aaa ctc aga gag ctg tgc aga gaa aac        288
Ser Ala Pro Ser Val Tyr Gln Lys Leu Arg Glu Leu Cys Arg Glu Asn
                85                  90                  95

ttt tcg ata tac atc ttt gaa tat gac aaa aga ttt gcc atg tat gga        336
Phe Ser Ile Tyr Ile Phe Glu Tyr Asp Lys Arg Phe Ala Met Tyr Gly
            100                 105                 110

gag gag ttt att ttc tat gat tac aat aat cca ttg gac tta ccc gaa        384
Glu Glu Phe Ile Phe Tyr Asp Tyr Asn Asn Pro Leu Asp Leu Pro Glu
        115                 120                 125

aga att gct gca cat agt ttt gac atc gta ata gca gat cct ccc tat        432
Arg Ile Ala Ala His Ser Phe Asp Ile Val Ile Ala Asp Pro Pro Tyr
    130                 135                 140

ctt tcg gag gaa tgt ctc aga aaa aca tcg gaa acc gtc aag tac ctg        480
Leu Ser Glu Glu Cys Leu Arg Lys Thr Ser Glu Thr Val Lys Tyr Leu
145                 150                 155                 160

acg cgg ggc aag att ctg ctg tgc aca ggt gcc atc atg gaa gaa cag        528
Thr Arg Gly Lys Ile Leu Leu Cys Thr Gly Ala Ile Met Glu Glu Gln
                165                 170                 175

gca gca gaa ctc ctt gga gtg aag atg tgc acg ttt gtt cca aga cac        576
Ala Ala Glu Leu Leu Gly Val Lys Met Cys Thr Phe Val Pro Arg His
            180                 185                 190

acc cgg aac ttg gca aat gag ttt cgc tgt tat gtg aat tat gat tct        624
Thr Arg Asn Leu Ala Asn Glu Phe Arg Cys Tyr Val Asn Tyr Asp Ser
        195                 200                 205

ggg ctg gac tgt ggg atc tga                                            645
Gly Leu Asp Cys Gly Ile  *
    210
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<210> 106
<211> 214
<212> PRT
<213> Homo sapiens

<400> 106
Met Ser Asp Leu Glu Asp Asp Glu Thr Pro Gln Leu Ser Ala His Ala
1 5 10 15
Leu Ala Ala Leu Gln Glu Phe Tyr Ala Glu Gln Lys Gln Gln Ile Glu
20 25 30
Pro Gly Glu Asp Asp Lys Tyr Asn Ile Gly Ile Ile Glu Glu Asn Trp
35 40 45
Gln Leu Ser Gln Phe Trp Tyr Ser Gln Glu Thr Ala Leu Gln Leu Ala
50 55 60
Gln Glu Ala Ile Ala Ala Val Gly Glu Gly Gly Arg Ile Ala Cys Val
65 70 75 80
Ser Ala Pro Ser Val Tyr Gln Lys Leu Arg Glu Leu Cys Arg Glu Asn
85 90 95
Phe Ser Ile Tyr Ile Phe Glu Tyr Asp Lys Arg Phe Ala Met Tyr Gly
100 105 110
Glu Glu Phe Ile Phe Tyr Asp Tyr Asn Asn Pro Leu Asp Leu Pro Glu
115 120 125
Arg Ile Ala Ala His Ser Phe Asp Ile Val Ile Ala Asp Pro Pro Tyr
130 135 140
Leu Ser Glu Glu Cys Leu Arg Lys Thr Ser Glu Thr Val Lys Tyr Leu
145 150 155 160
Thr Arg Gly Lys Ile Leu Leu Cys Thr Gly Ala Ile Met Glu Glu Gln
165 170 175
Ala Ala Glu Leu Leu Gly Val Lys Met Cys Thr Phe Val Pro Arg His
180 185 190
Thr Arg Asn Leu Ala Asn Glu Phe Arg Cys Tyr Val Asn Tyr Asp Ser
195 200 205
Gly Leu Asp Cys Gly Ile
210

<210> 107
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(264)

<400> 107
atg aag agc agc act ctg ttg acg atc cta gtt ctc cag gcc ctt ctg 48
Met Lys Ser Ser Thr Leu Leu Thr Ile Leu Val Leu Gln Ala Leu Leu
1 5 10 15

gtc tct acg gcc gtg ccc aaa gga cct gca ggc ccg aag aag cag tgc 96
Val Ser Thr Ala Val Pro Lys Gly Pro Ala Gly Pro Lys Lys Gln Cys
20 25 30

tgg tgc ggc gag tgc acc agc tgg tcg ggc gtg tgg acc tgc gac gac 144
Trp Cys Gly Glu Cys Thr Ser Trp Ser Gly Val Trp Thr Cys Asp Asp
35 40 45

ctc ctc acc aag tgc gcc gcc acc tgc aag aac tgc gtc ccc gtc tcc 192
Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro Val Ser
50 55 60

acg gac aag ggc gcc acc aag tac aga tgc cgc gac ttc ctc ccc gaa 240
Thr Asp Lys Gly Ala Thr Lys Tyr Arg Cys Arg Asp Phe Leu Pro Glu
65 70 75 80

aac tgc ggc tgc aag atc cac tag 264
Asn Cys Gly Cys Lys Ile His *
85

<210> 108
<211> 87
<212> PRT
<213> Homo sapiens

<400> 108
Met Lys Ser Ser Thr Leu Leu Thr Ile Leu Val Leu Gln Ala Leu Leu
1 5 10 15
Val Ser Thr Ala Val Pro Lys Gly Pro Ala Gly Pro Lys Lys Gln Cys
20 25 30
Trp Cys Gly Glu Cys Thr Ser Trp Ser Gly Val Trp Thr Cys Asp Asp
35 40 45
Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro Val Ser
50 55 60
Thr Asp Lys Gly Ala Thr Lys Tyr Arg Cys Arg Asp Phe Leu Pro Glu
65 70 75 80
Asn Cys Gly Cys Lys Ile His
85

<210> 109
<211> 378
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(378)

<400> 109

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atg aag gaa gaa gga aaa ctc cta ttt tat gcg aca agc cgt gcc tat       48
Met Lys Glu Glu Gly Lys Leu Leu Phe Tyr Ala Thr Ser Arg Ala Tyr
 1               5                  10                  15

gtg gaa tct atc tgt tcg aat aat ttt gac agt ttc cta cat gaa act       96
Val Glu Ser Ile Cys Ser Asn Asn Phe Asp Ser Phe Leu His Glu Thr
            20                  25                  30

cat gaa aac aaa tac gga aaa gga att tac ttt gca aaa gat gcc atc      144
His Glu Asn Lys Tyr Gly Lys Gly Ile Tyr Phe Ala Lys Asp Ala Ile
        35                  40                  45

tat tcc cac aaa aat tgc ccg tat gat gcc aaa aac gtc gtt atg ttt      192
Tyr Ser His Lys Asn Cys Pro Tyr Asp Ala Lys Asn Val Val Met Phe
    50                  55                  60

gta gcc caa gtt ctg gtt gga aag ttt act gaa gga aat ata acg tac      240
Val Ala Gln Val Leu Val Gly Lys Phe Thr Glu Gly Asn Ile Thr Tyr
65                  70                  75                  80

acg agc cct cct cca cag ttc gac agc tgt gtg gat acc aga tcg aat      288
Thr Ser Pro Pro Pro Gln Phe Asp Ser Cys Val Asp Thr Arg Ser Asn
                85                  90                  95

ccc tcc gtt ttt gtc atc ttt cag aaa gat cag gtt tac cca caa tat      336
Pro Ser Val Phe Val Ile Phe Gln Lys Asp Gln Val Tyr Pro Gln Tyr
            100                 105                 110

gtg att gaa tat act gaa gac aaa gcc tgc gtg att agt tag              378
Val Ile Glu Tyr Thr Glu Asp Lys Ala Cys Val Ile Ser  *
        115                 120                 125
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<210> 110
<211> 125
<212> PRT
<213> Homo sapiens

<400> 110
Met Lys Glu Glu Gly Lys Leu Leu Phe Tyr Ala Thr Ser Arg Ala Tyr
1 5 10 15
Val Glu Ser Ile Cys Ser Asn Asn Phe Asp Ser Phe Leu His Glu Thr
20 25 30
His Glu Asn Lys Tyr Gly Lys Gly Ile Tyr Phe Ala Lys Asp Ala Ile
35 40 45
Tyr Ser His Lys Asn Cys Pro Tyr Asp Ala Lys Asn Val Val Met Phe
50 55 60
Val Ala Gln Val Leu Val Gly Lys Phe Thr Glu Gly Asn Ile Thr Tyr
65 70 75 80
Thr Ser Pro Pro Pro Gln Phe Asp Ser Cys Val Asp Thr Arg Ser Asn
85 90 95
Pro Ser Val Phe Val Ile Phe Gln Lys Asp Gln Val Tyr Pro Gln Tyr
100 105 110
Val Ile Glu Tyr Thr Glu Asp Lys Ala Cys Val Ile Ser
115 120 125

<210> 111
<211> 1965
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1965)

<400> 111
atg gcg gcg gcg gca ttg ggc agc tcc tca ggc tcg gcg tcc ccg gcc 48
Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
1 5 10 15

gtg gct gag ctc tgc cag aac acc ccg gag acc ttt ttg gag gcc tcc 96
Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
20 25 30

aag ctg ctg ctc acc tat gct gac aac atc ctc aga aac cct aat gat 144
Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
35 40 45

gaa aaa tat aga tcc atc cgg att gga aac aca gcc ttt tct act aga 192
Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
50 55 60

```
ctc ttg cct gtc aga gga gct gtt gaa tgt tta ttt gaa atg ggc ttt       240
Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe
 65                  70                  75                  80

gaa gag gga gaa aca cat ctc atc ttt cct aaa aaa gct tca gtg gag       288
Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu
                 85                  90                  95

cag ctg caa aaa att cgt gac ctg att gcc ata gag aga agt agc aga       336
Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg
            100                 105                 110

ctg gat ggc tca aat aag agc cac aaa gta aag tca tct cag caa cct       384
Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro
        115                 120                 125

gca gcc agt acc cag ctt cct aca aca cca tct tca aat ccc agt ggg       432
Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly
    130                 135                 140

tta aac cag cac aca agg aac cgt caa ggg cag tca tca gat cca cca       480
Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro
145                 150                 155                 160

tct gct tca acg gtt gct gct gac tca gcc att cta gaa gtt ctt cag       528
Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
                165                 170                 175

tcc aac att cag cat gtg ctg gtc tat gaa aat cct gct ctt cag gag       576
Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
            180                 185                 190

aaa gcg ttg gct tgt att ccg gtc caa gaa cta aaa agg aaa tca caa       624
Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
        195                 200                 205

gaa aag tta tcg aga gct aga aaa ttg gat aaa ggt atc aat ata agt       672
Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
    210                 215                 220

gat gag gat ttt ctt ttg ctg gag ctt ttg cac tgg ttt aag gaa gaa       720
Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
225                 230                 235                 240
```

```
ttt ttt cac tgg gtg aat aac gtt ttg tgc agc aaa tgt ggt gga cag      768
Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
                245                 250                 255

act agg tct aga gat aga tca tta ctg ccc agt gat gat gag ctg aag      816
Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys
            260                 265                 270

tgg ggt gca aag gaa gtg gaa gat cat tac tgt gat gcc tgc cag ttc      864
Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe
        275                 280                 285

agc aat cga ttc cca aga tat aat aac cct gag aaa ctt ttg gaa aca      912
Ser Asn Arg Phe Pro Arg Tyr Asn Asn Pro Glu Lys Leu Leu Glu Thr
    290                 295                 300

aga tgt gga cgg tgt ggc gag tgg gcc aat tgt ttt aca ctg tgc tgc      960
Arg Cys Gly Arg Cys Gly Glu Trp Ala Asn Cys Phe Thr Leu Cys Cys
305                 310                 315                 320

cga gct gta ggg ttt gaa gct cgc tat gtt tgg gat tac aca gac cat     1008
Arg Ala Val Gly Phe Glu Ala Arg Tyr Val Trp Asp Tyr Thr Asp His
                325                 330                 335

gtc tgg aca gaa gtc tat tct cct tct cag cag cgg tgg ctg cac tgt     1056
Val Trp Thr Glu Val Tyr Ser Pro Ser Gln Gln Arg Trp Leu His Cys
            340                 345                 350

gat gca tgt gaa gat gtc tgt gac aag cca ctc ctt tat gaa ata gga     1104
Asp Ala Cys Glu Asp Val Cys Asp Lys Pro Leu Leu Tyr Glu Ile Gly
        355                 360                 365

tgg ggc aag aag ctt tcc tat gtc ata gca ttt tca aaa gat gag gta     1152
Trp Gly Lys Lys Leu Ser Tyr Val Ile Ala Phe Ser Lys Asp Glu Val
    370                 375                 380

gtt gat gtc act tgg cga tat tcc tgc aaa cat gaa gag gtg att gcc     1200
Val Asp Val Thr Trp Arg Tyr Ser Cys Lys His Glu Glu Val Ile Ala
385                 390                 395                 400

aga aga act aag gtt aaa gaa gca tta ctt cga gac act att aat ggg     1248
Arg Arg Thr Lys Val Lys Glu Ala Leu Leu Arg Asp Thr Ile Asn Gly
                405                 410                 415
```

ctt aat aag cag agg caa ctg ttt ttg tca gaa aac aga agg aaa gaa 1296
Leu Asn Lys Gln Arg Gln Leu Phe Leu Ser Glu Asn Arg Arg Lys Glu
420 425 430

ctt ctc cag agg ata att gtg gag ctt gtt gaa ttt ata tct ccc aaa 1344
Leu Leu Gln Arg Ile Ile Val Glu Leu Val Glu Phe Ile Ser Pro Lys
435 440 445

acc cct aaa cct gga gaa ctt ggg gga aga ata tct ggg tca gtg gct 1392
Thr Pro Lys Pro Gly Glu Leu Gly Gly Arg Ile Ser Gly Ser Val Ala
450 455 460

tgg aga gta gcc cga ggt gaa atg ggt cta cag aga aaa gaa acc ttg 1440
Trp Arg Val Ala Arg Gly Glu Met Gly Leu Gln Arg Lys Glu Thr Leu
465 470 475 480

ttt att ccc tgt gaa aat gag aag att tct aaa cag ctc cac ctt tgt 1488
Phe Ile Pro Cys Glu Asn Glu Lys Ile Ser Lys Gln Leu His Leu Cys
485 490 495

tac aat att gtg aaa gat cgt tat gtt cga gtt tca aat aac aat caa 1536
Tyr Asn Ile Val Lys Asp Arg Tyr Val Arg Val Ser Asn Asn Asn Gln
500 505 510

acc att tct gga tgg gag aat ggc gtg tgg aaa atg gaa tct ata ttc 1584
Thr Ile Ser Gly Trp Glu Asn Gly Val Trp Lys Met Glu Ser Ile Phe
515 520 525

aga aaa gtt gaa aca gac tgg cac atg gta tat ttg gcc cga aag gaa 1632
Arg Lys Val Glu Thr Asp Trp His Met Val Tyr Leu Ala Arg Lys Glu
530 535 540

gga tca tct ttt gct tat att tcc tgg aag ttt gag tgt ggg tca gtt 1680
Gly Ser Ser Phe Ala Tyr Ile Ser Trp Lys Phe Glu Cys Gly Ser Val
545 550 555 560

ggc cta aaa gta gat agc att tct att aga aca agt agt caa act ttt 1728
Gly Leu Lys Val Asp Ser Ile Ser Ile Arg Thr Ser Ser Gln Thr Phe
565 570 575

cag act gga aca gta gaa tgg aaa ttg cga tct gat aca gca caa gta 1776
Gln Thr Gly Thr Val Glu Trp Lys Leu Arg Ser Asp Thr Ala Gln Val
580 585 590

gaa ctg aca ggc gat aac agt ctt cac tcc tat gct gat ttt tct ggt 1824
Glu Leu Thr Gly Asp Asn Ser Leu His Ser Tyr Ala Asp Phe Ser Gly
595 600 605

gcc act gaa gtt att ttg gaa gca gaa tta agc aga gga gat ggt gat 1872
Ala Thr Glu Val Ile Leu Glu Ala Glu Leu Ser Arg Gly Asp Gly Asp
610 615 620

gtc gct tgg caa cac acc cag ctg ttt aga caa agc tta aat gac cat 1920
Val Ala Trp Gln His Thr Gln Leu Phe Arg Gln Ser Leu Asn Asp His
625 630 635 640

gaa gaa aat tgt ttg gag ata att ata aaa ttc agt gac ctt tga 1965
Glu Glu Asn Cys Leu Glu Ile Ile Ile Lys Phe Ser Asp Leu *
645 650

<210> 112
<211> 654
<212> PRT
<213> Homo sapiens

<400> 112
Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
1 5 10 15
Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
20 25 30
Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
35 40 45
Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
50 55 60
Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe
65 70 75 80
Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu
85 90 95
Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg
100 105 110
Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro
115 120 125
Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly
130 135 140
Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro
145 150 155 160

Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
165 170 175
Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
180 185 190
Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
195 200 205
Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
210 215 220
Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
225 230 235 240
Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
245 250 255
Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys
260 265 270
Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe
275 280 285
Ser Asn Arg Phe Pro Arg Tyr Asn Asn Pro Glu Lys Leu Leu Glu Thr
290 295 300
Arg Cys Gly Arg Cys Gly Glu Trp Ala Asn Cys Phe Thr Leu Cys Cys
305 310 315 320
Arg Ala Val Gly Phe Glu Ala Arg Tyr Val Trp Asp Tyr Thr Asp His
325 330 335
Val Trp Thr Glu Val Tyr Ser Pro Ser Gln Gln Arg Trp Leu His Cys
340 345 350
Asp Ala Cys Glu Asp Val Cys Asp Lys Pro Leu Leu Tyr Glu Ile Gly
355 360 365
Trp Gly Lys Lys Leu Ser Tyr Val Ile Ala Phe Ser Lys Asp Glu Val
370 375 380
Val Asp Val Thr Trp Arg Tyr Ser Cys Lys His Glu Glu Val Ile Ala
385 390 395 400
Arg Arg Thr Lys Val Lys Glu Ala Leu Leu Arg Asp Thr Ile Asn Gly
405 410 415
Leu Asn Lys Gln Arg Gln Leu Phe Leu Ser Glu Asn Arg Arg Lys Glu
420 425 430
Leu Leu Gln Arg Ile Ile Val Glu Leu Val Glu Phe Ile Ser Pro Lys
435 440 445
Thr Pro Lys Pro Gly Glu Leu Gly Gly Arg Ile Ser Gly Ser Val Ala
450 455 460
Trp Arg Val Ala Arg Gly Glu Met Gly Leu Gln Arg Lys Glu Thr Leu
465 470 475 480
Phe Ile Pro Cys Glu Asn Glu Lys Ile Ser Lys Gln Leu His Leu Cys
485 490 495
Tyr Asn Ile Val Lys Asp Arg Tyr Val Arg Val Ser Asn Asn Asn Gln
500 505 510

Thr Ile Ser Gly Trp Glu Asn Gly Val Trp Lys Met Glu Ser Ile Phe
515 520 525
Arg Lys Val Glu Thr Asp Trp His Met Val Tyr Leu Ala Arg Lys Glu
530 535 540
Gly Ser Ser Phe Ala Tyr Ile Ser Trp Lys Phe Glu Cys Gly Ser Val
545 550 555 560
Gly Leu Lys Val Asp Ser Ile Ser Ile Arg Thr Ser Ser Gln Thr Phe
565 570 575
Gln Thr Gly Thr Val Glu Trp Lys Leu Arg Ser Asp Thr Ala Gln Val
580 585 590
Glu Leu Thr Gly Asp Asn Ser Leu His Ser Tyr Ala Asp Phe Ser Gly
595 600 605
Ala Thr Glu Val Ile Leu Glu Ala Glu Leu Ser Arg Gly Asp Gly Asp
610 615 620
Val Ala Trp Gln His Thr Gln Leu Phe Arg Gln Ser Leu Asn Asp His
625 630 635 640
Glu Glu Asn Cys Leu Glu Ile Ile Ile Lys Phe Ser Asp Leu
645 650

<210> 113
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(585)

<400> 113
atg tct gca ttg tgg ctg ctg ctg ggc ctc ctt gcc ctg atg gac ttg 48
Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu
1 5 10 15

tct gaa agc agc aac tgg gga tgc tat gga aac atc caa agc ctg gac 96
Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp
20 25 30

acc cct gga gca tct tgt ggg att gga aga cgt cac ggc ctg aac tac 144
Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr
35 40 45

tgt gga gtt cgt gct tct gaa agg ctg gct gaa ata gac atg cca tac 192
Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr
50 55 60

ctc ctg aaa tat caa ccc atg atg caa acc att ggc caa aag tac tgc 240
Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys
65 70 75 80

atg gat cct gcc gtg atc gct ggt gtc ttg tcc agg aag tct ccc ggt 288
Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly
85 90 95

gac aaa att ctg gtc aac atg ggc gat agg act agc atg gtg cag gac 336
Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp
100 105 110

cct ggc tct caa gct ccc aca tcc tgg att agt gag tct cag gtt tcc 384
Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser
115 120 125

cag aca act gaa gtt ctg act act aga atc aaa gaa atc cag agg agg 432
Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg
130 135 140

ttt cca acc tgg acc cct gac cag tac ctg aga ggt gga ctc tgt gcc 480
Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala
145 150 155 160

tac agt ggg ggt gct ggc tat gtc cga agc agc cag gac ctg agc tgt 528
Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys
165 170 175

gac ttc tgc aat gat gtc ctt gca cga gcc aag tac ctc aag aga cat 576
Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His
180 185 190

ggc ttc taa 585
Gly Phe *

<210> 114
<211> 194
<212> PRT
<213> Homo sapiens

<400> 114

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu
1   5   10   15
Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp
            20   25   30
Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr
        35   40   45
Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr
    50   55   60
Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys
65   70   75   80
Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly
                85   90   95
Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp
            100   105   110
Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser
        115   120   125
Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg
    130   135   140
Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala
145   150   155   160
Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys
                165   170   175
Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His
            180   185   190
Gly Phe

<210> 115
<211> 933
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(933)

<221> misc_feature
<222> (1)...(933)
<223> n = A,T,C or G

<400> 115
atg ctg gtg gtg gag gtg gcg aac ggc cgc tcc ctg gtg tgg gga gcc 48
Met Leu Val Val Glu Val Ala Asn Gly Arg Ser Leu Val Trp Gly Ala
1   5   10   15

gag gcg gtg cag gcc ctc cgg gag cgc ctg ggt gtg ggg ggc cgc acg 96
Glu Ala Val Gln Ala Leu Arg Glu Arg Leu Gly Val Gly Gly Arg Thr
20 25 30

gta ggc gcc ctg ccc cgc ggg ccc cgc cag aac tcg cgc ctg ggc ctc 144
Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu
35 40 45

ccg ctg ctg ctg atg ccc gaa gag gcg cgg ctc ttg gcc gag atc ggc 192
Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly
50 55 60

gcc gtg act ctg gtc agc gcc ccg cgt cca gac tct cgg cac cac agc 240
Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser
65 70 75 80

ctg gcc ctg aca tcc ttc aag cgc can caa gag gag agc ttc cag gag 288
Leu Ala Leu Thr Ser Phe Lys Arg Xaa Gln Glu Glu Ser Phe Gln Glu
85 90 95

cag agc gcc ttg gca gct gag gcc cgg gag acc cgt cgt cag gag ctc 336
Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu
100 105 110

ctg gag aag att acg gag ggc cag gct gct aag aag cag aaa cta gaa 384
Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu
115 120 125

cag gct tca ggg gcc agc tca agc cag gag gcc ggc tcg agc cag gct 432
Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala
130 135 140

gcc aaa gag gat gag acc agt gat ggc cag gct tcg gga gag cag gag 480
Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu
145 150 155 160

gaa gct ggc ccc tcg tct tcc caa gca gga ccc tca aat ggg gta gcc 528
Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala
165 170 175

ccc ttg ccc aga tct gct ctc ctt gtc cag ctg gcc act gcc agg cct 576
Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro
180 185 190

```
cga ccg gtc aag gcc agg ccc ctg gac tgg cgt gtc cag tct aaa gac      624
Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp
        195                 200                 205

tgg ccc cac gcc ggc cgc cct gcc cac gag ctg cgc tac agt atc tac      672
Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr
    210                 215                 220

aga gac ctg tgg gag cga ggc ttc ttc ctc agt gcg gct ggc aag ttc      720
Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe
225                 230                 235                 240

gga ggt gac ttc ctg gtc tat cct ggt gac ccc ctc cgc ttc cac gcc      768
Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala
                245                 250                 255

cat tat atc gct cag tgc tgg gcc cct gag gac acc atc cca ctc caa      816
His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln
            260                 265                 270

gac ctg gtt gct gct ggg cgc ctt gga acc agc gtc aga aag acc ctg      864
Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu
        275                 280                 285

ctc ctc tgt tct ccg cag cct gat ggt aag gtg gtc tac acc tcc ctg      912
Leu Leu Cys Ser Pro Gln Pro Asp Gly Lys Val Val Tyr Thr Ser Leu
    290                 295                 300

caa tgg gcc agc ctg cag tga                                          933
Gln Trp Ala Ser Leu Gln  *
305                 310
```

<210> 116
<211> 310
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(310)
<223> Xaa = Any Amino Acid

<400> 116

Met Leu Val Val Glu Val Ala Asn Gly Arg Ser Leu Val Trp Gly Ala
1 5 10 15
Glu Ala Val Gln Ala Leu Arg Glu Arg Leu Gly Val Gly Gly Arg Thr
20 25 30
Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu
35 40 45
Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly
50 55 60
Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser
65 70 75 80
Leu Ala Leu Thr Ser Phe Lys Arg Xaa Gln Glu Glu Ser Phe Gln Glu
85 90 95
Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu
100 105 110
Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu
115 120 125
Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala
130 135 140
Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu
145 150 155 160
Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala
165 170 175
Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro
180 185 190
Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp
195 200 205
Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr
210 215 220
Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe
225 230 235 240
Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala
245 250 255
His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln
260 265 270
Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu
275 280 285
Leu Leu Cys Ser Pro Gln Pro Asp Gly Lys Val Val Tyr Thr Ser Leu
290 295 300
Gln Trp Ala Ser Leu Gln
305 310

<210> 117
<211> 828

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(828)

<400> 117
atg gca aat ttc aag ggc cac gcg ctt cca ggg agt ttc ttc ctg atc 48
Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile
1 5 10 15

att ggg ctg tgt tgg tca gtg aag tac ccg ctg aag tac ttt agc cac 96
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His
20 25 30

acg cgg aag aac agc cca cta cat tac tat cag cgt ctc gag atc gtc 144
Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
35 40 45

gaa gcc gca att agg act ttg ttt tcc gtc act ggg atc ctg gca gag 192
Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
50 55 60

cag ttt gtt ccg gat ggg ccc cac ctg cac ctc tac cat gag aac cac 240
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
65 70 75 80

tgg ata aag tta atg aat tgg cag cac agc acc atg tac cta ttc ttt 288
Trp Ile Lys Leu Met Asn Trp Gln His Ser Thr Met Tyr Leu Phe Phe
85 90 95

gca gtc tca gga att gtt gac atg ctc acc tat ctg gtc agc cac gtt 336
Ala Val Ser Gly Ile Val Asp Met Leu Thr Tyr Leu Val Ser His Val
100 105 110

ccc ttg ggg gtg gac aga ctg gtt atg gct gtg gca gta ttc atg gaa 384
Pro Leu Gly Val Asp Arg Leu Val Met Ala Val Ala Val Phe Met Glu
115 120 125

ggt ttc ctc ttc tac tac cac gtc cac aac cgg cct ccg ctg gac cag 432
Gly Phe Leu Phe Tyr Tyr His Val His Asn Arg Pro Pro Leu Asp Gln
130 135 140

cac atc cac tca ctc ctg ctg tat gct ctg ttc gga ggg tgt gtt agt 480
His Ile His Ser Leu Leu Leu Tyr Ala Leu Phe Gly Gly Cys Val Ser
145 150 155 160

atc tcc cta gag gtg atc ttc cgg gac cac att gtg ctg gaa ctt ttc 528
Ile Ser Leu Glu Val Ile Phe Arg Asp His Ile Val Leu Glu Leu Phe
165 170 175

cga acc agt ctc atc att ctt cag gga acc tgg ttc tgg cag att ggg 576
Arg Thr Ser Leu Ile Ile Leu Gln Gly Thr Trp Phe Trp Gln Ile Gly
180 185 190

ttt gtg ctg ttc cca cct ttt gga aca ccc gaa tgg gac cag aag gat 624
Phe Val Leu Phe Pro Pro Phe Gly Thr Pro Glu Trp Asp Gln Lys Asp
195 200 205

gat gcc aac ctc atg ttc atc acc atg tgc ttc tgc tgg cac tac ctg 672
Asp Ala Asn Leu Met Phe Ile Thr Met Cys Phe Cys Trp His Tyr Leu
210 215 220

gct gcc ctc agc att gtg gcc gtc aac tat tct ctt gtt tac tgc ctt 720
Ala Ala Leu Ser Ile Val Ala Val Asn Tyr Ser Leu Val Tyr Cys Leu
225 230 235 240

ttg act cgg atg aag aga cac gga agg gga gaa atc att gga att cag 768
Leu Thr Arg Met Lys Arg His Gly Arg Gly Glu Ile Ile Gly Ile Gln
245 250 255

aag ctg aat tca gat gac act tac cag acc gcc ctc ttg agt ggc tca 816
Lys Leu Asn Ser Asp Asp Thr Tyr Gln Thr Ala Leu Leu Ser Gly Ser
260 265 270

gat gag gaa tga 828
Asp Glu Glu *
275

<210> 118
<211> 275
<212> PRT
<213> Homo sapiens

<400> 118
Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile

```
1               5                   10                  15
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His
            20                  25                  30
Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
        35                  40                  45
Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
    50                  55                  60
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
65                  70                  75                  80
Trp Ile Lys Leu Met Asn Trp Gln His Ser Thr Met Tyr Leu Phe Phe
                85                  90                  95
Ala Val Ser Gly Ile Val Asp Met Leu Thr Tyr Leu Val Ser His Val
            100                 105                 110
Pro Leu Gly Val Asp Arg Leu Val Met Ala Val Ala Val Phe Met Glu
        115                 120                 125
Gly Phe Leu Phe Tyr Tyr His Val His Asn Arg Pro Pro Leu Asp Gln
    130                 135                 140
His Ile His Ser Leu Leu Leu Tyr Ala Leu Phe Gly Gly Cys Val Ser
145                 150                 155                 160
Ile Ser Leu Glu Val Ile Phe Arg Asp His Ile Val Leu Glu Leu Phe
                165                 170                 175
Arg Thr Ser Leu Ile Ile Leu Gln Gly Thr Trp Phe Trp Gln Ile Gly
            180                 185                 190
Phe Val Leu Phe Pro Pro Phe Gly Thr Pro Glu Trp Asp Gln Lys Asp
        195                 200                 205
Asp Ala Asn Leu Met Phe Ile Thr Met Cys Phe Cys Trp His Tyr Leu
    210                 215                 220
Ala Ala Leu Ser Ile Val Ala Val Asn Tyr Ser Leu Val Tyr Cys Leu
225                 230                 235                 240
Leu Thr Arg Met Lys Arg His Gly Arg Gly Glu Ile Ile Gly Ile Gln
                245                 250                 255
Lys Leu Asn Ser Asp Asp Thr Tyr Gln Thr Ala Leu Leu Ser Gly Ser
            260                 265                 270
Asp Glu Glu
        275
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<210> 119
<211> 867
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(867)

<400> 119

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atg ggg cgc ctg acg gaa gcg gcg gca gcg ggc agc ggc tct cgg gct      48
Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala
 1               5                  10                  15

gca ggc tgg gca ggg tcc cct ccc acg ctc ctg ccg ctg tct ccc acg      96
Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr
            20                  25                  30

tcc ccc agg tgc gcg gcc acc atg gcg tcc agc gac gag gac ggc acc     144
Ser Pro Arg Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr
        35                  40                  45

aac ggc ggc gcc tcg gag gcc ggc gag gac cgg gag gct ccc ggc aag     192
Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Lys
    50                  55                  60

cgg agg cgc ctg ggg ttc ttg gcc acc gcc tgg ctc acc ttc tac gac     240
Arg Arg Arg Leu Gly Phe Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp
65                  70                  75                  80

atc gcc atg acc gcg ggg tgg ttg gtt cta gct att gcc atg gta cgt     288
Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg
                85                  90                  95

ttt tat atg gaa aaa gga aca cac aga ggt tta tat aaa agt att cag     336
Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln
            100                 105                 110

aag aca ctt aaa ttt ttc cag aca ttt gcc ttg ctt gag ata gtt cac     384
Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His
        115                 120                 125

tgt tta att gga att gta cct act tct gtg att gtg act ggg gtc caa     432
Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln
    130                 135                 140

gtg agt tca aga atc ttt atg gtg tgg ctc att act cac agt ata aaa     480
Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys
145                 150                 155                 160

cca atc cag aat gaa gag agt gtg gtg ctt ttt ctg gtc gcg tgg act     528
Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr
```

165 170 175

gtg aca gag atc act cgc tat tcc ttc tac aca ttc agc ctt ctt gac 576
Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp
180 185 190

cac ttg cca tac ttc att aaa tgg gcc aga tat aat ttt ttt atc atc 624
His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile
195 200 205

tta tat cct gtt gga gtt gct ggt gaa ctt ctt aca ata tac gct gcc 672
Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala
210 215 220

ttg ccg cat gtg aag aaa aca gga atg ttt tca ata aga ctt cct aac 720
Leu Pro His Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu Pro Asn
225 230 235 240

aaa tac aat gtc tct ttt gac tac tat tat ttt ctt ctt ata acc atg 768
Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile Thr Met
245 250 255

gca tca tat ata cct ttg ttt cca caa ctc tat ttt cat atg tta cgt 816
Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met Leu Arg
260 265 270

caa aga aga aag gtg ctt cat gga gag gtg att gta gaa aag gat gat 864
Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys Asp Asp
275 280 285

taa 867
*

<210> 120
<211> 288
<212> PRT
<213> Homo sapiens

<400> 120
Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala
1 5 10 15
Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr

```
            20                  25                  30
Ser Pro Arg Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr
        35                  40                  45
Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Lys
    50                  55                  60
Arg Arg Arg Leu Gly Phe Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp
65                  70                  75                  80
Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg
                85                  90                  95
Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln
            100                 105                 110
Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His
        115                 120                 125
Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln
    130                 135                 140
Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys
145                 150                 155                 160
Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr
                165                 170                 175
Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp
            180                 185                 190
His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile
        195                 200                 205
Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala
    210                 215                 220
Leu Pro His Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu Pro Asn
225                 230                 235                 240
Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile Thr Met
                245                 250                 255
Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met Leu Arg
            260                 265                 270
Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys Asp Asp
        275                 280                 285
```

<210> 121
<211> 177
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(177)

<400> 121

```
atg gcc gcc acc ttc gac gac tgc ctg tat gcc ttg tgc gtg gtg gac       48
Met Ala Ala Thr Phe Asp Asp Cys Leu Tyr Ala Leu Cys Val Val Asp
 1               5                  10                  15

acc atc aag agg tcc agc cag acg ggc gag tgg cag aac att gcc atc       96
Thr Ile Lys Arg Ser Ser Gln Thr Gly Glu Trp Gln Asn Ile Ala Ile
            20                  25                  30

atg acc gag gag ccg gag ctg agc ccc gcc tac ctg atc agc gag gcc      144
Met Thr Glu Glu Pro Glu Leu Ser Pro Ala Tyr Leu Ile Ser Glu Ala
        35                  40                  45

atg cgc cgc agc agg atg tcc ctc tac tgt tag                          177
Met Arg Arg Ser Arg Met Ser Leu Tyr Cys  *
    50                  55
```

<210> 122
<211> 58
<212> PRT
<213> Homo sapiens

<400> 122

```
Met Ala Ala Thr Phe Asp Asp Cys Leu Tyr Ala Leu Cys Val Val Asp
 1               5                  10                  15
Thr Ile Lys Arg Ser Ser Gln Thr Gly Glu Trp Gln Asn Ile Ala Ile
            20                  25                  30
Met Thr Glu Glu Pro Glu Leu Ser Pro Ala Tyr Leu Ile Ser Glu Ala
        35                  40                  45
Met Arg Arg Ser Arg Met Ser Leu Tyr Cys
    50                  55
```

<210> 123
<211> 1158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1158)

<400> 123

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atg cag tac cac gcg ctg tcg ttg gcc atg cac ggc ttc tcg gtg acc       48
Met Gln Tyr His Ala Leu Ser Leu Ala Met His Gly Phe Ser Val Thr
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1 5 10 15

ctc ctg ggg ttc tgc aac tcc aaa ccc cat gat gag ctc ttg cag aac 96
Leu Leu Gly Phe Cys Asn Ser Lys Pro His Asp Glu Leu Leu Gln Asn
20 25 30

aac aga att cag att gtg ggg ttg aca gaa ctt cag agt ctt gca gtt 144
Asn Arg Ile Gln Ile Val Gly Leu Thr Glu Leu Gln Ser Leu Ala Val
35 40 45

ggg ccc cga gtt ttc cag tac gga gtc aaa gtt gta ctt cag gct atg 192
Gly Pro Arg Val Phe Gln Tyr Gly Val Lys Val Val Leu Gln Ala Met
50 55 60

tac ttg ctg tgg aag ttg atg tgg agg gag cca ggt gcc tat atc ttt 240
Tyr Leu Leu Trp Lys Leu Met Trp Arg Glu Pro Gly Ala Tyr Ile Phe
65 70 75 80

ctc cag aac ccc cca ggt ctg cct agc att gct gtc tgc tgg ttc gtg 288
Leu Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala Val Cys Trp Phe Val
85 90 95

ggc tgc ctt tgt gga agc aag ctc gtc att gac tgg cac aac tat ggc 336
Gly Cys Leu Cys Gly Ser Lys Leu Val Ile Asp Trp His Asn Tyr Gly
100 105 110

tac tcc atc atg ggt ctg gtg cat ggc ccc aac cat ccc ctc gtt ctg 384
Tyr Ser Ile Met Gly Leu Val His Gly Pro Asn His Pro Leu Val Leu
115 120 125

ctg gcc aag tgg tac gag aag ttc ttt ggg cgc ctg tcc cac ctg aac 432
Leu Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn
130 135 140

ctg tgt gtt acc aat gct atg cga gaa gac ctg gcg gat aac tgg cac 480
Leu Cys Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His
145 150 155 160

atc agg gct gtg acc gtc tac gac aag ccc gca tct ttc ttt aaa gag 528
Ile Arg Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu
165 170 175

aca cct ctg gac ctg cag cac cgg ctc ttc atg aag ctg ggc agc atg 576
Thr Pro Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met

180 185 190

cac tct ccg ttc agg gcc cgc tca gaa cct gag gac cca gtc acg gag 624
His Ser Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu
195 200 205

cgg tcg gcc ttc acg gag cgg gat gct ggg agc ggg ctg gtg acg cgt 672
Arg Ser Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg
210 215 220

ctc cgt gag cgg cca gcc ctg ctg gtc agc agc acg agc tgg aca gag 720
Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu
225 230 235 240

gac gaa gac ttc tcc atc ctg ctg gca gct tta gaa aag ttt gaa caa 768
Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln
245 250 255

ctg act ctt gat gga cac aac ctt cct tct ctc gtc tgt gtg ata aca 816
Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr
260 265 270

ggc aaa ggg cct ctg agg gag tat tat agc cgc ctc atc cac cag aag 864
Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys
275 280 285

cac ttc cag cac atc cag gtc tgc acc ccc tgg ctg gag gcc gag gac 912
His Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp
290 295 300

tac ccc ctg ctt cta ggg tcg gcg gac ctg ggt gtc tgt ctg cac acg 960
Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr
305 310 315 320

tcc tcc agt ggc ctg gac ctg ccc atg aag gtg gtg gac atg ttc ggg 1008
Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly
325 330 335

tgc tgt ttg cct gtg tgt gct gtg aac ttc aag tgt tta cat gag ctg 1056
Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu
340 345 350

gtg aaa cat gaa gaa aat ggc ctg gtc ttt gag gac tca gag gaa ctg 1104
Val Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu

355 360 365

gca gct cag ctg cag atg ctt ttc tca aac ttt cct gat ctg cgg gca 1152
Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Leu Arg Ala
370 375 380

agc taa 1158
Ser *
385

<210> 124
<211> 385
<212> PRT
<213> Homo sapiens

<400> 124
Met Gln Tyr His Ala Leu Ser Leu Ala Met His Gly Phe Ser Val Thr
1 5 10 15
Leu Leu Gly Phe Cys Asn Ser Lys Pro His Asp Glu Leu Leu Gln Asn
20 25 30
Asn Arg Ile Gln Ile Val Gly Leu Thr Glu Leu Gln Ser Leu Ala Val
35 40 45
Gly Pro Arg Val Phe Gln Tyr Gly Val Lys Val Val Leu Gln Ala Met
50 55 60
Tyr Leu Leu Trp Lys Leu Met Trp Arg Glu Pro Gly Ala Tyr Ile Phe
65 70 75 80
Leu Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala Val Cys Trp Phe Val
85 90 95
Gly Cys Leu Cys Gly Ser Lys Leu Val Ile Asp Trp His Asn Tyr Gly
100 105 110
Tyr Ser Ile Met Gly Leu Val His Gly Pro Asn His Pro Leu Val Leu
115 120 125
Leu Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn
130 135 140
Leu Cys Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His
145 150 155 160
Ile Arg Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu
165 170 175
Thr Pro Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met
180 185 190
His Ser Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu
195 200 205
Arg Ser Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg

```
    210                 215                 220
Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu
225                 230                 235                 240
Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln
                245                 250                 255
Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr
            260                 265                 270
Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys
        275                 280                 285
His Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp
    290                 295                 300
Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr
305                 310                 315                 320
Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly
                325                 330                 335
Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu
            340                 345                 350
Val Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu
        355                 360                 365
Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Leu Arg Ala
    370                 375                 380
Ser
385

      <210> 125
      <211> 1002
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(1002)

      <221> misc_feature
      <222> (1)...(1002)
      <223> n = A,T,C or G

      <400> 125
atg gcg gcc gcc gca ggn nga ncg ctc ctg ctg ctc ctc tcc tct cgg      48
Met Ala Ala Ala Ala Xaa Xaa Xaa Leu Leu Leu Leu Leu Ser Ser Arg
 1               5                  10                  15

ggc ggc ggc ggc ggg ggc gcc ggc ggc tgc ggg gcg ctg act gcc ggc      96
Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly
```

20 25 30

tgc ttc cct ggg ctg ggc gtc agc cgc cac cgg cag cag cag cac cac 144
Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln His His
35 40 45

cgg acg gta cac cag agg atc gct tcc tgg cag aat ttg gga gct gtt 192
Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val
50 55 60

tat tgc agc act gtt gtg ccc tct gat gat gtt aca gtg gtt tat caa 240
Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln
65 70 75 80

aat ggg tta cct gtg ata tct gtg agg cta cca tcc cgg cgt gaa cgc 288
Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg
85 90 95

tgt cag ttc aca ctc aag cct atc tct gac tct gtt ggt gta ttt tta 336
Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu
100 105 110

cga caa ctg caa gaa gag gat cgg gga att gac aga gtt gct atc tat 384
Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr
115 120 125

tca cca gat ggt gtt cgc gtt gct gct tca aca gga ata gac ctc ctc 432
Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu
130 135 140

ctc ctt gat gac ttt aag ctg gtc att aat gac tta aca tac cac gta 480
Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val
145 150 155 160

cga cca cca aaa aga gac ctc tta agt cat gaa aat gca gca acg ctg 528
Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu
165 170 175

aat gat gta aag aca ttg gtc cag caa cta tac acc aca ctg tgc att 576
Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile
180 185 190

gag cag cac cag tta aac aag gaa agg gag ctt att gaa aga cta gag 624
Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu

```
    195                 200                 205

gat ctc aaa gag cag ctg gct ccc ctg gaa aag gta cga att gag att     672
Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile
    210                 215                 220

agc aga aaa gct gag aag agg acc act ttg gtg cta tgg ggt ggc ctt     720
Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Gly Gly Leu
225                 230                 235                 240

gcc tac atg gcc aca cag ttt ggc att ttg gcc cgg ctt acc tgg tgg     768
Ala Tyr Met Ala Thr Gln Phe Gly Ile Leu Ala Arg Leu Thr Trp Trp
                245                 250                 255

gaa tat tcc tgg gac atc atg gag cca gta aca tac ttc atc act tat     816
Glu Tyr Ser Trp Asp Ile Met Glu Pro Val Thr Tyr Phe Ile Thr Tyr
            260                 265                 270

gga agt gcc atg gca atg tat gca tat ttt gta atg aca cgc cag gaa     864
Gly Ser Ala Met Ala Met Tyr Ala Tyr Phe Val Met Thr Arg Gln Glu
        275                 280                 285

tat gtt tat cca gaa gcc aga gac aga caa tac tta cta ttt ttc cat     912
Tyr Val Tyr Pro Glu Ala Arg Asp Arg Gln Tyr Leu Leu Phe Phe His
    290                 295                 300

aaa gga gcc aaa aag tca cgt ttt gac cta gag aaa tac aat caa ctc     960
Lys Gly Ala Lys Lys Ser Arg Phe Asp Leu Glu Lys Tyr Asn Gln Leu
305                 310                 315                 320

aag gat gca att gct cag cag aaa tgg acc tta aga gac tga            1002
Lys Asp Ala Ile Ala Gln Gln Lys Trp Thr Leu Arg Asp  *
                325                 330
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<210> 126
<211> 333
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(333)
<223> Xaa = Any Amino Acid

<400> 126

Met Ala Ala Ala Ala Xaa Xaa Xaa Leu Leu Leu Leu Leu Ser Ser Arg
1   5   10   15
Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly
            20   25   30
Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln His His
        35   40   45
Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val
    50   55   60
Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln
65   70   75   80
Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg
                85   90   95
Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu
            100   105   110
Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr
        115   120   125
Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu
    130   135   140
Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val
145   150   155   160
Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu
                165   170   175
Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile
            180   185   190
Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu
        195   200   205
Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile
    210   215   220
Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Gly Gly Leu
225   230   235   240
Ala Tyr Met Ala Thr Gln Phe Gly Ile Leu Ala Arg Leu Thr Trp Trp
                245   250   255
Glu Tyr Ser Trp Asp Ile Met Glu Pro Val Thr Tyr Phe Ile Thr Tyr
            260   265   270
Gly Ser Ala Met Ala Met Tyr Ala Tyr Phe Val Met Thr Arg Gln Glu
        275   280   285
Tyr Val Tyr Pro Glu Ala Arg Asp Arg Gln Tyr Leu Leu Phe Phe His
    290   295   300
Lys Gly Ala Lys Lys Ser Arg Phe Asp Leu Glu Lys Tyr Asn Gln Leu
305   310   315   320
Lys Asp Ala Ile Ala Gln Gln Lys Trp Thr Leu Arg Asp
                325   330

<210> 127
<211> 1164
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1164)

<221> misc_feature
<222> (1)...(1164)
<223> n = A,T,C or G

<400> 127
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atg gtc ata ccc act ttg gcc tcc ctg gct tct cca act aca cta cag       48
Met Val Ile Pro Thr Leu Ala Ser Leu Ala Ser Pro Thr Thr Leu Gln
 1               5                  10                  15

tcc cag atg ctt ggg ggc cta gga cag gat gtt ttg tta aat aat tca       96
Ser Gln Met Leu Gly Gly Leu Gly Gln Asp Val Leu Leu Asn Asn Ser
            20                  25                  30

ctc act cct aaa tat ctt ggc tgt aag caa gac aac agc tct tcc cct      144
Leu Thr Pro Lys Tyr Leu Gly Cys Lys Gln Asp Asn Ser Ser Ser Pro
        35                  40                  45

aag ccc agc tcc gtg ttc aga aat gga ttc tct ggc att aag aag cct      192
Lys Pro Ser Ser Val Phe Arg Asn Gly Phe Ser Gly Ile Lys Lys Pro
    50                  55                  60

tgg cac aga tgt cac gtc tgc aac cac cac ttc cag ttc aaa cag cac      240
Trp His Arg Cys His Val Cys Asn His His Phe Gln Phe Lys Gln His
 65                  70                  75                  80

ctt cga gac cac atg aat aca cac acc aac aga cgc cct tac agt tgt      288
Leu Arg Asp His Met Asn Thr His Thr Asn Arg Arg Pro Tyr Ser Cys
                85                  90                  95

cgg att tgt cgc aag tcc tat gta cgt cct ggc agc ctg agc aca cac      336
Arg Ile Cys Arg Lys Ser Tyr Val Arg Pro Gly Ser Leu Ser Thr His
            100                 105                 110

atg aaa ctt cat cat ggt gag aac cgt ctg aag aaa ctc atg tgt tgt      384
```

```
Met Lys Leu His His Gly Glu Asn Arg Leu Lys Lys Leu Met Cys Cys
        115                 120                 125

gag ttt tgt gca aaa gtg ttt ggc cac atc cga gtc tat ttt ggc cat      432
Glu Phe Cys Ala Lys Val Phe Gly His Ile Arg Val Tyr Phe Gly His
    130                 135                 140

ctg aaa gaa gtg cat agg gtt gtg atc agc act gag cct gcg ccc agt      480
Leu Lys Glu Val His Arg Val Val Ile Ser Thr Glu Pro Ala Pro Ser
145                 150                 155                 160

gaa ctg cag cca gga gac ata cca aag aac aga gac atg agt gtg cga      528
Glu Leu Gln Pro Gly Asp Ile Pro Lys Asn Arg Asp Met Ser Val Arg
                165                 170                 175

ggc atg gag gga tca ttg gag agg gaa aac aag tcc aac ctg gaa gaa      576
Gly Met Glu Gly Ser Leu Glu Arg Glu Asn Lys Ser Asn Leu Glu Glu
            180                 185                 190

gac ttc ctt cta aac cag gca gac gaa gtc aaa tta caa atc aaa tgt      624
Asp Phe Leu Leu Asn Gln Ala Asp Glu Val Lys Leu Gln Ile Lys Cys
        195                 200                 205

ggt cnt tgt cag att act gct cag tct ttt gcg gaa ata aaa ttt cat      672
Gly Xaa Cys Gln Ile Thr Ala Gln Ser Phe Ala Glu Ile Lys Phe His
    210                 215                 220

tta ctt gat gtt cat gga gag gaa att gag ggc agg cta caa gaa ggg      720
Leu Leu Asp Val His Gly Glu Glu Ile Glu Gly Arg Leu Gln Glu Gly
225                 230                 235                 240

acc ttc cca gga agc aag ggg act cag gaa gag ttg gtg cag cac gct      768
Thr Phe Pro Gly Ser Lys Gly Thr Gln Glu Glu Leu Val Gln His Ala
                245                 250                 255

agc ccc gac tgg aaa agg cat cct gag aga ggg aag ccg gag aag gtt      816
Ser Pro Asp Trp Lys Arg His Pro Glu Arg Gly Lys Pro Glu Lys Val
            260                 265                 270

cat tcc tcc tcc gag gaa tca cat gca tgt cca aga ctg aaa agg cag      864
His Ser Ser Ser Glu Glu Ser His Ala Cys Pro Arg Leu Lys Arg Gln
        275                 280                 285

ctc cac ctt cat cag aat ggc gtg gaa atg ctc atg gaa aat gaa gga      912
```

```
Leu His Leu His Gln Asn Gly Val Glu Met Leu Met Glu Asn Glu Gly
    290                 295                 300

ccc cag tca gga acc aac aag cca agg gaa acc tgc cag ggc cct gag      960
Pro Gln Ser Gly Thr Asn Lys Pro Arg Glu Thr Cys Gln Gly Pro Glu
305                 310                 315                 320

tgt cct ggc ctc cac acg ttt ctc ttg tgg tcc cat tca ggc ttt aac     1008
Cys Pro Gly Leu His Thr Phe Leu Leu Trp Ser His Ser Gly Phe Asn
                325                 330                 335

tgc ctg ctt tgt gca gag atg ctg gga cgg aaa gag gac ctc ctc cac     1056
Cys Leu Leu Cys Ala Glu Met Leu Gly Arg Lys Glu Asp Leu Leu His
            340                 345                 350

cac tgg aag cac cag cat aac tgt gag gac cct tcc aaa ctg tgg gct     1104
His Trp Lys His Gln His Asn Cys Glu Asp Pro Ser Lys Leu Trp Ala
        355                 360                 365

att tta aat acg gtc tcc aac cag gga gtg atc gaa ctt tcc agt gaa     1152
Ile Leu Asn Thr Val Ser Asn Gln Gly Val Ile Glu Leu Ser Ser Glu
    370                 375                 380

gct gag aaa tga                                                     1164
Ala Glu Lys  *
385


      <210> 128
      <211> 387
      <212> PRT
      <213> Homo sapiens

      <220>
      <221> VARIANT
      <222> (1)...(387)
      <223> Xaa = Any Amino Acid

      <400> 128
Met Val Ile Pro Thr Leu Ala Ser Leu Ala Ser Pro Thr Thr Leu Gln
 1               5                  10                  15
Ser Gln Met Leu Gly Gly Leu Gly Gln Asp Val Leu Leu Asn Asn Ser
            20                  25                  30
Leu Thr Pro Lys Tyr Leu Gly Cys Lys Gln Asp Asn Ser Ser Ser Pro
```

35 40 45
Lys Pro Ser Ser Val Phe Arg Asn Gly Phe Ser Gly Ile Lys Lys Pro
50 55 60
Trp His Arg Cys His Val Cys Asn His His Phe Gln Phe Lys Gln His
65 70 75 80
Leu Arg Asp His Met Asn Thr His Thr Asn Arg Arg Pro Tyr Ser Cys
85 90 95
Arg Ile Cys Arg Lys Ser Tyr Val Arg Pro Gly Ser Leu Ser Thr His
100 105 110
Met Lys Leu His His Gly Glu Asn Arg Leu Lys Lys Leu Met Cys Cys
115 120 125
Glu Phe Cys Ala Lys Val Phe Gly His Ile Arg Val Tyr Phe Gly His
130 135 140
Leu Lys Glu Val His Arg Val Val Ile Ser Thr Glu Pro Ala Pro Ser
145 150 155 160
Glu Leu Gln Pro Gly Asp Ile Pro Lys Asn Arg Asp Met Ser Val Arg
165 170 175
Gly Met Glu Gly Ser Leu Glu Arg Glu Asn Lys Ser Asn Leu Glu Glu
180 185 190
Asp Phe Leu Leu Asn Gln Ala Asp Glu Val Lys Leu Gln Ile Lys Cys
195 200 205
Gly Xaa Cys Gln Ile Thr Ala Gln Ser Phe Ala Glu Ile Lys Phe His
210 215 220
Leu Leu Asp Val His Gly Glu Glu Ile Glu Gly Arg Leu Gln Glu Gly
225 230 235 240
Thr Phe Pro Gly Ser Lys Gly Thr Gln Glu Glu Leu Val Gln His Ala
245 250 255
Ser Pro Asp Trp Lys Arg His Pro Glu Arg Gly Lys Pro Glu Lys Val
260 265 270
His Ser Ser Ser Glu Glu Ser His Ala Cys Pro Arg Leu Lys Arg Gln
275 280 285
Leu His Leu His Gln Asn Gly Val Glu Met Leu Met Glu Asn Glu Gly
290 295 300
Pro Gln Ser Gly Thr Asn Lys Pro Arg Glu Thr Cys Gln Gly Pro Glu
305 310 315 320
Cys Pro Gly Leu His Thr Phe Leu Leu Trp Ser His Ser Gly Phe Asn
325 330 335
Cys Leu Leu Cys Ala Glu Met Leu Gly Arg Lys Glu Asp Leu Leu His
340 345 350
His Trp Lys His Gln His Asn Cys Glu Asp Pro Ser Lys Leu Trp Ala
355 360 365
Ile Leu Asn Thr Val Ser Asn Gln Gly Val Ile Glu Leu Ser Ser Glu
370 375 380
Ala Glu Lys

385

<210> 129
<211> 2022
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2022)

<221> misc_feature
<222> (1)...(2022)
<223> n = A,T,C or G

<400> 129
atg aag aag gac tgc agt ctt cct ctt act gtc ctt acc tgt gct aaa 48
Met Lys Lys Asp Cys Ser Leu Pro Leu Thr Val Leu Thr Cys Ala Lys
1 5 10 15

gca tgt cca cac atg gct act tgt gga aat gtt ctg ttt gag gga aga 96
Ala Cys Pro His Met Ala Thr Cys Gly Asn Val Leu Phe Glu Gly Arg
20 25 30

aca gtt cag cta ggg aag ctt tgc tgc act gga gtt gaa act gaa gat 144
Thr Val Gln Leu Gly Lys Leu Cys Cys Thr Gly Val Glu Thr Glu Asp
35 40 45

gat gaa gat act gag tca aat tca tcg gta gaa caa gca tcg gtt gaa 192
Asp Glu Asp Thr Glu Ser Asn Ser Ser Val Glu Gln Ala Ser Val Glu
50 55 60

gta cct gat gga cca aca ctc cat gac cca gac ctc tat att gag att 240
Val Pro Asp Gly Pro Thr Leu His Asp Pro Asp Leu Tyr Ile Glu Ile
65 70 75 80

gtg aaa aat acg aag tct gtc cca gaa tat tca gag gtg gct tat ccc 288
Val Lys Asn Thr Lys Ser Val Pro Glu Tyr Ser Glu Val Ala Tyr Pro
85 90 95

gat tat ttt ggt cac att ccg cct cca ttc aaa gag cct att tta gaa 336
Asp Tyr Phe Gly His Ile Pro Pro Pro Phe Lys Glu Pro Ile Leu Glu
100 105 110

agg cct tat ggt gta caa agg aca aaa att gct caa gat att gaa agg 384
Arg Pro Tyr Gly Val Gln Arg Thr Lys Ile Ala Gln Asp Ile Glu Arg
115 120 125

cta ata cat cag agt gat atc ata gat cgt gtg gta tat gac ttg gat 432
Leu Ile His Gln Ser Asp Ile Ile Asp Arg Val Val Tyr Asp Leu Asp
130 135 140

aac cca aat tac acc att cca gaa gag gga gat att ttg aaa ttt aac 480
Asn Pro Asn Tyr Thr Ile Pro Glu Glu Gly Asp Ile Leu Lys Phe Asn
145 150 155 160

tcc aaa ttt gag tct ggg aat ctg cgc ana gta att caa att aga aaa 528
Ser Lys Phe Glu Ser Gly Asn Leu Arg Xaa Val Ile Gln Ile Arg Lys
165 170 175

aat gaa tat gat ctt att ctg aac tca gac ata aac agc aat cat tat 576
Asn Glu Tyr Asp Leu Ile Leu Asn Ser Asp Ile Asn Ser Asn His Tyr
180 185 190

cat cag tgg ttt tac ttt gaa gtc agt gga atg cga cca ggt gtt gct 624
His Gln Trp Phe Tyr Phe Glu Val Ser Gly Met Arg Pro Gly Val Ala
195 200 205

tac agg ttt aac atc att aac tgt gaa aag tcc aac agt cag ttt aat 672
Tyr Arg Phe Asn Ile Ile Asn Cys Glu Lys Ser Asn Ser Gln Phe Asn
210 215 220

tat ggt atg caa cca ctc atg tat tcg gtt cag gaa gca tta aat gcc 720
Tyr Gly Met Gln Pro Leu Met Tyr Ser Val Gln Glu Ala Leu Asn Ala
225 230 235 240

aga cca tgg tgg att cgt atg ggg act gac att tgt tac tat aaa aat 768
Arg Pro Trp Trp Ile Arg Met Gly Thr Asp Ile Cys Tyr Tyr Lys Asn
245 250 255

cat ttc tca aga agt tca gtt gct gca ggt ggg caa aag gga aaa tcc 816
His Phe Ser Arg Ser Ser Val Ala Ala Gly Gly Gln Lys Gly Lys Ser
260 265 270

tac tat aca att aca ttt act gtc aat ttt cca cat aaa gat gat gtt 864
Tyr Tyr Thr Ile Thr Phe Thr Val Asn Phe Pro His Lys Asp Asp Val
275 280 285

```
tgc tac ttt gct tat cac tat cca tat acg tat tca act tta cag atg      912
Cys Tyr Phe Ala Tyr His Tyr Pro Tyr Thr Tyr Ser Thr Leu Gln Met
    290                 295                 300

cat ctt caa aaa ttg gaa tca gca cac aat cct cag caa atc tat ttt      960
His Leu Gln Lys Leu Glu Ser Ala His Asn Pro Gln Gln Ile Tyr Phe
305                 310                 315                 320

cgg aaa gat gtg tta tgt gaa acc ctg tct gga aac agc tgc ccc ttg     1008
Arg Lys Asp Val Leu Cys Glu Thr Leu Ser Gly Asn Ser Cys Pro Leu
                325                 330                 335

gtg act ata aca gca atg cca gag tct aat tat tat gaa cat atc tgc     1056
Val Thr Ile Thr Ala Met Pro Glu Ser Asn Tyr Tyr Glu His Ile Cys
            340                 345                 350

cat ttc aga aat cgc cct tac gtt ttc ttg tct gct cgg gta cat cct     1104
His Phe Arg Asn Arg Pro Tyr Val Phe Leu Ser Ala Arg Val His Pro
        355                 360                 365

gga gaa act aat gca agt tgg gtt atg aaa gga acg ttg gaa tat ctc     1152
Gly Glu Thr Asn Ala Ser Trp Val Met Lys Gly Thr Leu Glu Tyr Leu
    370                 375                 380

atg agc aat aac ccc act gct cag agc tta cga gaa tct tat att ttt     1200
Met Ser Asn Asn Pro Thr Ala Gln Ser Leu Arg Glu Ser Tyr Ile Phe
385                 390                 395                 400

aaa att gtc cct atg tta aat cca gat ggt gtc atc aat gga aat cat     1248
Lys Ile Val Pro Met Leu Asn Pro Asp Gly Val Ile Asn Gly Asn His
                405                 410                 415

cgc tgt tct tta agt gga gag gat ttg aat agg cag tgg caa agt cca     1296
Arg Cys Ser Leu Ser Gly Glu Asp Leu Asn Arg Gln Trp Gln Ser Pro
            420                 425                 430

agt ccg gat tta cat cct aca att tac cat gct aag ggg ctg ttg caa     1344
Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala Lys Gly Leu Leu Gln
        435                 440                 445

tac ttg gct gca gtg aag cgt tta ccc ttg gtt tat tgt gat tat cat     1392
Tyr Leu Ala Ala Val Lys Arg Leu Pro Leu Val Tyr Cys Asp Tyr His
    450                 455                 460
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ggc cat tcc cga aag aag aat gta ttt atg tat ggt tgc agc atc aaa 1440
Gly His Ser Arg Lys Lys Asn Val Phe Met Tyr Gly Cys Ser Ile Lys
465 470 475 480

gag aca gtg tgg cat acc aat gat aat gca act tca tgt gat gtt gtg 1488
Glu Thr Val Trp His Thr Asn Asp Asn Ala Thr Ser Cys Asp Val Val
485 490 495

gag gat acg gga tac agg aca ttg cct aag ata ctg agc cat atc gcc 1536
Glu Asp Thr Gly Tyr Arg Thr Leu Pro Lys Ile Leu Ser His Ile Ala
500 505 510

cca gca ttt tgc atg agc agc tgt agc ttc gta gtg gaa aaa tct aaa 1584
Pro Ala Phe Cys Met Ser Ser Cys Ser Phe Val Val Glu Lys Ser Lys
515 520 525

gaa tcc aca gca cgt gtt gta gtt tgg agg gaa ata gga gta caa aga 1632
Glu Ser Thr Ala Arg Val Val Val Trp Arg Glu Ile Gly Val Gln Arg
530 535 540

agt tat acc atg gag agt act tta tgt ggc tgt gat cag gga aaa tac 1680
Ser Tyr Thr Met Glu Ser Thr Leu Cys Gly Cys Asp Gln Gly Lys Tyr
545 550 555 560

aag ggt tta cag att ggt acc cga gaa ctg gaa gag atg gga gca aaa 1728
Lys Gly Leu Gln Ile Gly Thr Arg Glu Leu Glu Glu Met Gly Ala Lys
565 570 575

ttt tgt gtt ggt ctt tta cgt ttg aaa aga ctg acc tct cca ttg gag 1776
Phe Cys Val Gly Leu Leu Arg Leu Lys Arg Leu Thr Ser Pro Leu Glu
580 585 590

tat aat ctg cct tcc agc ctg ctt gac ttt gaa aat gat tta att gaa 1824
Tyr Asn Leu Pro Ser Ser Leu Leu Asp Phe Glu Asn Asp Leu Ile Glu
595 600 605

tca agc tgc aaa gta act agc cct acc act tat gtc ttg gat gaa gat 1872
Ser Ser Cys Lys Val Thr Ser Pro Thr Thr Tyr Val Leu Asp Glu Asp
610 615 620

gaa cct cga ttc ctt gaa gaa gtt gat tac agt gca gaa agt aat gat 1920
Glu Pro Arg Phe Leu Glu Glu Val Asp Tyr Ser Ala Glu Ser Asn Asp
625 630 635 640

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gag tta gat att gag ttg gct gaa aat gta gga gat tat gaa cct tct      1968
Glu Leu Asp Ile Glu Leu Ala Glu Asn Val Gly Asp Tyr Glu Pro Ser
                645                 650                 655

gct caa gaa gaa gta ctt tct gac tct gaa tta tca aga aca tac cta      2016
Ala Gln Glu Glu Val Leu Ser Asp Ser Glu Leu Ser Arg Thr Tyr Leu
            660                 665                 670

cct tga                                                              2022
Pro  *


      <210> 130
      <211> 673
      <212> PRT
      <213> Homo sapiens

      <220>
      <221> VARIANT
      <222> (1)...(673)
      <223> Xaa = Any Amino Acid

      <400> 130
Met Lys Lys Asp Cys Ser Leu Pro Leu Thr Val Leu Thr Cys Ala Lys
 1               5                  10                  15
Ala Cys Pro His Met Ala Thr Cys Gly Asn Val Leu Phe Glu Gly Arg
            20                  25                  30
Thr Val Gln Leu Gly Lys Leu Cys Cys Thr Gly Val Glu Thr Glu Asp
        35                  40                  45
Asp Glu Asp Thr Glu Ser Asn Ser Ser Val Glu Gln Ala Ser Val Glu
    50                  55                  60
Val Pro Asp Gly Pro Thr Leu His Asp Pro Asp Leu Tyr Ile Glu Ile
65                  70                  75                  80
Val Lys Asn Thr Lys Ser Val Pro Glu Tyr Ser Glu Val Ala Tyr Pro
                85                  90                  95
Asp Tyr Phe Gly His Ile Pro Pro Pro Phe Lys Glu Pro Ile Leu Glu
            100                 105                 110
Arg Pro Tyr Gly Val Gln Arg Thr Lys Ile Ala Gln Asp Ile Glu Arg
        115                 120                 125
Leu Ile His Gln Ser Asp Ile Ile Asp Arg Val Val Tyr Asp Leu Asp
    130                 135                 140
Asn Pro Asn Tyr Thr Ile Pro Glu Glu Gly Asp Ile Leu Lys Phe Asn
145                 150                 155                 160
```

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Ser Lys Phe Glu Ser Gly Asn Leu Arg Xaa Val Ile Gln Ile Arg Lys
                165                 170                 175
Asn Glu Tyr Asp Leu Ile Leu Asn Ser Asp Ile Asn Ser Asn His Tyr
            180                 185                 190
His Gln Trp Phe Tyr Phe Glu Val Ser Gly Met Arg Pro Gly Val Ala
        195                 200                 205
Tyr Arg Phe Asn Ile Ile Asn Cys Glu Lys Ser Asn Ser Gln Phe Asn
    210                 215                 220
Tyr Gly Met Gln Pro Leu Met Tyr Ser Val Gln Glu Ala Leu Asn Ala
225                 230                 235                 240
Arg Pro Trp Trp Ile Arg Met Gly Thr Asp Ile Cys Tyr Tyr Lys Asn
                245                 250                 255
His Phe Ser Arg Ser Ser Val Ala Ala Gly Gly Gln Lys Gly Lys Ser
            260                 265                 270
Tyr Tyr Thr Ile Thr Phe Thr Val Asn Phe Pro His Lys Asp Asp Val
        275                 280                 285
Cys Tyr Phe Ala Tyr His Tyr Pro Tyr Thr Tyr Ser Thr Leu Gln Met
    290                 295                 300
His Leu Gln Lys Leu Glu Ser Ala His Asn Pro Gln Gln Ile Tyr Phe
305                 310                 315                 320
Arg Lys Asp Val Leu Cys Glu Thr Leu Ser Gly Asn Ser Cys Pro Leu
                325                 330                 335
Val Thr Ile Thr Ala Met Pro Glu Ser Asn Tyr Tyr Glu His Ile Cys
            340                 345                 350
His Phe Arg Asn Arg Pro Tyr Val Phe Leu Ser Ala Arg Val His Pro
        355                 360                 365
Gly Glu Thr Asn Ala Ser Trp Val Met Lys Gly Thr Leu Glu Tyr Leu
    370                 375                 380
Met Ser Asn Asn Pro Thr Ala Gln Ser Leu Arg Glu Ser Tyr Ile Phe
385                 390                 395                 400
Lys Ile Val Pro Met Leu Asn Pro Asp Gly Val Ile Asn Gly Asn His
                405                 410                 415
Arg Cys Ser Leu Ser Gly Glu Asp Leu Asn Arg Gln Trp Gln Ser Pro
            420                 425                 430
Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala Lys Gly Leu Leu Gln
        435                 440                 445
Tyr Leu Ala Ala Val Lys Arg Leu Pro Leu Val Tyr Cys Asp Tyr His
    450                 455                 460
Gly His Ser Arg Lys Lys Asn Val Phe Met Tyr Gly Cys Ser Ile Lys
465                 470                 475                 480
Glu Thr Val Trp His Thr Asn Asp Asn Ala Thr Ser Cys Asp Val Val
                485                 490                 495
Glu Asp Thr Gly Tyr Arg Thr Leu Pro Lys Ile Leu Ser His Ile Ala
            500                 505                 510
```

Pro Ala Phe Cys Met Ser Ser Cys Ser Phe Val Val Glu Lys Ser Lys
515 520 525
Glu Ser Thr Ala Arg Val Val Val Trp Arg Glu Ile Gly Val Gln Arg
530 535 540
Ser Tyr Thr Met Glu Ser Thr Leu Cys Gly Cys Asp Gln Gly Lys Tyr
545 550 555 560
Lys Gly Leu Gln Ile Gly Thr Arg Glu Leu Glu Glu Met Gly Ala Lys
565 570 575
Phe Cys Val Gly Leu Leu Arg Leu Lys Arg Leu Thr Ser Pro Leu Glu
580 585 590
Tyr Asn Leu Pro Ser Ser Leu Leu Asp Phe Glu Asn Asp Leu Ile Glu
595 600 605
Ser Ser Cys Lys Val Thr Ser Pro Thr Thr Tyr Val Leu Asp Glu Asp
610 615 620
Glu Pro Arg Phe Leu Glu Glu Val Asp Tyr Ser Ala Glu Ser Asn Asp
625 630 635 640
Glu Leu Asp Ile Glu Leu Ala Glu Asn Val Gly Asp Tyr Glu Pro Ser
645 650 655
Ala Gln Glu Glu Val Leu Ser Asp Ser Glu Leu Ser Arg Thr Tyr Leu
660 665 670
Pro

<210> 131
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(375)

<400> 131
atg att gga cct gca gta ttc ctg gta gct gct ggc ttc att ggc tgt 48
Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys
1 5 10 15

gat tat tct ttg gcc gtt gct ttc cta act ata tca aca aca ctg gga 96
Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly
20 25 30

ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat att gct cct 144
Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro
35 40 45

```
tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt gcc act att      192
Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile
     50                  55                  60

cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc cct gat aac      240
Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn
 65                  70                  75                  80

act gtt gga gaa tgg caa acc gtg ttc tat att gct gct gct att aat      288
Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn
                 85                  90                  95

gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt gaa gta caa      336
Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln
            100                 105                 110

aac tgg gct ctc aat gat cac cat gga cac aga cac tga                  375
Asn Trp Ala Leu Asn Asp His His Gly His Arg His  *
        115                 120
```

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      <210> 132
      <211> 124
      <212> PRT
      <213> Homo sapiens

      <400> 132
Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys
 1               5                  10                  15
Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly
            20                  25                  30
Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro
        35                  40                  45
Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile
    50                  55                  60
Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn
65                  70                  75                  80
Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn
                85                  90                  95
Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln
            100                 105                 110
Asn Trp Ala Leu Asn Asp His His Gly His Arg His
        115                 120
```

<210> 133
<211> 1485
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1485)

<221> misc_feature
<222> (1)...(1485)
<223> n = A,T,C or G

<400> 133
atg ccc gca gag tct gga aag aga ttc aaa ccc agc aag tat gtc ccg 48
Met Pro Ala Glu Ser Gly Lys Arg Phe Lys Pro Ser Lys Tyr Val Pro
1 5 10 15

gtc tct gca gcc gcc atc ttc cta gtg gga gct acg aca ctc ttc ttt 96
Val Ser Ala Ala Ala Ile Phe Leu Val Gly Ala Thr Thr Leu Phe Phe
20 25 30

gcc ttt acg tgt cca gga cta agc ctg tat gtg tca cct gca gtg ccc 144
Ala Phe Thr Cys Pro Gly Leu Ser Leu Tyr Val Ser Pro Ala Val Pro
35 40 45

atc tac aat gca att atg ttt ctc ttt gtg ttg gcc aac ttc agc atg 192
Ile Tyr Asn Ala Ile Met Phe Leu Phe Val Leu Ala Asn Phe Ser Met
50 55 60

gcc acc ttc atg gac cca ggg att ttc cct cga gct gag gag gat gag 240
Ala Thr Phe Met Asp Pro Gly Ile Phe Pro Arg Ala Glu Glu Asp Glu
65 70 75 80

gac aag gaa gat gat ttc cga gct ccc ctt tac aaa aca gtg gag ata 288
Asp Lys Glu Asp Asp Phe Arg Ala Pro Leu Tyr Lys Thr Val Glu Ile
85 90 95

aag ggc atc cag gtg cgc atg aaa tgg tgt gcc acc tgc cgc ttt tac 336
Lys Gly Ile Gln Val Arg Met Lys Trp Cys Ala Thr Cys Arg Phe Tyr
100 105 110

cgt ccc cct cga tgt tcc cac tgc agt gtc tgt gac aac tgt gtg gag 384

Arg Pro Pro Arg Cys Ser His Cys Ser Val Cys Asp Asn Cys Val Glu
115 120 125

gaa ttt gat cat cac tgc ccc tgg gtg aat aac tgt att ggt cgc cgg 432
Glu Phe Asp His His Cys Pro Trp Val Asn Asn Cys Ile Gly Arg Arg
130 135 140

aac tac cgt tat ttt ttc ctt ttc ctc ctt tcc ctg aca gcc cac att 480
Asn Tyr Arg Tyr Phe Phe Leu Phe Leu Leu Ser Leu Thr Ala His Ile
145 150 155 160

atg ggt gtg ttt ggc ttt ggc ctc ctt tat gtc ctc tac cac ata gag 528
Met Gly Val Phe Gly Phe Gly Leu Leu Tyr Val Leu Tyr His Ile Glu
165 170 175

gaa ctc tca ggg gtc cgc acg gct gtc aca atg gca gta atg tgt gtg 576
Glu Leu Ser Gly Val Arg Thr Ala Val Thr Met Ala Val Met Cys Val
180 185 190

gct ggc tta ttc ttc atc cct gta gct ggc ctc acg gga ttt cac gtg 624
Ala Gly Leu Phe Phe Ile Pro Val Ala Gly Leu Thr Gly Phe His Val
195 200 205

gtt ctg gtg gcc agg gga cgc aca acc aat gaa cag gtt acg ggt aaa 672
Val Leu Val Ala Arg Gly Arg Thr Thr Asn Glu Gln Val Thr Gly Lys
210 215 220

ttc cgg gga ggt gtg aac ccc ttc acc aat ggc tgc tgt aac aat gtc 720
Phe Arg Gly Gly Val Asn Pro Phe Thr Asn Gly Cys Cys Asn Asn Val
225 230 235 240

agc cgt gtt ctc tgc agt tct cca gca ccc agg tat ttg ggg aga cca 768
Ser Arg Val Leu Cys Ser Ser Pro Ala Pro Arg Tyr Leu Gly Arg Pro
245 250 255

aag aaa gag aag aca att gta atc aga cct ccc ttc ctt cga cca gaa 816
Lys Lys Glu Lys Thr Ile Val Ile Arg Pro Pro Phe Leu Arg Pro Glu
260 265 270

gtt tca gat ggg cag ata act gtg aag atc atg gat aat ggc atc cag 864
Val Ser Asp Gly Gln Ile Thr Val Lys Ile Met Asp Asn Gly Ile Gln
275 280 285

gga gag ctg agg aga aca aag tct aag gga agc ctg gag ata aca gag 912

```
Gly Glu Leu Arg Arg Thr Lys Ser Lys Gly Ser Leu Glu Ile Thr Glu
    290                 295                 300

agc cag tct gca gat gct gaa cct cca cct cct cct aag cca gac ctg      960
Ser Gln Ser Ala Asp Ala Glu Pro Pro Pro Pro Pro Lys Pro Asp Leu
305                 310                 315                 320

agc cgt tac aca ggg ttg cga aca cac ctc ggc ttg gct act aat gag     1008
Ser Arg Tyr Thr Gly Leu Arg Thr His Leu Gly Leu Ala Thr Asn Glu
                325                 330                 335

gat agt agc tta ttg gcc aag gac agc ccc ccg aca cct acc atg tac     1056
Asp Ser Ser Leu Leu Ala Lys Asp Ser Pro Pro Thr Pro Thr Met Tyr
            340                 345                 350

aag tat cgg ccg ggt tac agt agc agc agt acg tca gct gcc atg ccg     1104
Lys Tyr Arg Pro Gly Tyr Ser Ser Ser Ser Thr Ser Ala Ala Met Pro
        355                 360                 365

cat tcc tcc agc gcc aag ttg agt cgt ggg gac agc ttg aag gag cca     1152
His Ser Ser Ser Ala Lys Leu Ser Arg Gly Asp Ser Leu Lys Glu Pro
    370                 375                 380

acc tca att gca gag agc agc cgt cac ccc agc tac cgc tca gag ccc     1200
Thr Ser Ile Ala Glu Ser Ser Arg His Pro Ser Tyr Arg Ser Glu Pro
385                 390                 395                 400

agc ttg gaa cca gag agc ttc cgt tct cct acc ttt ggc aaa agt ttt     1248
Ser Leu Glu Pro Glu Ser Phe Arg Ser Pro Thr Phe Gly Lys Ser Phe
                405                 410                 415

cac ttc gat cca cta tcc agt ggc tca cgc tcc tcc agc ctc aag tca     1296
His Phe Asp Pro Leu Ser Ser Gly Ser Arg Ser Ser Ser Leu Lys Ser
            420                 425                 430

ncc cag ggc aca ggc ttt gag ctg ggc cag ttg caa tcc att cgt tca     1344
Xaa Gln Gly Thr Gly Phe Glu Leu Gly Gln Leu Gln Ser Ile Arg Ser
        435                 440                 445

gag ggc acc acc tcc acc tcc tat aag agc ctg gcc aac cag aca cgc     1392
Glu Gly Thr Thr Ser Thr Ser Tyr Lys Ser Leu Ala Asn Gln Thr Arg
    450                 455                 460

aat gga agc cta tct tat gac agc ttg ctc aca cct tca gac agc cct     1440
```

Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro
465 470 475 480

gat ttt gag tca gtg cag gca ggg ctg agc cag acc cac ctt tag 1485
Asp Phe Glu Ser Val Gln Ala Gly Leu Ser Gln Thr His Leu *
485 490

<210> 134
<211> 494
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(494)
<223> Xaa = Any Amino Acid

<400> 134
Met Pro Ala Glu Ser Gly Lys Arg Phe Lys Pro Ser Lys Tyr Val Pro
1 5 10 15
Val Ser Ala Ala Ala Ile Phe Leu Val Gly Ala Thr Thr Leu Phe Phe
20 25 30
Ala Phe Thr Cys Pro Gly Leu Ser Leu Tyr Val Ser Pro Ala Val Pro
35 40 45
Ile Tyr Asn Ala Ile Met Phe Leu Phe Val Leu Ala Asn Phe Ser Met
50 55 60
Ala Thr Phe Met Asp Pro Gly Ile Phe Pro Arg Ala Glu Glu Asp Glu
65 70 75 80
Asp Lys Glu Asp Asp Phe Arg Ala Pro Leu Tyr Lys Thr Val Glu Ile
85 90 95
Lys Gly Ile Gln Val Arg Met Lys Trp Cys Ala Thr Cys Arg Phe Tyr
100 105 110
Arg Pro Pro Arg Cys Ser His Cys Ser Val Cys Asp Asn Cys Val Glu
115 120 125
Glu Phe Asp His His Cys Pro Trp Val Asn Asn Cys Ile Gly Arg Arg
130 135 140
Asn Tyr Arg Tyr Phe Phe Leu Phe Leu Leu Ser Leu Thr Ala His Ile
145 150 155 160
Met Gly Val Phe Gly Phe Gly Leu Leu Tyr Val Leu Tyr His Ile Glu
165 170 175
Glu Leu Ser Gly Val Arg Thr Ala Val Thr Met Ala Val Met Cys Val
180 185 190
Ala Gly Leu Phe Phe Ile Pro Val Ala Gly Leu Thr Gly Phe His Val

195 200 205
Val Leu Val Ala Arg Gly Arg Thr Thr Asn Glu Gln Val Thr Gly Lys
210 215 220
Phe Arg Gly Gly Val Asn Pro Phe Thr Asn Gly Cys Cys Asn Asn Val
225 230 235 240
Ser Arg Val Leu Cys Ser Ser Pro Ala Pro Arg Tyr Leu Gly Arg Pro
245 250 255
Lys Lys Glu Lys Thr Ile Val Ile Arg Pro Pro Phe Leu Arg Pro Glu
260 265 270
Val Ser Asp Gly Gln Ile Thr Val Lys Ile Met Asp Asn Gly Ile Gln
275 280 285
Gly Glu Leu Arg Arg Thr Lys Ser Lys Gly Ser Leu Glu Ile Thr Glu
290 295 300
Ser Gln Ser Ala Asp Ala Glu Pro Pro Pro Pro Pro Lys Pro Asp Leu
305 310 315 320
Ser Arg Tyr Thr Gly Leu Arg Thr His Leu Gly Leu Ala Thr Asn Glu
325 330 335
Asp Ser Ser Leu Leu Ala Lys Asp Ser Pro Pro Thr Pro Thr Met Tyr
340 345 350
Lys Tyr Arg Pro Gly Tyr Ser Ser Ser Ser Thr Ser Ala Ala Met Pro
355 360 365
His Ser Ser Ser Ala Lys Leu Ser Arg Gly Asp Ser Leu Lys Glu Pro
370 375 380
Thr Ser Ile Ala Glu Ser Ser Arg His Pro Ser Tyr Arg Ser Glu Pro
385 390 395 400
Ser Leu Glu Pro Glu Ser Phe Arg Ser Pro Thr Phe Gly Lys Ser Phe
405 410 415
His Phe Asp Pro Leu Ser Ser Gly Ser Arg Ser Ser Ser Leu Lys Ser
420 425 430
Xaa Gln Gly Thr Gly Phe Glu Leu Gly Gln Leu Gln Ser Ile Arg Ser
435 440 445
Glu Gly Thr Thr Ser Thr Ser Tyr Lys Ser Leu Ala Asn Gln Thr Arg
450 455 460
Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro
465 470 475 480
Asp Phe Glu Ser Val Gln Ala Gly Leu Ser Gln Thr His Leu
485 490

<210> 135
<211> 246
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)...(246)

<400> 135
atg gtt ggg ggg gac gca gat gcc agg tcc aag gcc ttg ctg gga gtc 48
Met Val Gly Gly Asp Ala Asp Ala Arg Ser Lys Ala Leu Leu Gly Val
1 5 10 15

tgc gtc ggg tca ggc acg gaa gcc tat gtc ctg gta ttg gac cct cac 96
Cys Val Gly Ser Gly Thr Glu Ala Tyr Val Leu Val Leu Asp Pro His
20 25 30

tac tgg ggc act cca aaa agc ccc agt gaa cta cag gct gct ggg tgg 144
Tyr Trp Gly Thr Pro Lys Ser Pro Ser Glu Leu Gln Ala Ala Gly Trp
35 40 45

gtg ggc tgg caa gag gtg agt gca gcc ttt gac ccc aac tcc ttc tac 192
Val Gly Trp Gln Glu Val Ser Ala Ala Phe Asp Pro Asn Ser Phe Tyr
50 55 60

aac ctg tgc ttg acc agc ctt agc tcc caa cag cag cag cgc acc ttg 240
Asn Leu Cys Leu Thr Ser Leu Ser Ser Gln Gln Gln Gln Arg Thr Leu
65 70 75 80

gac tga 246
Asp *

<210> 136
<211> 81
<212> PRT
<213> Homo sapiens

<400> 136
Met Val Gly Gly Asp Ala Asp Ala Arg Ser Lys Ala Leu Leu Gly Val
1 5 10 15
Cys Val Gly Ser Gly Thr Glu Ala Tyr Val Leu Val Leu Asp Pro His
20 25 30
Tyr Trp Gly Thr Pro Lys Ser Pro Ser Glu Leu Gln Ala Ala Gly Trp
35 40 45
Val Gly Trp Gln Glu Val Ser Ala Ala Phe Asp Pro Asn Ser Phe Tyr
50 55 60
Asn Leu Cys Leu Thr Ser Leu Ser Ser Gln Gln Gln Gln Arg Thr Leu

65 70 75 80
Asp

<210> 137
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(552)

<400> 137
atg gaa cag cgg tta gct gag ttt cgg gcg gcg cgg aaa cgg gcg ggt 48
Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly
1 5 10 15

ctg gcg gcc caa ccc cct gct gcc agt cag ggc gca caa acc cca gga 96
Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly
20 25 30

gag aag gcg gaa gca gca gcg act cta aag gca gcc cca ggc tgg cta 144
Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu
35 40 45

aag cgg ttc ctg gta tgg aaa cct agg ccc gcg agt gcc cgg gcc cag 192
Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln
50 55 60

ccc ggc cta gtt cag gaa gcg gct cag ccc cag ggc agc aca tca gag 240
Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu
65 70 75 80

aca cca tgg aac aca gcc att cct ctg ccg tcg tgc tgg gac cag tct 288
Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser
85 90 95

ttc ctg acc aat atc acc ttc ttg aag gtt ctt ctc tgg ttg gtc ctg 336
Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu
100 105 110

ctg gga ctg ttt gtg gaa ctg gaa ttt ggc ctg gca tat ttt gtc ctg 384
Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu

115 120 125

tcc ttg ttc tat tgg atg tac gtc ggg aca cga ggc cct gaa gag aag 432
Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys
130 135 140

aaa gag gga gag aag agc gcc tac tct gtg ttc aat cca ggc tgt gaa 480
Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu
145 150 155 160

gcc atc cag ggc acc ctg act gca gag cag ttg gag cgc gag tta cag 528
Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln
165 170 175

ttg aga ccc ctg gca ggg aga tag 552
Leu Arg Pro Leu Ala Gly Arg *
180

<210> 138
<211> 183
<212> PRT
<213> Homo sapiens

<400> 138
Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly
1 5 10 15
Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly
20 25 30
Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu
35 40 45
Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln
50 55 60
Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu
65 70 75 80
Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser
85 90 95
Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu
100 105 110
Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu
115 120 125
Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys
130 135 140
Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu

```
145                 150                 155                 160
Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln
                165                 170                 175
Leu Arg Pro Leu Ala Gly Arg
            180

      <210> 139
      <211> 912
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(912)

      <400> 139
atg gcg gcg gcg gca ttg ggc agc tcc tca ggc tcg gcg tcc ccg gcc      48
Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
 1               5                  10                  15

gtg gct gag ctc tgc cag aac acc ccg gag acc ttt ttg gag gcc tcc      96
Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
            20                  25                  30

aag ctg ctg ctc acc tat gct gac aac atc ctc aga aac cct aat gat     144
Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
        35                  40                  45

gaa aaa tat aga tcc atc cgg att gga aac aca gcc ttt tct act aga     192
Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
    50                  55                  60

ctc ttg cct gtc aga gga gct gtt gaa tgt tta ttt gaa atg ggc ttt     240
Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe
 65                 70                  75                  80

gaa gag gga gaa aca cat ctc atc ttt cct aaa aaa gct tca gtg gag     288
Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu
                85                  90                  95

cag ctg caa aaa att cgt gac ctg att gcc ata gag aga agt agc aga     336
Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg
            100                 105                 110
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ctg gat ggc tca aat aag agc cac aaa gta aag tca tct cag caa cct 384
Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro
115 120 125

gca gcc agt acc cag ctt cct aca aca cca tct tca aat ccc agt ggg 432
Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly
130 135 140

tta aac cag cac aca agg aac cgt caa ggg cag tca tca gat cca cca 480
Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro
145 150 155 160

tct gct tca acg gtt gct gct gac tca gcc att cta gaa gtt ctt cag 528
Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
165 170 175

tcc aac att cag cat gtg ctg gtc tat gaa aat cct gct ctt cag gag 576
Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
180 185 190

aaa gcg ttg gct tgt att ccg gtc caa gaa cta aaa agg aaa tca caa 624
Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
195 200 205

gaa aag tta tcg aga gct aga aaa ttg gat aaa ggt atc aat ata agt 672
Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
210 215 220

gat gag gat ttt ctt ttg ctg gag ctt ttg cac tgg ttt aag gaa gaa 720
Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
225 230 235 240

ttt ttt cac tgg gtg aat aac gtt ttg tgc agc aaa tgt ggt gga cag 768
Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
245 250 255

act agg tct aga gat aga tca tta ctg ccc agt gat gat gag ctg aag 816
Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys
260 265 270

tgg ggt gca aag gaa gtg gaa gat cat tac tgt gat gcc tgc cag ttc 864
Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe
275 280 285

agc aat cga ttc cca aga tgg gtg ccc tgg atg gta aaa tca gaa taa 912
Ser Asn Arg Phe Pro Arg Trp Val Pro Trp Met Val Lys Ser Glu *
290 295 300

<210> 140
<211> 303
<212> PRT
<213> Homo sapiens

<400> 140
Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
1 5 10 15
Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
20 25 30
Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
35 40 45
Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
50 55 60
Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe
65 70 75 80
Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu
85 90 95
Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg
100 105 110
Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro
115 120 125
Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly
130 135 140
Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro
145 150 155 160
Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
165 170 175
Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
180 185 190
Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
195 200 205
Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
210 215 220
Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
225 230 235 240
Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
245 250 255
Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys

```
            260                 265                 270
Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe
        275                 280                 285
Ser Asn Arg Phe Pro Arg Trp Val Pro Trp Met Val Lys Ser Glu
    290                 295                 300

      &lt;210&gt; 141
      &lt;211&gt; 750
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapiens

      &lt;220&gt;
      &lt;221&gt; CDS
      &lt;222&gt; (1)...(750)

      &lt;400&gt; 141
atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc      48
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1               5                  10                  15

ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg      96
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
            20                  25                  30

cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca gaa gac     144
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
        35                  40                  45

tta act gat ggt tca tat gat gat gtt cta aat gct gaa caa ctt cag     192
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
    50                  55                  60

aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta att att gaa     240
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
65                  70                  75                  80

aga gct ttg att act ttg ggt aac aat gca gcc ttt tca gtt aac caa     288
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
                85                  90                  95

gct att att cgt gaa ttg ggt ggt att cca att gtt gca aac aaa atc     336
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
            100                 105                 110
```

aac cat tcc aac cag agt att aaa gag aaa gct tta aat gca cta aat 384
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
115 120 125

aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag gtg caa gtt 432
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val
130 135 140

ttg aaa ctg ctt ttg aat ttg tct gaa aat cca gcc atg aca gaa gga 480
Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly
145 150 155 160

ctt ctc cgt gcc caa gtg gat tca tca ttc ctt tcc ctt tat gac agc 528
Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser
165 170 175

cac gta gca aag gag att ctt ctt cga gta ctt acg cta ttt cag aat 576
His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn
180 185 190

ata aag aac tgc ctc aaa ata gaa ggc cat tta gct gtg cag cct act 624
Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr
195 200 205

ttc act gaa ggt tca ttg ttt ttc ctg tta cat gga gaa gaa tgt gcc 672
Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala
210 215 220

cag aaa ata aga gct tta gtt gat cac cat gat gca gag gtg aag gaa 720
Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu
225 230 235 240

aag gtt gta aca ata ata ccc aaa atc tga 750
Lys Val Val Thr Ile Ile Pro Lys Ile *
245

<210> 142
<211> 249
<212> PRT
<213> Homo sapiens

<400> 142
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu

1 5 10 15
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
20 25 30
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
35 40 45
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
50 55 60
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
65 70 75 80
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
85 90 95
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
100 105 110
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
115 120 125
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val
130 135 140
Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly
145 150 155 160
Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser
165 170 175
His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn
180 185 190
Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr
195 200 205
Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala
210 215 220
Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu
225 230 235 240
Lys Val Val Thr Ile Ile Pro Lys Ile
245

<210> 143
<211> 846
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(846)

<221> misc_feature
<222> (1)...(846)
<223> n = A,T,C or G

<400> 143

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atg ctg ccc aag tcc cgg cga gcc cta act atc cag gng atc gct gcg      48
Met Leu Pro Lys Ser Arg Arg Ala Leu Thr Ile Gln Xaa Ile Ala Ala
1               5                   10                  15

ctg gcc agg tcc tcc ctg cat ggt att tcc cag gtg gtg aag gac cac      96
Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val Lys Asp His
            20                  25                  30

gtg acc aag cct acc gcc atg gcc cag ggc cga gtg gct cac ctc att     144
Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile
        35                  40                  45

gag tgg aag ggc tgg agc aag ccg agt gac tca cct gct gcc ctg gaa     192
Glu Trp Lys Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu
    50                  55                  60

tca gcc ttt tcc tcc tat tca gac ctc agc gag ggc gaa caa gag gct     240
Ser Ala Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala
65                  70                  75                  80

cgc ttt gca gca gga gtg gct gag cag ttt gcc atc gcg gaa gcc aag     288
Arg Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
                85                  90                  95

ctc cga gca tgg tct tcg gtg gat ggc gag gac tcc act gat gac tcc     336
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp Ser
            100                 105                 110

tat gat gag gac ttt gct ggg gga atg gac aca gac atg gct ggg cag     384
Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala Gly Gln
        115                 120                 125

ctg ccc ctg ggg ccg cac ctc cag gac ctg ttc acc ggc cac cgg ttc     432
Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly His Arg Phe
    130                 135                 140

tcc cgg cct gtg cgc cag ggc tcc gtg gag cct gag agc gac tgc tca     480
Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu Ser Asp Cys Ser
145                 150                 155                 160

cag acc gtg tcc cca gac acc ctg tgc tct agt ctg tgc agc ctg gag     528
Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser Leu Cys Ser Leu Glu
```

165 170 175

gat ggg ttg ttg ggc tcc ccg gcc cgg ctg gcc tcc cag ctg ctg ggc 576
Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu Ala Ser Gln Leu Leu Gly
180 185 190

gat gag ctg ctt ctc gcc aaa ctg ccc ccc agc cgg gaa agt gcc ttc 624
Asp Glu Leu Leu Leu Ala Lys Leu Pro Pro Ser Arg Glu Ser Ala Phe
195 200 205

cgc agc ctg ggc cca ctg gag gcc cag gac tca ctc tac aac tcg ccc 672
Arg Ser Leu Gly Pro Leu Glu Ala Gln Asp Ser Leu Tyr Asn Ser Pro
210 215 220

ctc aca gag tcc tgc ctt tcc ccc gcg gag gag gag cca gcc ccc tgc 720
Leu Thr Glu Ser Cys Leu Ser Pro Ala Glu Glu Glu Pro Ala Pro Cys
225 230 235 240

aag gac tgc cag cca ctc tgc cca cca cta acg ggc agc tgg gaa cgg 768
Lys Asp Cys Gln Pro Leu Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg
245 250 255

cag cgg caa gcc tct gac ctg gcc tct tct ggg gtg gtg tcc tta gat 816
Gln Arg Gln Ala Ser Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp
260 265 270

gag gat gag gca gag cca gag gaa cag tga 846
Glu Asp Glu Ala Glu Pro Glu Glu Gln *
275 280

<210> 144
<211> 281
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(281)
<223> Xaa = Any Amino Acid

<400> 144
Met Leu Pro Lys Ser Arg Arg Ala Leu Thr Ile Gln Xaa Ile Ala Ala
1 5 10 15

Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val Lys Asp His
20 25 30
Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile
35 40 45
Glu Trp Lys Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu
50 55 60
Ser Ala Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala
65 70 75 80
Arg Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
85 90 95
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp Ser
100 105 110
Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala Gly Gln
115 120 125
Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly His Arg Phe
130 135 140
Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu Ser Asp Cys Ser
145 150 155 160
Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser Leu Cys Ser Leu Glu
165 170 175
Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu Ala Ser Gln Leu Leu Gly
180 185 190
Asp Glu Leu Leu Leu Ala Lys Leu Pro Pro Ser Arg Glu Ser Ala Phe
195 200 205
Arg Ser Leu Gly Pro Leu Glu Ala Gln Asp Ser Leu Tyr Asn Ser Pro
210 215 220
Leu Thr Glu Ser Cys Leu Ser Pro Ala Glu Glu Glu Pro Ala Pro Cys
225 230 235 240
Lys Asp Cys Gln Pro Leu Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg
245 250 255
Gln Arg Gln Ala Ser Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp
260 265 270
Glu Asp Glu Ala Glu Pro Glu Glu Gln
275 280

<210> 145
<211> 1353
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1353)

<400> 145

atg ctg gtg act gcc tac ctt gct ttt gta ggc ctc ctg gcc tcc tgc 48
Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser Cys
1 5 10 15

ctg ggg ctg gaa ctg tca aga tgc cgg gct aaa ccc cct gga agg gcc 96
Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly Arg Ala
20 25 30

tgc agc aat ccc tcc ttc ctt cgg ttt caa ctg gac ttc tat cag gtc 144
Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe Tyr Gln Val
35 40 45

tac ttc ctg gcc ctg gca gct gat tgg ctt cag gcc ccc tac ctc tat 192
Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala Pro Tyr Leu Tyr
50 55 60

aaa ctc tac cag cat tac tac ttc ctg gaa ggt caa att gcc atc ctc 240
Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly Gln Ile Ala Ile Leu
65 70 75 80

tat gtc tgt ggc ctt gcc tct aca gtc ctc ttt ggc cta gtg gcc tcc 288
Tyr Val Cys Gly Leu Ala Ser Thr Val Leu Phe Gly Leu Val Ala Ser
85 90 95

tcc ctt gtg gat tgg ctg ggt cgc aag aat tct tgt gtc ctc ttc tcc 336
Ser Leu Val Asp Trp Leu Gly Arg Lys Asn Ser Cys Val Leu Phe Ser
100 105 110

ctg act tac tca cta tgc tgc tta acc aaa ctc tct caa gac tac ttt 384
Leu Thr Tyr Ser Leu Cys Cys Leu Thr Lys Leu Ser Gln Asp Tyr Phe
115 120 125

gtg ctg cta gtg ggg cga gca ctt ggt ggg ctg tcc aca gcc ctg ctc 432
Val Leu Leu Val Gly Arg Ala Leu Gly Gly Leu Ser Thr Ala Leu Leu
130 135 140

ttc tca gcc ttc gag gcc tgg tat atc cat gag cac gtg gaa cgg cat 480
Phe Ser Ala Phe Glu Ala Trp Tyr Ile His Glu His Val Glu Arg His
145 150 155 160

gac ttc cct gct gag tgg atc cca gct acc ttt gct cga gct gcc ttc 528
Asp Phe Pro Ala Glu Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe
165 170 175

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tgg aac cat gtg ctg gct gta gtg gca ggt gtg gca gct gag gct gta      576
Trp Asn His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val
            180                 185                 190

gcc agc tgg ata ggg ctg ggg cct gta gcg ccc ttt gtg gct gcc atc      624
Ala Ser Trp Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile
        195                 200                 205

cct ctc ctg gct ctg gca ggg gcc ttg gcc ctt cga aac tgg ggg gag      672
Pro Leu Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu
    210                 215                 220

aac tat gac cgg cag cgt gcc ttc tca agg acc tgt gct gga ggc ctg      720
Asn Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
225                 230                 235                 240

cgc tgc ctc ctg tcg gac cgc cgc gtg ctg ctg ttg ggc acc ata caa      768
Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile Gln
                245                 250                 255

gct cta ttt gag agt gtc atc ttc atc ttt gtc ttc ctc tgg aca cct      816
Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp Thr Pro
            260                 265                 270

gtg ctg gac cca cac ggg gcc cct ctg ggc att atc ttc tcc agc ttc      864
Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe Ser Ser Phe
        275                 280                 285

atg gca gcc agc ctg ctt ggc tct tcc ctg tac cgt atc gcc acc tcc      912
Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg Ile Ala Thr Ser
    290                 295                 300

aag agg tac cac ctt cag ccc atg cac ctg ctg tcc ctt gct gtg ctc      960
Lys Arg Tyr His Leu Gln Pro Met His Leu Leu Ser Leu Ala Val Leu
305                 310                 315                 320

atc gtc gtc ttc tct ctc ttc atg ttg act ttc tct acc agc cca ggc     1008
Ile Val Val Phe Ser Leu Phe Met Leu Thr Phe Ser Thr Ser Pro Gly
                325                 330                 335

cag gag agt ccg gtg gag tcc ttc ata gcc ttt cta ctt att gag ttg     1056
Gln Glu Ser Pro Val Glu Ser Phe Ile Ala Phe Leu Leu Ile Glu Leu
            340                 345                 350
```

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gct tgt gga tta tac ttt ccc agc atg agc ttc cta cgg aga aag gtg      1104
Ala Cys Gly Leu Tyr Phe Pro Ser Met Ser Phe Leu Arg Arg Lys Val
        355                 360                 365

atc cct gag aca gag cag gct ggt gta ctc aac tgg ttc cgg gta cct      1152
Ile Pro Glu Thr Glu Gln Ala Gly Val Leu Asn Trp Phe Arg Val Pro
    370                 375                 380

ctg cac tca ctg gct tgc cta ggg ctc ctt gtc ctc cat gac agt gat      1200
Leu His Ser Leu Ala Cys Leu Gly Leu Leu Val Leu His Asp Ser Asp
385                 390                 395                 400

cga aaa aca ggc act cgg aat atg ttc agc att tgc tct gct gtc atg      1248
Arg Lys Thr Gly Thr Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met
                405                 410                 415

gtg atg gct ctg ctg gca gtg gtg gga ctc ttc acc gtg gta agg cat      1296
Val Met Ala Leu Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His
            420                 425                 430

gat gct gag ctg cgg gta cct tca cct act gag gag ccc tat gcc cct      1344
Asp Ala Glu Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro
        435                 440                 445

gag ctg taa                                                          1353
Glu Leu  *
    450


      <210> 146
      <211> 450
      <212> PRT
      <213> Homo sapiens

      <400> 146
Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser Cys
 1               5                  10                  15
Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly Arg Ala
            20                  25                  30
Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe Tyr Gln Val
        35                  40                  45
Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala Pro Tyr Leu Tyr
    50                  55                  60
```

Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly Gln Ile Ala Ile Leu
65 70 75 80
Tyr Val Cys Gly Leu Ala Ser Thr Val Leu Phe Gly Leu Val Ala Ser
85 90 95
Ser Leu Val Asp Trp Leu Gly Arg Lys Asn Ser Cys Val Leu Phe Ser
100 105 110
Leu Thr Tyr Ser Leu Cys Cys Leu Thr Lys Leu Ser Gln Asp Tyr Phe
115 120 125
Val Leu Leu Val Gly Arg Ala Leu Gly Gly Leu Ser Thr Ala Leu Leu
130 135 140
Phe Ser Ala Phe Glu Ala Trp Tyr Ile His Glu His Val Glu Arg His
145 150 155 160
Asp Phe Pro Ala Glu Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe
165 170 175
Trp Asn His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val
180 185 190
Ala Ser Trp Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile
195 200 205
Pro Leu Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu
210 215 220
Asn Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
225 230 235 240
Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile Gln
245 250 255
Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp Thr Pro
260 265 270
Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe Ser Ser Phe
275 280 285
Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg Ile Ala Thr Ser
290 295 300
Lys Arg Tyr His Leu Gln Pro Met His Leu Leu Ser Leu Ala Val Leu
305 310 315 320
Ile Val Val Phe Ser Leu Phe Met Leu Thr Phe Ser Thr Ser Pro Gly
325 330 335
Gln Glu Ser Pro Val Glu Ser Phe Ile Ala Phe Leu Leu Ile Glu Leu
340 345 350
Ala Cys Gly Leu Tyr Phe Pro Ser Met Ser Phe Leu Arg Arg Lys Val
355 360 365
Ile Pro Glu Thr Glu Gln Ala Gly Val Leu Asn Trp Phe Arg Val Pro
370 375 380
Leu His Ser Leu Ala Cys Leu Gly Leu Leu Val Leu His Asp Ser Asp
385 390 395 400
Arg Lys Thr Gly Thr Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met
405 410 415

Val Met Ala Leu Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His
420 425 430

Asp Ala Glu Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro
435 440 445

Glu Leu
450

<210> 147
<211> 465
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(465)

<221> misc_feature
<222> (1)...(465)
<223> n = A,T,C or G

<400> 147
atg gcg ggg ccg gtg aag gac cgc gag gcc ttc cag agg ctc aac ttc 48
Met Ala Gly Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn Phe
1 5 10 15

ctg tac cag gcc gcc cat tgt gtc ctt gcc cag gac ccc gag aac cag 96
Leu Tyr Gln Ala Ala His Cys Val Leu Ala Gln Asp Pro Glu Asn Gln
20 25 30

gcg ctg gcg agg ttt tac tgc tac act gag agg acc att gcg aag ngg 144
Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr Ile Ala Lys Xaa
35 40 45

ctc gtc ttg cgg cgg gat ccc tcg gtg aag agg act ctc tgt cga ggc 192
Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr Leu Cys Arg Gly
50 55 60

tgc tct tcc ctc ctc gtc ccg ggc ctc acc tgc acc cag cgc cag aga 240
Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys Thr Gln Arg Gln Arg
65 70 75 80

cgc tgc agg gga cag cgc tgg acc gta cag acc tgc cta aca tgc cag 288
Arg Cys Arg Gly Gln Arg Trp Thr Val Gln Thr Cys Leu Thr Cys Gln
85 90 95

```
cgc agc caa cgc ttc ctc aat gat ccc ggg cat tta ctc tgg gga gac      336
Arg Ser Gln Arg Phe Leu Asn Asp Pro Gly His Leu Leu Trp Gly Asp
            100                 105                 110

agg cct gag gcc cag ctc ggg agc caa gca gat tcc aaa cca cta caa      384
Arg Pro Glu Ala Gln Leu Gly Ser Gln Ala Asp Ser Lys Pro Leu Gln
        115                 120                 125

ccc ttg cca aac aca gcc cac tcc att tca gac cgc ctt cct gag gag      432
Pro Leu Pro Asn Thr Ala His Ser Ile Ser Asp Arg Leu Pro Glu Glu
    130                 135                 140

aaa atg cag act cag ggt tcc agt aac cag tga                          465
Lys Met Gln Thr Gln Gly Ser Ser Asn Gln  *
145                 150


      <210> 148
      <211> 154
      <212> PRT
      <213> Homo sapiens

      <400> 148
Met Ala Gly Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn Phe
 1               5                  10                  15
Leu Tyr Gln Ala Ala His Cys Val Leu Ala Gln Asp Pro Glu Asn Gln
            20                  25                  30
Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr Ile Ala Lys Xaa
        35                  40                  45
Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr Leu Cys Arg Gly
    50                  55                  60
Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys Thr Gln Arg Gln Arg
65                  70                  75                  80
Arg Cys Arg Gly Gln Arg Trp Thr Val Gln Thr Cys Leu Thr Cys Gln
                85                  90                  95
Arg Ser Gln Arg Phe Leu Asn Asp Pro Gly His Leu Leu Trp Gly Asp
            100                 105                 110
Arg Pro Glu Ala Gln Leu Gly Ser Gln Ala Asp Ser Lys Pro Leu Gln
        115                 120                 125
Pro Leu Pro Asn Thr Ala His Ser Ile Ser Asp Arg Leu Pro Glu Glu
    130                 135                 140
Lys Met Gln Thr Gln Gly Ser Ser Asn Gln
145                 150
```

<210> 149
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(390)

<400> 149

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atg atc ccc ctc ctc aga gag agc tta cac ccc atg ctg ctc tcc atc      48
Met Ile Pro Leu Leu Arg Glu Ser Leu His Pro Met Leu Leu Ser Ile
 1               5                  10                  15

atc atc act gtt gca gac aac ctc aac tcc aag aac tca ggg att tac      96
Ile Ile Thr Val Ala Asp Asn Leu Asn Ser Lys Asn Ser Gly Ile Tyr
            20                  25                  30

gct gct gcc gtg gca gtg ctg gtg gcc tca gtt tac ccc cgg aag cct     144
Ala Ala Ala Val Ala Val Leu Val Ala Ser Val Tyr Pro Arg Lys Pro
        35                  40                  45

caa gct gta gag cgg cat gtc ctt ccc atc ctc tgg cac ttc ctg aac     192
Gln Ala Val Glu Arg His Val Leu Pro Ile Leu Trp His Phe Leu Asn
    50                  55                  60

acc gcc acc agg aat ggc acc ctg cct gga ccc agc ggg aac atc cgc     240
Thr Ala Thr Arg Asn Gly Thr Leu Pro Gly Pro Ser Gly Asn Ile Arg
65                  70                  75                  80

ggg gtg gtg tgc cgg ctg tcc agg agc ctc cag gag cac cat ggg ctc     288
Gly Val Val Cys Arg Leu Ser Arg Ser Leu Gln Glu His His Gly Leu
                85                  90                  95

ccg cct gct gga ctt tgc cgc cag cca gcc aaa gca cgt cct caa gac     336
Pro Pro Ala Gly Leu Cys Arg Gln Pro Ala Lys Ala Arg Pro Gln Asp
            100                 105                 110

gct cca gga act ctt aga ctc aga gtc ctt ggg agg cag ccg caa ggc     384
Ala Pro Gly Thr Leu Arg Leu Arg Val Leu Gly Arg Gln Pro Gln Gly
        115                 120                 125

cac tga                                                             390
```

His *

<210> 150
<211> 129
<212> PRT
<213> Homo sapiens

<400> 150
Met Ile Pro Leu Leu Arg Glu Ser Leu His Pro Met Leu Leu Ser Ile
 1   5   10   15
Ile Ile Thr Val Ala Asp Asn Leu Asn Ser Lys Asn Ser Gly Ile Tyr
            20   25   30
Ala Ala Ala Val Ala Val Leu Val Ala Ser Val Tyr Pro Arg Lys Pro
        35   40   45
Gln Ala Val Glu Arg His Val Leu Pro Ile Leu Trp His Phe Leu Asn
    50   55   60
Thr Ala Thr Arg Asn Gly Thr Leu Pro Gly Pro Ser Gly Asn Ile Arg
65   70   75   80
Gly Val Val Cys Arg Leu Ser Arg Ser Leu Gln Glu His His Gly Leu
                85   90   95
Pro Pro Ala Gly Leu Cys Arg Gln Pro Ala Lys Ala Arg Pro Gln Asp
            100   105   110
Ala Pro Gly Thr Leu Arg Leu Arg Val Leu Gly Arg Gln Pro Gln Gly
        115   120   125
His

<210> 151
<211> 567
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(567)

<400> 151
atg gtc cct gcc cct cag cat gtc act gag cta gag ctg ggc atg tac 48
Met Val Pro Ala Pro Gln His Val Thr Glu Leu Glu Leu Gly Met Tyr
 1   5   10   15

gcc ctg ctg gga gtc ttc tgc gtg gcc atc ttc atc ttc ttg gtc aat 96

```
Ala Leu Leu Gly Val Phe Cys Val Ala Ile Phe Ile Phe Leu Val Asn
            20                  25                  30

ggt gtg gtc ttc gtc ctg cgc tat cag cgc aaa gaa cct ccc gac agt      144
Gly Val Val Phe Val Leu Arg Tyr Gln Arg Lys Glu Pro Pro Asp Ser
        35                  40                  45

gcc act gac ccc acc tcc ccc cag ccc cac aac tgg gtc tgg ctg ggc      192
Ala Thr Asp Pro Thr Ser Pro Gln Pro His Asn Trp Val Trp Leu Gly
    50                  55                  60

act gac cag gag gaa ctg agc cgc cag ctg gac cgg cag tcc cct ggc      240
Thr Asp Gln Glu Glu Leu Ser Arg Gln Leu Asp Arg Gln Ser Pro Gly
65                  70                  75                  80

ccg ccc aag ggg gag ggg agc tgc ccc tgt gag agt ggg gga gga ggg      288
Pro Pro Lys Gly Glu Gly Ser Cys Pro Cys Glu Ser Gly Gly Gly Gly
                85                  90                  95

gag gcc cct acc ctg gcc cct ggc cct cct ggg ggc acc acc agc tcc      336
Glu Ala Pro Thr Leu Ala Pro Gly Pro Pro Gly Gly Thr Thr Ser Ser
            100                 105                 110

tca agc acc ctg gcc cga aag gag gct ggg ggg cgg cgg aag cga gta      384
Ser Ser Thr Leu Ala Arg Lys Glu Ala Gly Gly Arg Arg Lys Arg Val
        115                 120                 125

gag ttt gtg aca ttt gcg cca gcc cct cca gcc cag tca cct gag gag      432
Glu Phe Val Thr Phe Ala Pro Ala Pro Pro Ala Gln Ser Pro Glu Glu
    130                 135                 140

cct gta ggg gcc cct gct gtg cag tcc atc ctt gtg gca ggc gag gag      480
Pro Val Gly Ala Pro Ala Val Gln Ser Ile Leu Val Ala Gly Glu Glu
145                 150                 155                 160

gac atc cgc tgg gtg tgt gag gac atg ggg ctg aag gac cct gag gag      528
Asp Ile Arg Trp Val Cys Glu Asp Met Gly Leu Lys Asp Pro Glu Glu
                165                 170                 175

ctt cgc aac tac atg gag agg atc cgg ggc agc tcc tga                  567
Leu Arg Asn Tyr Met Glu Arg Ile Arg Gly Ser Ser  *
            180                 185
```

<210> 152
<211> 188
<212> PRT
<213> Homo sapiens

<400> 152
Met Val Pro Ala Pro Gln His Val Thr Glu Leu Glu Leu Gly Met Tyr
1 5 10 15
Ala Leu Leu Gly Val Phe Cys Val Ala Ile Phe Ile Phe Leu Val Asn
20 25 30
Gly Val Val Phe Val Leu Arg Tyr Gln Arg Lys Glu Pro Pro Asp Ser
35 40 45
Ala Thr Asp Pro Thr Ser Pro Gln Pro His Asn Trp Val Trp Leu Gly
50 55 60
Thr Asp Gln Glu Glu Leu Ser Arg Gln Leu Asp Arg Gln Ser Pro Gly
65 70 75 80
Pro Pro Lys Gly Glu Gly Ser Cys Pro Cys Glu Ser Gly Gly Gly Gly
85 90 95
Glu Ala Pro Thr Leu Ala Pro Gly Pro Pro Gly Gly Thr Thr Ser Ser
100 105 110
Ser Ser Thr Leu Ala Arg Lys Glu Ala Gly Gly Arg Arg Lys Arg Val
115 120 125
Glu Phe Val Thr Phe Ala Pro Ala Pro Pro Ala Gln Ser Pro Glu Glu
130 135 140
Pro Val Gly Ala Pro Ala Val Gln Ser Ile Leu Val Ala Gly Glu Glu
145 150 155 160
Asp Ile Arg Trp Val Cys Glu Asp Met Gly Leu Lys Asp Pro Glu Glu
165 170 175
Leu Arg Asn Tyr Met Glu Arg Ile Arg Gly Ser Ser
180 185

<210> 153
<211> 735
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(735)

<400> 153
atg gct acg gga acg cgc tat gcc ggg aag gtg gtg gtc gtg acc ggg 48
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr Gly
1 5 10 15

```
ggc ggg cgc ggc atc gga gct ggg atc gtg cgc gcc ttc gtg aac agc        96
Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val Asn Ser
                20                  25                  30

ggg gcc cga gtg gtt atc tgc gac aag gat gag tct ggg ggc cgg gcc       144
Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly Gly Arg Ala
            35                  40                  45

ctg gag cag gag ctc cct gga gct gtc ttt atc ctc tgt gat gtg act       192
Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu Cys Asp Val Thr
        50                  55                  60

cag gaa gat gat gtg aag acc ctg gtt tct gag acc atc cgc cga ttt       240
Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu Thr Ile Arg Arg Phe
    65                  70                  75                  80

ggc cgc ctg gat tgt gtt gtc aac aac gct ggc cac cac cca ccc cca       288
Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro
                    85                  90                  95

cag agg cct gag gag acc tct gcc cag gga ttc cgc cag ctg ctg gag       336
Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu
                100                 105                 110

ctg aac cta ctg ggg acg tac acc ttg acc aag ctc gcc ctc ccc tac       384
Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr
            115                 120                 125

ctg cgg aag agt caa ggg aat gtc atc aac atc tcc agc ctg gtg ggg       432
Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly
        130                 135                 140

gca atc ggc cag gcc cag gca gtt ccc tat gtg gcc acc aag ggg gca       480
Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala
145                 150                 155                 160

gta aca gcc atg acc aaa gct ttg gcc ctg gat gaa agt cca tat ggt       528
Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly
                165                 170                 175

gtc cga gtc aac tgt atc tcc cca gga aac atc tgg acc ccg ctg tgg       576
Val Arg Val Asn Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp
                180                 185                 190
```

```
gag gag ctg gca gcc tta atg cca gac cct agg gcc aca atc cga gag       624
Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu
        195                 200                 205

ggc atg ctg ccc agc cac tgg gcc gca tgg gcc agc ccg ctg agg tcg       672
Gly Met Leu Pro Ser His Trp Ala Ala Trp Ala Ser Pro Leu Arg Ser
    210                 215                 220

ggg ctg cgg cag tgt tcc tgg cct ccg aag cca act tct gca cgg gca       720
Gly Leu Arg Gln Cys Ser Trp Pro Pro Lys Pro Thr Ser Ala Arg Ala
225                 230                 235                 240

ttg aac tgc tcg tga                                                   735
Leu Asn Cys Ser  *


      <210> 154
      <211> 244
      <212> PRT
      <213> Homo sapiens

      <400> 154
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr Gly
 1               5                  10                  15
Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val Asn Ser
            20                  25                  30
Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly Gly Arg Ala
        35                  40                  45
Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu Cys Asp Val Thr
    50                  55                  60
Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu Thr Ile Arg Arg Phe
65                  70                  75                  80
Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro
                85                  90                  95
Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu
            100                 105                 110
Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr
        115                 120                 125
Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly
    130                 135                 140
Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala
145                 150                 155                 160
```

Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly
165 170 175
Val Arg Val Asn Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp
180 185 190
Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu
195 200 205
Gly Met Leu Pro Ser His Trp Ala Ala Trp Ala Ser Pro Leu Arg Ser
210 215 220
Gly Leu Arg Gln Cys Ser Trp Pro Pro Lys Pro Thr Ser Ala Arg Ala
225 230 235 240
Leu Asn Cys Ser

<210> 155
<211> 975
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(975)

<221> misc_feature
<222> (1)...(975)
<223> n = A,T,C or G

<400> 155
atg atg ctg gca cag ggc ctt ctg ctg cat tnc ntn ccn nna gac tgg 48
Met Met Leu Ala Gln Gly Leu Leu Leu His Xaa Xaa Xaa Xaa Asp Trp
1 5 10 15

aca tgg gcc gag ggc atg ggc ctg ggc ccc cct gag ctg tca ggg tca 96
Thr Trp Ala Glu Gly Met Gly Leu Gly Pro Pro Glu Leu Ser Gly Ser
20 25 30

gcc tct ccc agc cgg tac cat ggg cct gcc cgc tgg atg ccc cca cgc 144
Ala Ser Pro Ser Arg Tyr His Gly Pro Ala Arg Trp Met Pro Pro Arg
35 40 45

tgg gcc cag ggt gcc cct gag ctg gag cag gaa cgc cgg cac cgg cag 192
Trp Ala Gln Gly Ala Pro Glu Leu Glu Gln Glu Arg Arg His Arg Gln
50 55 60

att gtg tcc tgg ttc gcc gac cac ccc cgg gcc ccc ttt ggc cta cac 240

Ile Val Ser Trp Phe Ala Asp His Pro Arg Ala Pro Phe Gly Leu His
65 70 75 80

cgg ctg gtg gag ctt ggg cag agc tca ggc aag aag gca ggt gac tgg 288
Arg Leu Val Glu Leu Gly Gln Ser Ser Gly Lys Lys Ala Gly Asp Trp
85 90 95

tat ggg cca tcg cta gtg gca cac atc ctc agg aaa gcc gtg gag agc 336
Tyr Gly Pro Ser Leu Val Ala His Ile Leu Arg Lys Ala Val Glu Ser
100 105 110

tgc tcc gac gtc acc cgc ctg gtg gtg tac gtt tct cag gac tgc aca 384
Cys Ser Asp Val Thr Arg Leu Val Val Tyr Val Ser Gln Asp Cys Thr
115 120 125

gtg tac aag gcg gat gtg gca cgc ctg gtg gcc agg cca gac ccc aca 432
Val Tyr Lys Ala Asp Val Ala Arg Leu Val Ala Arg Pro Asp Pro Thr
130 135 140

gcc gag tgg aag tct gtg gtc atc ctg gtg ccc gtg cga ctg ggt ggc 480
Ala Glu Trp Lys Ser Val Val Ile Leu Val Pro Val Arg Leu Gly Gly
145 150 155 160

gag act ctc aac ccc gtg tat gtg ccc tgc gtg aag gaa ctc ctg cgt 528
Glu Thr Leu Asn Pro Val Tyr Val Pro Cys Val Lys Glu Leu Leu Arg
165 170 175

tgc gag ctg tgc ctg ggc atc atg ggt ggg aaa ccg cga cac tca ctg 576
Cys Glu Leu Cys Leu Gly Ile Met Gly Gly Lys Pro Arg His Ser Leu
180 185 190

tac ttc att ggc tac caa gat gac ttc ctg ctg tac ctg gac cct cac 624
Tyr Phe Ile Gly Tyr Gln Asp Asp Phe Leu Leu Tyr Leu Asp Pro His
195 200 205

tac tgc cag ccc act gtg gat gtc agc cag gcc gac ttc ccc ctg gag 672
Tyr Cys Gln Pro Thr Val Asp Val Ser Gln Ala Asp Phe Pro Leu Glu
210 215 220

tcc ttc cac tgc acc tcg ccc cgc aag atg gcc ttt gcc aag atg gac 720
Ser Phe His Cys Thr Ser Pro Arg Lys Met Ala Phe Ala Lys Met Asp
225 230 235 240

cca agc tgt acc gtg ggc ttc tat gct gga gac agg aag gag ttt gag 768

Pro Ser Cys Thr Val Gly Phe Tyr Ala Gly Asp Arg Lys Glu Phe Glu
245 250 255

aca ctc tgc tca gag ctg acc agg gtc ctc agc tcc tcc tca gcc aca 816
Thr Leu Cys Ser Glu Leu Thr Arg Val Leu Ser Ser Ser Ser Ala Thr
260 265 270

gag cgg tac ccc atg ttc acc ctg gcc gag ggc cat gct cag gac cac 864
Glu Arg Tyr Pro Met Phe Thr Leu Ala Glu Gly His Ala Gln Asp His
275 280 285

agc ctg gac gac ctc tgc tcc cag ctc gcc cag ccc aca ctc cgg ctc 912
Ser Leu Asp Asp Leu Cys Ser Gln Leu Ala Gln Pro Thr Leu Arg Leu
290 295 300

cct cgc aca ggg cgg ctc ctc agg gcc aaa cgc ccc agc tct gag gac 960
Pro Arg Thr Gly Arg Leu Leu Arg Ala Lys Arg Pro Ser Ser Glu Asp
305 310 315 320

ttt gtg ttt tta taa 975
Phe Val Phe Leu *

<210> 156
<211> 324
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(324)
<223> Xaa = Any Amino Acid

<400> 156
Met Met Leu Ala Gln Gly Leu Leu Leu His Xaa Xaa Xaa Xaa Asp Trp
1 5 10 15
Thr Trp Ala Glu Gly Met Gly Leu Gly Pro Pro Glu Leu Ser Gly Ser
20 25 30
Ala Ser Pro Ser Arg Tyr His Gly Pro Ala Arg Trp Met Pro Pro Arg
35 40 45
Trp Ala Gln Gly Ala Pro Glu Leu Glu Gln Glu Arg Arg His Arg Gln
50 55 60
Ile Val Ser Trp Phe Ala Asp His Pro Arg Ala Pro Phe Gly Leu His

65 70 75 80
Arg Leu Val Glu Leu Gly Gln Ser Ser Gly Lys Lys Ala Gly Asp Trp
85 90 95
Tyr Gly Pro Ser Leu Val Ala His Ile Leu Arg Lys Ala Val Glu Ser
100 105 110
Cys Ser Asp Val Thr Arg Leu Val Val Tyr Val Ser Gln Asp Cys Thr
115 120 125
Val Tyr Lys Ala Asp Val Ala Arg Leu Val Ala Arg Pro Asp Pro Thr
130 135 140
Ala Glu Trp Lys Ser Val Val Ile Leu Val Pro Val Arg Leu Gly Gly
145 150 155 160
Glu Thr Leu Asn Pro Val Tyr Val Pro Cys Val Lys Glu Leu Leu Arg
165 170 175
Cys Glu Leu Cys Leu Gly Ile Met Gly Gly Lys Pro Arg His Ser Leu
180 185 190
Tyr Phe Ile Gly Tyr Gln Asp Asp Phe Leu Leu Tyr Leu Asp Pro His
195 200 205
Tyr Cys Gln Pro Thr Val Asp Val Ser Gln Ala Asp Phe Pro Leu Glu
210 215 220
Ser Phe His Cys Thr Ser Pro Arg Lys Met Ala Phe Ala Lys Met Asp
225 230 235 240
Pro Ser Cys Thr Val Gly Phe Tyr Ala Gly Asp Arg Lys Glu Phe Glu
245 250 255
Thr Leu Cys Ser Glu Leu Thr Arg Val Leu Ser Ser Ser Ser Ala Thr
260 265 270
Glu Arg Tyr Pro Met Phe Thr Leu Ala Glu Gly His Ala Gln Asp His
275 280 285
Ser Leu Asp Asp Leu Cys Ser Gln Leu Ala Gln Pro Thr Leu Arg Leu
290 295 300
Pro Arg Thr Gly Arg Leu Leu Arg Ala Lys Arg Pro Ser Ser Glu Asp
305 310 315 320
Phe Val Phe Leu

<210> 157
<211> 669
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(669)

<400> 157

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atg atc ctt gta gga ctc tgg tta att cag tgg ctg ctc tta aaa tac      48
Met Ile Leu Val Gly Leu Trp Leu Ile Gln Trp Leu Leu Leu Lys Tyr
 1               5                  10                  15

aag tct att att agc aga aga ttt ttc tgc ata gtt ggc acg ctg tac      96
Lys Ser Ile Ile Ser Arg Arg Phe Phe Cys Ile Val Gly Thr Leu Tyr
            20                  25                  30

ctg tat cgg tgt att aca atg tat gta act aca ctc cca gta cct ggt     144
Leu Tyr Arg Cys Ile Thr Met Tyr Val Thr Thr Leu Pro Val Pro Gly
        35                  40                  45

atg cat ttc aac tgt tct ccg aag ctt ttc gga gac tgg gaa gcc caa     192
Met His Phe Asn Cys Ser Pro Lys Leu Phe Gly Asp Trp Glu Ala Gln
    50                  55                  60

ctg cga aga ata atg aag ctc att gct gga ggt ggc ttg tct atc act     240
Leu Arg Arg Ile Met Lys Leu Ile Ala Gly Gly Gly Leu Ser Ile Thr
65                  70                  75                  80

ggc tct cac aac atg tgt ggg gac tat ctg tac agc ggc cac acg gtc     288
Gly Ser His Asn Met Cys Gly Asp Tyr Leu Tyr Ser Gly His Thr Val
                85                  90                  95

atg cta aca ctt acc tac tta ttt atc aaa gag tat tcc cct cgg cga     336
Met Leu Thr Leu Thr Tyr Leu Phe Ile Lys Glu Tyr Ser Pro Arg Arg
            100                 105                 110

ctc tgg tgg tat cac tgg att tgc tgg ctt ctc agc gta gtt gga atc     384
Leu Trp Trp Tyr His Trp Ile Cys Trp Leu Leu Ser Val Val Gly Ile
        115                 120                 125

ttc tgt att ctc tta gcg cat gac cac tac act gtg gac gtg gtg gtg     432
Phe Cys Ile Leu Leu Ala His Asp His Tyr Thr Val Asp Val Val Val
    130                 135                 140

gca tat tac atc acc acg aga ctc ttc tgg tgg tat cac act atg gcc     480
Ala Tyr Tyr Ile Thr Thr Arg Leu Phe Trp Trp Tyr His Thr Met Ala
145                 150                 155                 160

aat cag caa gtg cta aag gaa gct tcc cag atg aac ctc ctg gcc agg     528
Asn Gln Gln Val Leu Lys Glu Ala Ser Gln Met Asn Leu Leu Ala Arg
                165                 170                 175
```

```
gtg tgg tgg tac agg cca ttt cag tac ttt gaa aag aat gtc caa gga        576
Val Trp Trp Tyr Arg Pro Phe Gln Tyr Phe Glu Lys Asn Val Gln Gly
            180                 185                 190

att gta cct cga tct tac cat tgg cct ttc ccc tgg cca gta gtc cac        624
Ile Val Pro Arg Ser Tyr His Trp Pro Phe Pro Trp Pro Val Val His
        195                 200                 205

ctc agt agg caa gtt aaa tac agc cgg ctg gtg aat gac aca taa            669
Leu Ser Arg Gln Val Lys Tyr Ser Arg Leu Val Asn Asp Thr  *
    210                 215                 220


      <210> 158
      <211> 222
      <212> PRT
      <213> Homo sapiens

      <400> 158
Met Ile Leu Val Gly Leu Trp Leu Ile Gln Trp Leu Leu Leu Lys Tyr
 1               5                  10                  15
Lys Ser Ile Ile Ser Arg Arg Phe Phe Cys Ile Val Gly Thr Leu Tyr
            20                  25                  30
Leu Tyr Arg Cys Ile Thr Met Tyr Val Thr Thr Leu Pro Val Pro Gly
        35                  40                  45
Met His Phe Asn Cys Ser Pro Lys Leu Phe Gly Asp Trp Glu Ala Gln
    50                  55                  60
Leu Arg Arg Ile Met Lys Leu Ile Ala Gly Gly Gly Leu Ser Ile Thr
65                  70                  75                  80
Gly Ser His Asn Met Cys Gly Asp Tyr Leu Tyr Ser Gly His Thr Val
                85                  90                  95
Met Leu Thr Leu Thr Tyr Leu Phe Ile Lys Glu Tyr Ser Pro Arg Arg
            100                 105                 110
Leu Trp Trp Tyr His Trp Ile Cys Trp Leu Leu Ser Val Val Gly Ile
        115                 120                 125
Phe Cys Ile Leu Leu Ala His Asp His Tyr Thr Val Asp Val Val Val
    130                 135                 140
Ala Tyr Tyr Ile Thr Thr Arg Leu Phe Trp Trp Tyr His Thr Met Ala
145                 150                 155                 160
Asn Gln Gln Val Leu Lys Glu Ala Ser Gln Met Asn Leu Leu Ala Arg
                165                 170                 175
Val Trp Trp Tyr Arg Pro Phe Gln Tyr Phe Glu Lys Asn Val Gln Gly
            180                 185                 190
Ile Val Pro Arg Ser Tyr His Trp Pro Phe Pro Trp Pro Val Val His
```

```
    195                 200                 205
Leu Ser Arg Gln Val Lys Tyr Ser Arg Leu Val Asn Asp Thr
210                 215                 220

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(540)

<221> misc_feature
<222> (1)...(540)
<223> n = A,T,C or G

<400> 159
atg gcc gct ccc cgc ngn agg gcc gcg ccc tgg acg acg gcc ctg ctg      48
Met Ala Ala Pro Arg Xaa Arg Ala Ala Pro Trp Thr Thr Ala Leu Leu
 1               5                  10                  15

ctg ctc cta gcc tcg cag gtc ctg tct ccg gga agc tgc gcg gac gag      96
Leu Leu Leu Ala Ser Gln Val Leu Ser Pro Gly Ser Cys Ala Asp Glu
            20                  25                  30

gag gag gtc ccc gag gag tgg gtg ctc ctg cac gtc gtc cag ggc cag     144
Glu Glu Val Pro Glu Glu Trp Val Leu Leu His Val Val Gln Gly Gln
        35                  40                  45

ata ggc gcc ggg aac tac agc tac ctg cgg ctg aac cac gag ggc aag     192
Ile Gly Ala Gly Asn Tyr Ser Tyr Leu Arg Leu Asn His Glu Gly Lys
    50                  55                  60

ata gtc ctc agg atg cgc acc tnc aag gga gat gcg gat ctg tac gtc     240
Ile Val Leu Arg Met Arg Thr Xaa Lys Gly Asp Ala Asp Leu Tyr Val
65                  70                  75                  80

tcc gcc agc agc ctg cac ccc agc ttc gac gac tac gag ctg caa tcg     288
Ser Ala Ser Ser Leu His Pro Ser Phe Asp Asp Tyr Glu Leu Gln Ser
                85                  90                  95

gcc acc tgn cgg ccc gga cgc cgt gtc cat ccc cgc gca ctt ccg gcg     336
Ala Thr Xaa Arg Pro Gly Arg Arg Val His Pro Arg Ala Leu Pro Ala
```

100 105 110

ccc agt ggg cat cgg cgt cta tgg aca ccc ctc cca cct gga gag cga 384
Pro Ser Gly His Arg Arg Leu Trp Thr Pro Leu Pro Pro Gly Glu Arg
115 120 125

gtt cga gat gaa ggt gta cta cga cgg cac ggt ncg agc agc acc cgt 432
Val Arg Asp Glu Gly Val Leu Arg Arg His Gly Xaa Ser Ser Thr Arg
130 135 140

tcg gcg agg ccg cct acc ccg ccg acg gcg cag atg ccg gcc aga agc 480
Ser Ala Arg Pro Pro Thr Pro Pro Thr Ala Gln Met Pro Ala Arg Ser
145 150 155 160

acg ctg gtg ccc cgg aag acg cct cgc aag agg agg aat ctg ttc tct 528
Thr Leu Val Pro Arg Lys Thr Pro Arg Lys Arg Arg Asn Leu Phe Ser
165 170 175

gga cga tat taa 540
Gly Arg Tyr *

<210> 160
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(179)
<223> Xaa = Any Amino Acid

<400> 160
Met Ala Ala Pro Arg Xaa Arg Ala Ala Pro Trp Thr Thr Ala Leu Leu
1 5 10 15
Leu Leu Leu Ala Ser Gln Val Leu Ser Pro Gly Ser Cys Ala Asp Glu
20 25 30
Glu Glu Val Pro Glu Glu Trp Val Leu Leu His Val Val Gln Gly Gln
35 40 45
Ile Gly Ala Gly Asn Tyr Ser Tyr Leu Arg Leu Asn His Glu Gly Lys
50 55 60
Ile Val Leu Arg Met Arg Thr Xaa Lys Gly Asp Ala Asp Leu Tyr Val
65 70 75 80

```
Ser Ala Ser Ser Leu His Pro Ser Phe Asp Asp Tyr Glu Leu Gln Ser
                85                  90                  95
Ala Thr Xaa Arg Pro Gly Arg Arg Val His Pro Arg Ala Leu Pro Ala
            100                 105                 110
Pro Ser Gly His Arg Arg Leu Trp Thr Pro Leu Pro Pro Gly Glu Arg
        115                 120                 125
Val Arg Asp Glu Gly Val Leu Arg Arg His Gly Xaa Ser Ser Thr Arg
    130                 135                 140
Ser Ala Arg Pro Pro Thr Pro Pro Thr Ala Gln Met Pro Ala Arg Ser
145                 150                 155                 160
Thr Leu Val Pro Arg Lys Thr Pro Arg Lys Arg Arg Asn Leu Phe Ser
                165                 170                 175
Gly Arg Tyr
```

<210> 161
<211> 1290
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1290)

<400> 161

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atg act gct gct ctg gcc gtc gtc acg acg tcg ggt ttg gaa gat ggg      48
Met Thr Ala Ala Leu Ala Val Val Thr Thr Ser Gly Leu Glu Asp Gly
 1               5                  10                  15

gtg cct agg tcc cgt ggc gaa ggg acc ggg gaa gtg gtc ttg gag cgg      96
Val Pro Arg Ser Arg Gly Glu Gly Thr Gly Glu Val Val Leu Glu Arg
            20                  25                  30

ggg ccc ggc gcg gcc tac cac atg ttc gtg gtg atg gag gac ttg gtg     144
Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
        35                  40                  45

gag aag ctg aag ctg ctc cgc tac gag gag gag ttc ctc cgg aag agc     192
Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Phe Leu Arg Lys Ser
    50                  55                  60

aac ctg aag gcc ccg tcc aga cac tat ttt gca ctg cct acc aac cct     240
Asn Leu Lys Ala Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro
65                  70                  75                  80
```

ggc gaa cag ttc tac atg ttt tgt act ctt gct gct tgg ttg att aat 288
Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn
85 90 95

aaa gcg gga cgt ccc ttt gag cag cct caa gaa tat gat gac cct aat 336
Lys Ala Gly Arg Pro Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn
100 105 110

gca aca ata tct aac ata cta tcc gag ctt cgg tca ttt gga aga act 384
Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr
115 120 125

gca gat ttt cct cct tca aaa tta aag tca ggt tat gga gaa cat gta 432
Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu His Val
130 135 140

tgc tat gtt ctt gat tgc ttc gct gaa gaa gca ttg aaa tat att ggt 480
Cys Tyr Val Leu Asp Cys Phe Ala Glu Glu Ala Leu Lys Tyr Ile Gly
145 150 155 160

ttc acc tgg aaa agg cca ata tac cca gta gaa gaa tta gaa gaa gaa 528
Phe Thr Trp Lys Arg Pro Ile Tyr Pro Val Glu Glu Leu Glu Glu Glu
165 170 175

agc gtt gca gaa gat gat gca gaa tta aca tta aat aaa gtg gat gaa 576
Ser Val Ala Glu Asp Asp Ala Glu Leu Thr Leu Asn Lys Val Asp Glu
180 185 190

gaa ttt gtg gaa gaa gag aca gat aat gaa gaa aac ttt att gat ctc 624
Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu
195 200 205

aac gtt tta aag gcc cag aca tat cac ttg gat atg aac gag act gcc 672
Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala
210 215 220

aaa caa gaa gat att ttg gaa tcc aca aca gat gct gca gaa tgg agc 720
Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser
225 230 235 240

cta gaa gtg gaa cgt gta cta ccg caa ctg aaa gtc acg att agg act 768
Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr
245 250 255

```
gac aat aag gat tgg aga atc cat gtt gac caa atg cac cag cac aga      816
Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg
            260                 265                 270

agt gga att gaa tct gct cta aag gag acc aag gga ttt ttg gac aaa      864
Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
        275                 280                 285

ctc cat aat gaa att act agg act ttg gaa aag atc agc agc cga gaa      912
Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu
    290                 295                 300

aag tac atc aac aat cag ctt gag aat ttg gtt caa gaa tat cgt gca      960
Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala
305                 310                 315                 320

gct caa gcc cag ctg agt gag gca aag gag cga tac cag cag gga aat     1008
Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn
                325                 330                 335

gga gga gtg acg gaa aga acc aga ctc ctc tct gag gtt atg gaa gaa     1056
Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu
            340                 345                 350

tta gaa aag gta aaa caa gaa atg gaa gaa aag ggc agc agc atg act     1104
Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
        355                 360                 365

gat ggt gct cct ttg gtg aag att aaa cag agc tta aca aaa ctg aag     1152
Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
    370                 375                 380

caa gaa act gta gag atg gac att aga att ggc att gtg gaa cac aca     1200
Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr
385                 390                 395                 400

cta ctc caa tca aag ctg aag gag aag tcc aac atg act agg aac atg     1248
Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met
                405                 410                 415

cat gcc aca gtt att cca gaa cca gca aca ggc ttt tat taa             1290
His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr  *
            420                 425
```

<210> 162
<211> 429
<212> PRT
<213> Homo sapiens

<400> 162
Met Thr Ala Ala Leu Ala Val Val Thr Thr Ser Gly Leu Glu Asp Gly
1   5   10   15
Val Pro Arg Ser Arg Gly Glu Gly Thr Gly Glu Val Val Leu Glu Arg
            20   25   30
Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
        35   40   45
Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Phe Leu Arg Lys Ser
    50   55   60
Asn Leu Lys Ala Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro
65   70   75   80
Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn
                85   90   95
Lys Ala Gly Arg Pro Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn
            100   105   110
Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr
        115   120   125
Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu His Val
    130   135   140
Cys Tyr Val Leu Asp Cys Phe Ala Glu Glu Ala Leu Lys Tyr Ile Gly
145   150   155   160
Phe Thr Trp Lys Arg Pro Ile Tyr Pro Val Glu Glu Leu Glu Glu Glu
                165   170   175
Ser Val Ala Glu Asp Asp Ala Glu Leu Thr Leu Asn Lys Val Asp Glu
            180   185   190
Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu
        195   200   205
Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala
    210   215   220
Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser
225   230   235   240
Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr
                245   250   255
Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg
            260   265   270
Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
        275   280   285

Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu
290 295 300
Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala
305 310 315 320
Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn
325 330 335
Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu
340 345 350
Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
355 360 365
Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
370 375 380
Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr
385 390 395 400
Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met
405 410 415
His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr
420 425

<210> 163
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(456)

<400> 163
atg gaa gga cag cgg caa gaa agc cac gca acc cta aca ctc gcc cag 48
Met Glu Gly Gln Arg Gln Glu Ser His Ala Thr Leu Thr Leu Ala Gln
1 5 10 15

gct cat ttc aac aat gga gag tac gcg gag gcc gag gca ctg tac tcc 96
Ala His Phe Asn Asn Gly Glu Tyr Ala Glu Ala Glu Ala Leu Tyr Ser
20 25 30

gct tac att cgc cgg tgc gct tgc gcg gcc tcc agc gac gag agt ccc 144
Ala Tyr Ile Arg Arg Cys Ala Cys Ala Ala Ser Ser Asp Glu Ser Pro
35 40 45

ggg agc aaa tgc agc cct gag gat ttg gct act gca tat aac aac agg 192
Gly Ser Lys Cys Ser Pro Glu Asp Leu Ala Thr Ala Tyr Asn Asn Arg
50 55 60

```
ggg caa atc aag tac ttc agg gtt gat ttt tat gaa gcc atg gat gac      240
Gly Gln Ile Lys Tyr Phe Arg Val Asp Phe Tyr Glu Ala Met Asp Asp
 65                 70                  75                  80

tac aca tct gcc ata gaa gtc caa ccc aat ttt gaa gtt cca tat tac      288
Tyr Thr Ser Ala Ile Glu Val Gln Pro Asn Phe Glu Val Pro Tyr Tyr
                85                  90                  95

aac aga ggg ttg ata ctg tat agg ctg gga tat ttt gat gat gct ttg      336
Asn Arg Gly Leu Ile Leu Tyr Arg Leu Gly Tyr Phe Asp Asp Ala Leu
            100                 105                 110

gaa gat ttc aag aag gtc tta gac tta aat cct gga ttt caa gat gct      384
Glu Asp Phe Lys Lys Val Leu Asp Leu Asn Pro Gly Phe Gln Asp Ala
        115                 120                 125

act ttg agc tta aaa cag act att cta gac aaa gaa gaa aaa caa aga      432
Thr Leu Ser Leu Lys Gln Thr Ile Leu Asp Lys Glu Glu Lys Gln Arg
    130                 135                 140

aga aat gtt gca aaa aat tat tga                                      456
Arg Asn Val Ala Lys Asn Tyr  *
145                 150
```

<210> 164
<211> 151
<212> PRT
<213> Homo sapiens

<400> 164

```
Met Glu Gly Gln Arg Gln Glu Ser His Ala Thr Leu Thr Leu Ala Gln
 1               5                  10                  15
Ala His Phe Asn Asn Gly Glu Tyr Ala Glu Ala Glu Ala Leu Tyr Ser
            20                  25                  30
Ala Tyr Ile Arg Arg Cys Ala Cys Ala Ala Ser Ser Asp Glu Ser Pro
        35                  40                  45
Gly Ser Lys Cys Ser Pro Glu Asp Leu Ala Thr Ala Tyr Asn Asn Arg
    50                  55                  60
Gly Gln Ile Lys Tyr Phe Arg Val Asp Phe Tyr Glu Ala Met Asp Asp
65                  70                  75                  80
Tyr Thr Ser Ala Ile Glu Val Gln Pro Asn Phe Glu Val Pro Tyr Tyr
                85                  90                  95
```

Asn Arg Gly Leu Ile Leu Tyr Arg Leu Gly Tyr Phe Asp Asp Ala Leu
100 105 110
Glu Asp Phe Lys Lys Val Leu Asp Leu Asn Pro Gly Phe Gln Asp Ala
115 120 125
Thr Leu Ser Leu Lys Gln Thr Ile Leu Asp Lys Glu Glu Lys Gln Arg
130 135 140
Arg Asn Val Ala Lys Asn Tyr
145 150

<210> 165
<211> 1032
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1032)

<400> 165
atg atg ctg ctg ctc tat gaa gaa ggc ctc cgg gtt gtc ata cac acc 48
Met Met Leu Leu Leu Tyr Glu Glu Gly Leu Arg Val Val Ile His Thr
1 5 10 15

tcc aac ctc atc cat gct gac tgg cac cag aaa act caa gga ata tgg 96
Ser Asn Leu Ile His Ala Asp Trp His Gln Lys Thr Gln Gly Ile Trp
20 25 30

ttg agc ccc tta tac cca cga att gct gat gga acc cac aaa tct gga 144
Leu Ser Pro Leu Tyr Pro Arg Ile Ala Asp Gly Thr His Lys Ser Gly
35 40 45

gag tcg cca aca cat ttt aaa gct gat ctc atc agt tac ttg atg gct 192
Glu Ser Pro Thr His Phe Lys Ala Asp Leu Ile Ser Tyr Leu Met Ala
50 55 60

tat aat gcc cct tct ctc aag gag tgg ata gat gtc att cac aag cac 240
Tyr Asn Ala Pro Ser Leu Lys Glu Trp Ile Asp Val Ile His Lys His
65 70 75 80

gat ctc tct gaa aca aat gtt tat ctt att ggt tca acc cca gga cgc 288
Asp Leu Ser Glu Thr Asn Val Tyr Leu Ile Gly Ser Thr Pro Gly Arg
85 90 95

ttt caa gga agt caa aaa gat aat tgg gga cat ttt aga ctt aag aag 336

Phe Gln Gly Ser Gln Lys Asp Asn Trp Gly His Phe Arg Leu Lys Lys
100 105 110

ctt ctg aaa gac cat gcc tca tcc atg cct aac gca gag tcc tgg cct 384
Leu Leu Lys Asp His Ala Ser Ser Met Pro Asn Ala Glu Ser Trp Pro
115 120 125

gtc gta ggt cag ttt tca agc gtt ggc tcc ttg gga gcc gat gaa tca 432
Val Val Gly Gln Phe Ser Ser Val Gly Ser Leu Gly Ala Asp Glu Ser
130 135 140

aag tgg tta tgt tct gag ttt aaa gag agc atg ctg aca ctg ggg aag 480
Lys Trp Leu Cys Ser Glu Phe Lys Glu Ser Met Leu Thr Leu Gly Lys
145 150 155 160

gaa agc aag act cca gga aaa agc tct gtt cct ctt tac ttg atc tat 528
Glu Ser Lys Thr Pro Gly Lys Ser Ser Val Pro Leu Tyr Leu Ile Tyr
165 170 175

cct tct gtg gaa aat gtg cgg acc agt tta gaa gga tat cct gct ggg 576
Pro Ser Val Glu Asn Val Arg Thr Ser Leu Glu Gly Tyr Pro Ala Gly
180 185 190

ggc tct ctt ccc tat agc atc cag aca gct gaa aaa cag aat tgg ctg 624
Gly Ser Leu Pro Tyr Ser Ile Gln Thr Ala Glu Lys Gln Asn Trp Leu
195 200 205

cat tcc tat ttt cac aaa tgg tca gct gag act tct ggc cgc agc aat 672
His Ser Tyr Phe His Lys Trp Ser Ala Glu Thr Ser Gly Arg Ser Asn
210 215 220

gcc atg cca cat att aag aca tat atg agg cct tct cca gac ttc agt 720
Ala Met Pro His Ile Lys Thr Tyr Met Arg Pro Ser Pro Asp Phe Ser
225 230 235 240

aaa att gct tgg ttc ctt gtc aca agc gca aat ctg tcc aag gct gcc 768
Lys Ile Ala Trp Phe Leu Val Thr Ser Ala Asn Leu Ser Lys Ala Ala
245 250 255

tgg gga gca ttg gag aag aat ggc acc cag ctg atg atc cgc tcc tac 816
Trp Gly Ala Leu Glu Lys Asn Gly Thr Gln Leu Met Ile Arg Ser Tyr
260 265 270

gag ctc ggg gtc ctt ttc ctc cct tca gca ttt ggt cta gac agt ttc 864

```
Glu Leu Gly Val Leu Phe Leu Pro Ser Ala Phe Gly Leu Asp Ser Phe
        275                 280                 285

aaa gtg aaa cag aag ttc ttc gct ggc agc cag gag cca atg gcc acc      912
Lys Val Lys Gln Lys Phe Phe Ala Gly Ser Gln Glu Pro Met Ala Thr
    290                 295                 300

ttt cct gtg cca tat gat ttg cct cca gaa ctg tat gga agt aaa gat      960
Phe Pro Val Pro Tyr Asp Leu Pro Pro Glu Leu Tyr Gly Ser Lys Asp
305                 310                 315                 320

cgg cca tgg ata tgg aac att cct tat gtc aaa gca ccg gat acg cat     1008
Arg Pro Trp Ile Trp Asn Ile Pro Tyr Val Lys Ala Pro Asp Thr His
                325                 330                 335

ggg aac atg tgg gtg ccc tcc tga                                     1032
Gly Asn Met Trp Val Pro Ser  *
            340


      <210> 166
      <211> 343
      <212> PRT
      <213> Homo sapiens

      <400> 166
Met Met Leu Leu Leu Tyr Glu Glu Gly Leu Arg Val Val Ile His Thr
 1               5                  10                  15
Ser Asn Leu Ile His Ala Asp Trp His Gln Lys Thr Gln Gly Ile Trp
            20                  25                  30
Leu Ser Pro Leu Tyr Pro Arg Ile Ala Asp Gly Thr His Lys Ser Gly
        35                  40                  45
Glu Ser Pro Thr His Phe Lys Ala Asp Leu Ile Ser Tyr Leu Met Ala
    50                  55                  60
Tyr Asn Ala Pro Ser Leu Lys Glu Trp Ile Asp Val Ile His Lys His
65                  70                  75                  80
Asp Leu Ser Glu Thr Asn Val Tyr Leu Ile Gly Ser Thr Pro Gly Arg
                85                  90                  95
Phe Gln Gly Ser Gln Lys Asp Asn Trp Gly His Phe Arg Leu Lys Lys
            100                 105                 110
Leu Leu Lys Asp His Ala Ser Ser Met Pro Asn Ala Glu Ser Trp Pro
        115                 120                 125
Val Val Gly Gln Phe Ser Ser Val Gly Ser Leu Gly Ala Asp Glu Ser
    130                 135                 140
```

Lys Trp Leu Cys Ser Glu Phe Lys Glu Ser Met Leu Thr Leu Gly Lys
145 150 155 160
Glu Ser Lys Thr Pro Gly Lys Ser Ser Val Pro Leu Tyr Leu Ile Tyr
165 170 175
Pro Ser Val Glu Asn Val Arg Thr Ser Leu Glu Gly Tyr Pro Ala Gly
180 185 190
Gly Ser Leu Pro Tyr Ser Ile Gln Thr Ala Glu Lys Gln Asn Trp Leu
195 200 205
His Ser Tyr Phe His Lys Trp Ser Ala Glu Thr Ser Gly Arg Ser Asn
210 215 220
Ala Met Pro His Ile Lys Thr Tyr Met Arg Pro Ser Pro Asp Phe Ser
225 230 235 240
Lys Ile Ala Trp Phe Leu Val Thr Ser Ala Asn Leu Ser Lys Ala Ala
245 250 255
Trp Gly Ala Leu Glu Lys Asn Gly Thr Gln Leu Met Ile Arg Ser Tyr
260 265 270
Glu Leu Gly Val Leu Phe Leu Pro Ser Ala Phe Gly Leu Asp Ser Phe
275 280 285
Lys Val Lys Gln Lys Phe Phe Ala Gly Ser Gln Glu Pro Met Ala Thr
290 295 300
Phe Pro Val Pro Tyr Asp Leu Pro Pro Glu Leu Tyr Gly Ser Lys Asp
305 310 315 320
Arg Pro Trp Ile Trp Asn Ile Pro Tyr Val Lys Ala Pro Asp Thr His
325 330 335
Gly Asn Met Trp Val Pro Ser
340

<210> 167
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(594)

<400> 167
atg cca ccc gcg ggg ctc cgc cgg gcc gcg ccg ctc acc gca atc gct 48
Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile Ala
1 5 10 15

ctg ttg gtg ctg ggg gct ccc cta gtg ctg gcc ggc gag gac tgc ctg 96
Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp Cys Leu
20 25 30

tgg tac ctg gac cgg aat ggc tcc tgg cat ccg ggg ttt aac tgc gag 144
Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe Asn Cys Glu
35 40 45

ttc ttc acc ttc tgc tgc ggg acc tgc tac cat cgg tac tgc tgc agg 192
Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg
50 55 60

gac ctg acc ttg ctt atc acc gag agg cag cag aag cac tgc ctg gcc 240
Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala
65 70 75 80

ttc agc ccc aag acc ata gca ggc atc gcc tca gct gtg atc ctc ttt 288
Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe
85 90 95

gtt gct gtg gtt gcc acc acc atc tgc tgc ttc ctc tgt tcc tgt tgc 336
Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys
100 105 110

tac ctg tac cgc cgg cgc cag cag ctc cag agc cca ttt gaa ggc cag 384
Tyr Leu Tyr Arg Arg Arg Gln Gln Leu Gln Ser Pro Phe Glu Gly Gln
115 120 125

gag att cca atg aca ggc atc cca gtg cag cca gta tac cca tac ccc 432
Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro
130 135 140

cag gac ccc aaa gct ggc cct gca ccc cca cag cct ggc ttc atg tac 480
Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr
145 150 155 160

cca cct agt ggt cct gct ccc caa tat cca ctc tac cca gct ggg ccc 528
Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro
165 170 175

cca gtc tac aac cct gca gct cct cct ccc tat atg cca cca cag ccc 576
Pro Val Tyr Asn Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro
180 185 190

tct tac ccg gga gcc tga 594
Ser Tyr Pro Gly Ala *
195

<210> 168
<211> 197
<212> PRT
<213> Homo sapiens

<400> 168
Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile Ala
1 5 10 15
Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp Cys Leu
20 25 30
Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe Asn Cys Glu
35 40 45
Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg
50 55 60
Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala
65 70 75 80
Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe
85 90 95
Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys
100 105 110
Tyr Leu Tyr Arg Arg Arg Gln Gln Leu Gln Ser Pro Phe Glu Gly Gln
115 120 125
Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro
130 135 140
Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr
145 150 155 160
Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro
165 170 175
Pro Val Tyr Asn Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro
180 185 190
Ser Tyr Pro Gly Ala
195

<210> 169
<211> 669
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(669)

<400> 169

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atg cgt gtg ggc ctc gcg ctg atc ttg gtg ggc cac gtg aac ctg ctg        48
Met Arg Val Gly Leu Ala Leu Ile Leu Val Gly His Val Asn Leu Leu
 1               5                  10                  15

ctg ggg gcc gtg ctg cat ggc acc gtc ctg cgg cac gtg gcc aat ccc        96
Leu Gly Ala Val Leu His Gly Thr Val Leu Arg His Val Ala Asn Pro
            20                  25                  30

cgc ggc gct gtc acg ccg gag tac acc gta gcc aat gtc atc tct gtc       144
Arg Gly Ala Val Thr Pro Glu Tyr Thr Val Ala Asn Val Ile Ser Val
        35                  40                  45

ggc tcg ggg ctg ctg agc gtt tcc gtg gga ctt gtg gcc ctc ctg gcg       192
Gly Ser Gly Leu Leu Ser Val Ser Val Gly Leu Val Ala Leu Leu Ala
    50                  55                  60

tcc agg aac ctt ctt cgc cct cca ctg cac tgg gtc ctg ctg gca cta       240
Ser Arg Asn Leu Leu Arg Pro Pro Leu His Trp Val Leu Leu Ala Leu
65                  70                  75                  80

gct ctg gtg aac ctg ctc ttg tcc gtt gcc tgc tcc ctg ggc ctc ctt       288
Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu
                85                  90                  95

ctt gct gtg tca ctc act gtg gcc aac ggt ggc cgc cgc ctt att gct       336
Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly Arg Arg Leu Ile Ala
            100                 105                 110

gac tgc cac cca gga ctg ctg gat cct ctg gta cca ctg gat gag ggg       384
Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val Pro Leu Asp Glu Gly
        115                 120                 125

ccg gga cat act gac tgc ccc ttt gac ccc aca aga atc tat gat aca       432
Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr
    130                 135                 140

gcc ttg gct ctc tgg atc cct tct ttg ctc atg tct gca ggg gag gct       480
Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met Ser Ala Gly Glu Ala
145                 150                 155                 160

gct cta tct ggt tac tgc tgt gtg gct gca ctc act cta cgt gga gtt       528
Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu Thr Leu Arg Gly Val
                165                 170                 175
```

```
ggg ccc tgc agg aag gac gga ctt cag ggg cag cta gag gaa atg aca      576
Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln Leu Glu Glu Met Thr
            180                 185                 190

gag ctt gaa tct cct aaa tgt aaa agg cag gaa aat gag cag cta ctg      624
Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu Asn Glu Gln Leu Leu
        195                 200                 205

gat caa aat caa gaa atc cgg gca tca cag aga agt tgg gtt tag          669
Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg Ser Trp Val  *
    210                 215                 220


      <210> 170
      <211> 222
      <212> PRT
      <213> Homo sapiens

      <400> 170
Met Arg Val Gly Leu Ala Leu Ile Leu Val Gly His Val Asn Leu Leu
 1               5                  10                  15
Leu Gly Ala Val Leu His Gly Thr Val Leu Arg His Val Ala Asn Pro
            20                  25                  30
Arg Gly Ala Val Thr Pro Glu Tyr Thr Val Ala Asn Val Ile Ser Val
        35                  40                  45
Gly Ser Gly Leu Leu Ser Val Ser Val Gly Leu Val Ala Leu Leu Ala
    50                  55                  60
Ser Arg Asn Leu Leu Arg Pro Pro Leu His Trp Val Leu Leu Ala Leu
65                  70                  75                  80
Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu
                85                  90                  95
Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly Arg Arg Leu Ile Ala
            100                 105                 110
Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val Pro Leu Asp Glu Gly
        115                 120                 125
Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr
    130                 135                 140
Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met Ser Ala Gly Glu Ala
145                 150                 155                 160
Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu Thr Leu Arg Gly Val
                165                 170                 175
Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln Leu Glu Glu Met Thr
            180                 185                 190
```

```
Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu Asn Glu Gln Leu Leu
        195                 200                 205
Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg Ser Trp Val
    210                 215                 220

      <210> 171
      <211> 345
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(345)

      <400> 171
atg ctg ctg tgg ctt ctt gtc ttc tct gct ctg ggt atc cag gcc tgg       48
Met Leu Leu Trp Leu Leu Val Phe Ser Ala Leu Gly Ile Gln Ala Trp
 1               5                  10                  15

ggt gat tcc tcc tgg aac aaa aca caa gct aaa cag gta tca gag ggg       96
Gly Asp Ser Ser Trp Asn Lys Thr Gln Ala Lys Gln Val Ser Glu Gly
             20                  25                  30

ctc cag tac cta ttt gag aac atc tcc cag ctc act gaa aaa gat gtc      144
Leu Gln Tyr Leu Phe Glu Asn Ile Ser Gln Leu Thr Glu Lys Asp Val
         35                  40                  45

tcc acc acg gtc tct cgc aag gca tgg ggg gca gaa gct gtt ggc tgc      192
Ser Thr Thr Val Ser Arg Lys Ala Trp Gly Ala Glu Ala Val Gly Cys
     50                  55                  60

agt att cag ctg acc acg cca gtg aat gtc ctt gtt ata cac cat gtc      240
Ser Ile Gln Leu Thr Thr Pro Val Asn Val Leu Val Ile His His Val
 65                  70                  75                  80

cct gga ctg gag tgt cac gac cag aca gtc tgc agc cag aga ctg cgg      288
Pro Gly Leu Glu Cys His Asp Gln Thr Val Cys Ser Gln Arg Leu Arg
                 85                  90                  95

gaa ctg cag gcc cat cat gtc cac aac aac agt ggg tgt gat gtg gcc      336
Glu Leu Gln Ala His His Val His Asn Asn Ser Gly Cys Asp Val Ala
            100                 105                 110

tac aag taa                                                          345
```

Tyr Lys *

<210> 172
<211> 114
<212> PRT
<213> Homo sapiens

<400> 172
Met Leu Leu Trp Leu Leu Val Phe Ser Ala Leu Gly Ile Gln Ala Trp
1 5 10 15
Gly Asp Ser Ser Trp Asn Lys Thr Gln Ala Lys Gln Val Ser Glu Gly
20 25 30
Leu Gln Tyr Leu Phe Glu Asn Ile Ser Gln Leu Thr Glu Lys Asp Val
35 40 45
Ser Thr Thr Val Ser Arg Lys Ala Trp Gly Ala Glu Ala Val Gly Cys
50 55 60
Ser Ile Gln Leu Thr Thr Pro Val Asn Val Leu Val Ile His His Val
65 70 75 80
Pro Gly Leu Glu Cys His Asp Gln Thr Val Cys Ser Gln Arg Leu Arg
85 90 95
Glu Leu Gln Ala His His Val His Asn Asn Ser Gly Cys Asp Val Ala
100 105 110
Tyr Lys

<210> 173
<211> 924
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(924)

<400> 173
atg gag cag ctg cag gag gcc ctg aag gta cgc aag gat gat gcc cac 48
Met Glu Gln Leu Gln Glu Ala Leu Lys Val Arg Lys Asp Asp Ala His
1 5 10 15

gcc ctc cac ctg ctg gca ctg ctc ttc tct gcc cag aag cac cac cag 96
Ala Leu His Leu Leu Ala Leu Leu Phe Ser Ala Gln Lys His His Gln
20 25 30

```
cat gcc ctg gat gtt gtc aac atg gcc atc acc gag cac cct gag aac      144
His Ala Leu Asp Val Val Asn Met Ala Ile Thr Glu His Pro Glu Asn
         35                  40                  45

ttc aac ctg atg ttc acc aag gtg aag ctg gag cag gtg ctg aaa ggc      192
Phe Asn Leu Met Phe Thr Lys Val Lys Leu Glu Gln Val Leu Lys Gly
     50                  55                  60

cca gag gaa gcc ctc gtg acc tgc aga caa gtg ctg agg ctg tgg cag      240
Pro Glu Glu Ala Leu Val Thr Cys Arg Gln Val Leu Arg Leu Trp Gln
 65                  70                  75                  80

acc ctg tac agc ttc tcc cag ctg gga ggc cta gaa aag gat ggc agc      288
Thr Leu Tyr Ser Phe Ser Gln Leu Gly Gly Leu Glu Lys Asp Gly Ser
                 85                  90                  95

ttc ggt gag ggc ctc acc atg aag aag cag agt ggc atg cac ctg act      336
Phe Gly Glu Gly Leu Thr Met Lys Lys Gln Ser Gly Met His Leu Thr
            100                 105                 110

ttg cct gat gcc cat gat gca gac tct ggc tcc cgg cgg gct tcg tcc      384
Leu Pro Asp Ala His Asp Ala Asp Ser Gly Ser Arg Arg Ala Ser Ser
        115                 120                 125

atc gcc gcc tcc cgg ctg gag gag gcc atg tca gag ctg act atg ccc      432
Ile Ala Ala Ser Arg Leu Glu Glu Ala Met Ser Glu Leu Thr Met Pro
    130                 135                 140

tct tcg gtc ctg aag cag ggc ccc atg cag ctg tgg acc acg ctg gaa      480
Ser Ser Val Leu Lys Gln Gly Pro Met Gln Leu Trp Thr Thr Leu Glu
145                 150                 155                 160

cag atc tgg ctg cag gct gct gag ctg ttc atg gag cag cag cac ctc      528
Gln Ile Trp Leu Gln Ala Ala Glu Leu Phe Met Glu Gln Gln His Leu
                165                 170                 175

aag gaa gca ggt ttc tgc atc cag gag gcg gcg ggc ctc ttc ccc act      576
Lys Glu Ala Gly Phe Cys Ile Gln Glu Ala Ala Gly Leu Phe Pro Thr
            180                 185                 190

tct cac tca gta ctc tat atg cgg ggc cgg ctg gct gag gtg aag ggc      624
Ser His Ser Val Leu Tyr Met Arg Gly Arg Leu Ala Glu Val Lys Gly
        195                 200                 205
```

```
aac ctg gag gag gcc aag cag ctg tac aag gag gcg ctc acg gtg aac      672
Asn Leu Glu Glu Ala Lys Gln Leu Tyr Lys Glu Ala Leu Thr Val Asn
    210                 215                 220

cca gat ggc gtg cgc atc atg cat agc ctg ggt ctg atg ctg agt cgg      720
Pro Asp Gly Val Arg Ile Met His Ser Leu Gly Leu Met Leu Ser Arg
225                 230                 235                 240

ctg ggc cac aag agc ttg gcc cag aag gtg ctt cgt gat gcc gtg gag      768
Leu Gly His Lys Ser Leu Ala Gln Lys Val Leu Arg Asp Ala Val Glu
                245                 250                 255

agg cag agt acg tgc cac gag gcg tgg cag ggc ctg ggc gag gtg ctg      816
Arg Gln Ser Thr Cys His Glu Ala Trp Gln Gly Leu Gly Glu Val Leu
            260                 265                 270

cag gcc cag ggc cag aac gag gct gcc gtt gac tgc ttc ctc acc gcc      864
Gln Ala Gln Gly Gln Asn Glu Ala Ala Val Asp Cys Phe Leu Thr Ala
        275                 280                 285

ctt gag ctg gag gcc agc agc cct gta ctg ccc ttc tcc atc atc ccc      912
Leu Glu Leu Glu Ala Ser Ser Pro Val Leu Pro Phe Ser Ile Ile Pro
    290                 295                 300

aga gag ctc tga                                                      924
Arg Glu Leu  *
305
```

<210> 174
<211> 307
<212> PRT
<213> Homo sapiens

<400> 174

```
Met Glu Gln Leu Gln Glu Ala Leu Lys Val Arg Lys Asp Asp Ala His
 1               5                  10                  15
Ala Leu His Leu Leu Ala Leu Leu Phe Ser Ala Gln Lys His His Gln
            20                  25                  30
His Ala Leu Asp Val Val Asn Met Ala Ile Thr Glu His Pro Glu Asn
        35                  40                  45
Phe Asn Leu Met Phe Thr Lys Val Lys Leu Glu Gln Val Leu Lys Gly
    50                  55                  60
```

Pro Glu Glu Ala Leu Val Thr Cys Arg Gln Val Leu Arg Leu Trp Gln
65 70 75 80
Thr Leu Tyr Ser Phe Ser Gln Leu Gly Gly Leu Glu Lys Asp Gly Ser
85 90 95
Phe Gly Glu Gly Leu Thr Met Lys Lys Gln Ser Gly Met His Leu Thr
100 105 110
Leu Pro Asp Ala His Asp Ala Asp Ser Gly Ser Arg Arg Ala Ser Ser
115 120 125
Ile Ala Ala Ser Arg Leu Glu Glu Ala Met Ser Glu Leu Thr Met Pro
130 135 140
Ser Ser Val Leu Lys Gln Gly Pro Met Gln Leu Trp Thr Thr Leu Glu
145 150 155 160
Gln Ile Trp Leu Gln Ala Ala Glu Leu Phe Met Glu Gln Gln His Leu
165 170 175
Lys Glu Ala Gly Phe Cys Ile Gln Glu Ala Ala Gly Leu Phe Pro Thr
180 185 190
Ser His Ser Val Leu Tyr Met Arg Gly Arg Leu Ala Glu Val Lys Gly
195 200 205
Asn Leu Glu Glu Ala Lys Gln Leu Tyr Lys Glu Ala Leu Thr Val Asn
210 215 220
Pro Asp Gly Val Arg Ile Met His Ser Leu Gly Leu Met Leu Ser Arg
225 230 235 240
Leu Gly His Lys Ser Leu Ala Gln Lys Val Leu Arg Asp Ala Val Glu
245 250 255
Arg Gln Ser Thr Cys His Glu Ala Trp Gln Gly Leu Gly Glu Val Leu
260 265 270
Gln Ala Gln Gly Gln Asn Glu Ala Ala Val Asp Cys Phe Leu Thr Ala
275 280 285
Leu Glu Leu Glu Ala Ser Ser Pro Val Leu Pro Phe Ser Ile Ile Pro
290 295 300
Arg Glu Leu
305

<210> 175
<211> 627
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(627)

<221> misc_feature
<222> (1)...(627)

<223> n = A,T,C or G

<400> 175

```
atg gga ctc ggc gcg cga ggt gct tgg gcc gcg ctg ctc ctg ggg acg      48
Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr
1               5                   10                  15

ctg cag gtg cta gcg ctg ctg ggg gcc gcc cat gaa agc gca ncc atg      96
Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Xaa Met
            20                  25                  30

gcg gca tct gca aac ata gag aat tct ggg ctt cca cac aac tcc agt      144
Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser
        35                  40                  45

gct aac tca aca gag act ctc caa cat gtg cct tct gac cat aca aat      192
Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn
    50                  55                  60

gaa act tcc aac agt act gtg aaa cca cca act tca gtt gcc tca gac      240
Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp
65                  70                  75                  80

tcc agt aat aca acg gtc acc acc atg aaa cct aca gcg gca tct aat      288
Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn
                85                  90                  95

aca aca aca cca ggg atg gtc tca aca aat atg act tct acc acc tta      336
Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu
            100                 105                 110

aag tct aca ccc aaa aca aca agt gtt tca cag aac aca tct cag ata      384
Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile
        115                 120                 125

tca aca tcc aca atg acc gta acc cac aat agt tca gtg aca tct gct      432
Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala
    130                 135                 140

gct tca tca gta aca atc aca aca act atg cat tct gaa gca aag aaa      480
Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys
145                 150                 155                 160

gga tca aaa ttt gat act ggg agc ttt gtt ggt ggt att gta tta acg      528
```

Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr
165 170 175

ctg gga gtt tta tct att ctt tac att gga tgc aaa atg tat tac tca 576
Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser
180 185 190

aga aga ggc att cgg tat cga acc ata gat gaa cat gat gcc atc att 624
Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile
195 200 205

taa 627
*

<210> 176
<211> 208
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(208)
<223> Xaa = Any Amino Acid

<400> 176
Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr
1 5 10 15
Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Xaa Met
20 25 30
Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser
35 40 45
Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn
50 55 60
Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp
65 70 75 80
Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn
85 90 95
Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu
100 105 110
Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile
115 120 125
Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala

```
    130                 135                 140
Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys
145                 150                 155                 160
Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr
                165                 170                 175
Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser
            180                 185                 190
Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile
        195                 200                 205

      <210> 177
      <211> 1401
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(1401)

      <221> misc_feature
      <222> (1)...(1401)
      <223> n = A,T,C or G

      <400> 177
atg gtc tgg gcc tct ctg ggg gct gcc tgg gtg gca nat ggt gtt cag      48
Met Val Trp Ala Ser Leu Gly Ala Ala Trp Val Ala Xaa Gly Val Gln
 1               5                  10                  15

tgc gac agg aca gtt gta aac ggc atc atc gca acc gtc gtg gtc agt      96
Cys Asp Arg Thr Val Val Asn Gly Ile Ile Ala Thr Val Val Val Ser
            20                  25                  30

tgg atc atc atc gct gcc aca gtg gtt tcc att atc att gtc ttt gac     144
Trp Ile Ile Ile Ala Ala Thr Val Val Ser Ile Ile Ile Val Phe Asp
        35                  40                  45

cct ctt ggg ggg aaa atg gct cca tat tcc tct gcc ggc ccc agc cac     192
Pro Leu Gly Gly Lys Met Ala Pro Tyr Ser Ser Ala Gly Pro Ser His
    50                  55                  60

ctg gat agt cat gat tca agc cag tta ctt aat ggc ctc aag aca gca     240
Leu Asp Ser His Asp Ser Ser Gln Leu Leu Asn Gly Leu Lys Thr Ala
65                  70                  75                  80
```

gct aca agc gtg tgg gaa acc aga atc aag ctc ttg tgc tgt tgc att 288
Ala Thr Ser Val Trp Glu Thr Arg Ile Lys Leu Leu Cys Cys Cys Ile
85 90 95

ggg aaa gac gac cat act cgg gtt gct ttt tcg agt acg gca gag ctt 336
Gly Lys Asp Asp His Thr Arg Val Ala Phe Ser Ser Thr Ala Glu Leu
100 105 110

ttc tca acc tac ttt tca gac aca gat ctg gtg ccc agc gac att gcg 384
Phe Ser Thr Tyr Phe Ser Asp Thr Asp Leu Val Pro Ser Asp Ile Ala
115 120 125

gcg ggc ctc gcc ctg ctt cat cag caa cag gac aat atc agg aac aac 432
Ala Gly Leu Ala Leu Leu His Gln Gln Gln Asp Asn Ile Arg Asn Asn
130 135 140

caa gag cct gcc cag gtg gtc tgc cat gcc cca ggg agc tcc cag gaa 480
Gln Glu Pro Ala Gln Val Val Cys His Ala Pro Gly Ser Ser Gln Glu
145 150 155 160

gct gat ctg gat gca gaa tta gaa aac tgc cat cat tac atg cag ttt 528
Ala Asp Leu Asp Ala Glu Leu Glu Asn Cys His His Tyr Met Gln Phe
165 170 175

gca gca gcg gcc tat ggg tgg ccc ctc tac atc tac aga aac ccc ctc 576
Ala Ala Ala Ala Tyr Gly Trp Pro Leu Tyr Ile Tyr Arg Asn Pro Leu
180 185 190

acg ggg ctg tgc agg att ggt ggt gac tgc tgc aga agc aga acc aca 624
Thr Gly Leu Cys Arg Ile Gly Gly Asp Cys Cys Arg Ser Arg Thr Thr
195 200 205

gac tat gac ttg gtc gga ggc gat cag ctc aac tgt cac ttc ggc tcc 672
Asp Tyr Asp Leu Val Gly Gly Asp Gln Leu Asn Cys His Phe Gly Ser
210 215 220

atc ctg cac acc aca ggg ctg cag tac agg gac ttc atc cac gtc agc 720
Ile Leu His Thr Thr Gly Leu Gln Tyr Arg Asp Phe Ile His Val Ser
225 230 235 240

ttc cat gac aag gtt tac gag ctg ccg ttt tta gtg gct ctg gat cac 768
Phe His Asp Lys Val Tyr Glu Leu Pro Phe Leu Val Ala Leu Asp His
245 250 255

agg aaa gag tct gtt gtg gtc gct gtg agg ggg acc atg tct ctg cag 816
Arg Lys Glu Ser Val Val Val Ala Val Arg Gly Thr Met Ser Leu Gln
260 265 270

gat gtc ctt acg gac ctg tca gcg gag agt gag gtg ctg gac gtg gag 864
Asp Val Leu Thr Asp Leu Ser Ala Glu Ser Glu Val Leu Asp Val Glu
275 280 285

tgt gag gtg cag gac cgc ctg gca cac aag ggt att tct caa gct gcc 912
Cys Glu Val Gln Asp Arg Leu Ala His Lys Gly Ile Ser Gln Ala Ala
290 295 300

aga tac gtt tac caa cga ctc atc aac gac ggg att ttg agc caa gcc 960
Arg Tyr Val Tyr Gln Arg Leu Ile Asn Asp Gly Ile Leu Ser Gln Ala
305 310 315 320

ttc agc att gct cct gag tac cgg ctg gtc ata gtg ggc cac agc ctc 1008
Phe Ser Ile Ala Pro Glu Tyr Arg Leu Val Ile Val Gly His Ser Leu
325 330 335

ggg ggn ggg gcg gcc gcc ctg ctg gcc acc atg ctc aga gcc gcc tac 1056
Gly Xaa Gly Ala Ala Ala Leu Leu Ala Thr Met Leu Arg Ala Ala Tyr
340 345 350

ccg cag gtc agg tgc tac gcc ttc tcc cca ccc cgg ggg ctg tgg agc 1104
Pro Gln Val Arg Cys Tyr Ala Phe Ser Pro Pro Arg Gly Leu Trp Ser
355 360 365

aaa gct ctg cag gaa tat tct cag agc ttc atc gtg tca ctc gtc ctg 1152
Lys Ala Leu Gln Glu Tyr Ser Gln Ser Phe Ile Val Ser Leu Val Leu
370 375 380

ggg aag gat gtg att ccc agg ctc agt gtg acc aac ttg gaa gat ctg 1200
Gly Lys Asp Val Ile Pro Arg Leu Ser Val Thr Asn Leu Glu Asp Leu
385 390 395 400

aag aga aga atc ttg cga gtg gtc gcg cac tgc aat aaa ccc aag tac 1248
Lys Arg Arg Ile Leu Arg Val Val Ala His Cys Asn Lys Pro Lys Tyr
405 410 415

aag atc ttg ctg cac ggt ttg tgg tac gaa ctg ttt gga gga aac ccc 1296
Lys Ile Leu Leu His Gly Leu Trp Tyr Glu Leu Phe Gly Gly Asn Pro
420 425 430

aac aac ttg ccc agc aca agg ggt ctc cag tgt gga cgt ggc ctg acc 1344
Asn Asn Leu Pro Ser Thr Arg Gly Leu Gln Cys Gly Arg Gly Leu Thr
435 440 445

agg gcc act gga aac tgt ccc agg aac gat gga ctc acg ctt ttg tcc 1392
Arg Ala Thr Gly Asn Cys Pro Arg Asn Asp Gly Leu Thr Leu Leu Ser
450 455 460

tta aac tga 1401
Leu Asn *
465

<210> 178
<211> 466
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(466)
<223> Xaa = Any Amino Acid

<400> 178
Met Val Trp Ala Ser Leu Gly Ala Ala Trp Val Ala Xaa Gly Val Gln
1 5 10 15
Cys Asp Arg Thr Val Val Asn Gly Ile Ile Ala Thr Val Val Val Ser
20 25 30
Trp Ile Ile Ile Ala Ala Thr Val Val Ser Ile Ile Ile Val Phe Asp
35 40 45
Pro Leu Gly Gly Lys Met Ala Pro Tyr Ser Ser Ala Gly Pro Ser His
50 55 60
Leu Asp Ser His Asp Ser Ser Gln Leu Leu Asn Gly Leu Lys Thr Ala
65 70 75 80
Ala Thr Ser Val Trp Glu Thr Arg Ile Lys Leu Leu Cys Cys Cys Ile
85 90 95
Gly Lys Asp Asp His Thr Arg Val Ala Phe Ser Ser Thr Ala Glu Leu
100 105 110
Phe Ser Thr Tyr Phe Ser Asp Thr Asp Leu Val Pro Ser Asp Ile Ala
115 120 125
Ala Gly Leu Ala Leu Leu His Gln Gln Gln Asp Asn Ile Arg Asn Asn
130 135 140
Gln Glu Pro Ala Gln Val Val Cys His Ala Pro Gly Ser Ser Gln Glu
145 150 155 160

Ala Asp Leu Asp Ala Glu Leu Glu Asn Cys His His Tyr Met Gln Phe
165 170 175
Ala Ala Ala Ala Tyr Gly Trp Pro Leu Tyr Ile Tyr Arg Asn Pro Leu
180 185 190
Thr Gly Leu Cys Arg Ile Gly Gly Asp Cys Cys Arg Ser Arg Thr Thr
195 200 205
Asp Tyr Asp Leu Val Gly Gly Asp Gln Leu Asn Cys His Phe Gly Ser
210 215 220
Ile Leu His Thr Thr Gly Leu Gln Tyr Arg Asp Phe Ile His Val Ser
225 230 235 240
Phe His Asp Lys Val Tyr Glu Leu Pro Phe Leu Val Ala Leu Asp His
245 250 255
Arg Lys Glu Ser Val Val Val Ala Val Arg Gly Thr Met Ser Leu Gln
260 265 270
Asp Val Leu Thr Asp Leu Ser Ala Glu Ser Glu Val Leu Asp Val Glu
275 280 285
Cys Glu Val Gln Asp Arg Leu Ala His Lys Gly Ile Ser Gln Ala Ala
290 295 300
Arg Tyr Val Tyr Gln Arg Leu Ile Asn Asp Gly Ile Leu Ser Gln Ala
305 310 315 320
Phe Ser Ile Ala Pro Glu Tyr Arg Leu Val Ile Val Gly His Ser Leu
325 330 335
Gly Xaa Gly Ala Ala Ala Leu Leu Ala Thr Met Leu Arg Ala Ala Tyr
340 345 350
Pro Gln Val Arg Cys Tyr Ala Phe Ser Pro Pro Arg Gly Leu Trp Ser
355 360 365
Lys Ala Leu Gln Glu Tyr Ser Gln Ser Phe Ile Val Ser Leu Val Leu
370 375 380
Gly Lys Asp Val Ile Pro Arg Leu Ser Val Thr Asn Leu Glu Asp Leu
385 390 395 400
Lys Arg Arg Ile Leu Arg Val Val Ala His Cys Asn Lys Pro Lys Tyr
405 410 415
Lys Ile Leu Leu His Gly Leu Trp Tyr Glu Leu Phe Gly Gly Asn Pro
420 425 430
Asn Asn Leu Pro Ser Thr Arg Gly Leu Gln Cys Gly Arg Gly Leu Thr
435 440 445
Arg Ala Thr Gly Asn Cys Pro Arg Asn Asp Gly Leu Thr Leu Leu Ser
450 455 460
Leu Asn
465

<210> 179
<211> 909
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(909)

<221> misc_feature
<222> (1)...(909)
<223> n = A,T,C or G

<400> 179
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atg tcc cca agg act agg cca cgc agg tcc act ggc tat tct gag gtg        48
Met Ser Pro Arg Thr Arg Pro Arg Arg Ser Thr Gly Tyr Ser Glu Val
 1               5                  10                  15

ata gtt gtc gtt gga gga tgt gag cga gtt gga gga ttt aat ctt cca        96
Ile Val Val Val Gly Gly Cys Glu Arg Val Gly Gly Phe Asn Leu Pro
            20                  25                  30

tac act gag tgc tac gat cct gta aca gga gaa tgg aag tct ttg gct       144
Tyr Thr Glu Cys Tyr Asp Pro Val Thr Gly Glu Trp Lys Ser Leu Ala
        35                  40                  45

aag ctt cca gaa ttt acc aaa tca gag tat gca gtc tgt gct cta agg       192
Lys Leu Pro Glu Phe Thr Lys Ser Glu Tyr Ala Val Cys Ala Leu Arg
    50                  55                  60

aat gac att ctt gtt tca ggt gga aga atc aac agc cgt gat gtc tgg       240
Asn Asp Ile Leu Val Ser Gly Gly Arg Ile Asn Ser Arg Asp Val Trp
65                  70                  75                  80

att tat aac tca cag tta aat att tgg ntc aga gtt gcc tct ctc aat       288
Ile Tyr Asn Ser Gln Leu Asn Ile Trp Xaa Arg Val Ala Ser Leu Asn
                85                  90                  95

aaa ggc aga tgg cgt cac aaa atg gct gtc ctc ctt ggt aaa gta tat       336
Lys Gly Arg Trp Arg His Lys Met Ala Val Leu Leu Gly Lys Val Tyr
            100                 105                 110

gtt gtc ggt ggc tat gat ggg caa aac aga ctt agc agc gta gaa tgt       384
Val Val Gly Gly Tyr Asp Gly Gln Asn Arg Leu Ser Ser Val Glu Cys
        115                 120                 125

tat gat tcc ttt tca aat cga tgg act gaa gtt gct ccc ctt aag gaa       432
```

```
Tyr Asp Ser Phe Ser Asn Arg Trp Thr Glu Val Ala Pro Leu Lys Glu
    130                 135                 140

gcc gtg agt tct cct gca gtg act agc tgt gta ggc aaa ctg ttt gtg      480
Ala Val Ser Ser Pro Ala Val Thr Ser Cys Val Gly Lys Leu Phe Val
145                 150                 155                 160

att ggt gga gga cct gat gat aat act tgt tct gat aag gtt caa tct      528
Ile Gly Gly Gly Pro Asp Asp Asn Thr Cys Ser Asp Lys Val Gln Ser
                165                 170                 175

tat gat cca gaa acc aat tct tgg cta ctt cgt gca gct atc cca att      576
Tyr Asp Pro Glu Thr Asn Ser Trp Leu Leu Arg Ala Ala Ile Pro Ile
            180                 185                 190

gcc aaa agg tgt ata aca gct gta tcc cta aac aac ctg atc tat gtt      624
Ala Lys Arg Cys Ile Thr Ala Val Ser Leu Asn Asn Leu Ile Tyr Val
        195                 200                 205

gcc ggt gga ctg acc aag gca ata tac tgt tac gat cca gtt gaa gat      672
Ala Gly Gly Leu Thr Lys Ala Ile Tyr Cys Tyr Asp Pro Val Glu Asp
    210                 215                 220

tac tgg atg cac gta cag aat aca ttc agc cgt cag gaa aac tgt ggt      720
Tyr Trp Met His Val Gln Asn Thr Phe Ser Arg Gln Glu Asn Cys Gly
225                 230                 235                 240

atg tct gtg tgt aat ggt aaa ata tat atc ctg ggc gga aga cgg gaa      768
Met Ser Val Cys Asn Gly Lys Ile Tyr Ile Leu Gly Gly Arg Arg Glu
                245                 250                 255

aat gga gaa gcc aca gac act att ctc tgt tat gat cct gca aca agt      816
Asn Gly Glu Ala Thr Asp Thr Ile Leu Cys Tyr Asp Pro Ala Thr Ser
            260                 265                 270

atc atc aca ggg gta gct gca atg ccc agg cca gtg tcc tat cat ggc      864
Ile Ile Thr Gly Val Ala Ala Met Pro Arg Pro Val Ser Tyr His Gly
        275                 280                 285

tgt gtg act att cat aga tac aat gag aaa tgc ttt aaa ctc tga          909
Cys Val Thr Ile His Arg Tyr Asn Glu Lys Cys Phe Lys Leu  *
    290                 295                 300
```

<210> 180
<211> 302
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(302)
<223> Xaa = Any Amino Acid

<400> 180
Met Ser Pro Arg Thr Arg Pro Arg Arg Ser Thr Gly Tyr Ser Glu Val
1 5 10 15
Ile Val Val Val Gly Gly Cys Glu Arg Val Gly Gly Phe Asn Leu Pro
20 25 30
Tyr Thr Glu Cys Tyr Asp Pro Val Thr Gly Glu Trp Lys Ser Leu Ala
35 40 45
Lys Leu Pro Glu Phe Thr Lys Ser Glu Tyr Ala Val Cys Ala Leu Arg
50 55 60
Asn Asp Ile Leu Val Ser Gly Gly Arg Ile Asn Ser Arg Asp Val Trp
65 70 75 80
Ile Tyr Asn Ser Gln Leu Asn Ile Trp Xaa Arg Val Ala Ser Leu Asn
85 90 95
Lys Gly Arg Trp Arg His Lys Met Ala Val Leu Leu Gly Lys Val Tyr
100 105 110
Val Val Gly Gly Tyr Asp Gly Gln Asn Arg Leu Ser Ser Val Glu Cys
115 120 125
Tyr Asp Ser Phe Ser Asn Arg Trp Thr Glu Val Ala Pro Leu Lys Glu
130 135 140
Ala Val Ser Ser Pro Ala Val Thr Ser Cys Val Gly Lys Leu Phe Val
145 150 155 160
Ile Gly Gly Gly Pro Asp Asp Asn Thr Cys Ser Asp Lys Val Gln Ser
165 170 175
Tyr Asp Pro Glu Thr Asn Ser Trp Leu Leu Arg Ala Ala Ile Pro Ile
180 185 190
Ala Lys Arg Cys Ile Thr Ala Val Ser Leu Asn Asn Leu Ile Tyr Val
195 200 205
Ala Gly Gly Leu Thr Lys Ala Ile Tyr Cys Tyr Asp Pro Val Glu Asp
210 215 220
Tyr Trp Met His Val Gln Asn Thr Phe Ser Arg Gln Glu Asn Cys Gly
225 230 235 240
Met Ser Val Cys Asn Gly Lys Ile Tyr Ile Leu Gly Gly Arg Arg Glu
245 250 255
Asn Gly Glu Ala Thr Asp Thr Ile Leu Cys Tyr Asp Pro Ala Thr Ser

```
                260                 265                 270
Ile Ile Thr Gly Val Ala Ala Met Pro Arg Pro Val Ser Tyr His Gly
            275                 280                 285
Cys Val Thr Ile His Arg Tyr Asn Glu Lys Cys Phe Lys Leu
    290                 295                 300

      <210> 181
      <211> 405
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(405)

      <221> misc_feature
      <222> (1)...(405)
      <223> n = A,T,C or G

      <400> 181
atg ccg ctc cta cga gga ctg ctg tgg ctc cag gtg ctg tgt gcg ggc        48
Met Pro Leu Leu Arg Gly Leu Leu Trp Leu Gln Val Leu Cys Ala Gly
 1               5                  10                  15

cct ctc cat aca gag gct gtg gta ctt ctg gtt cct tct gat gat ggg        96
Pro Leu His Thr Glu Ala Val Val Leu Leu Val Pro Ser Asp Asp Gly
                20                  25                  30

cgt gct ttt ctg ctg cgg anc ggc ttc ttc atc cgg agg cgc atg tac       144
Arg Ala Phe Leu Leu Arg Xaa Gly Phe Phe Ile Arg Arg Arg Met Tyr
            35                  40                  45

ccc ccg ccg ctg atc gag gag cca gcc ttc aat gtg tcc tac acc agg       192
Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
        50                  55                  60

cag ccc cca aat ccc ggc cca gga gcc cag cag ccg ggg ccg ccc tat       240
Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
65                  70                  75                  80

tac acc gac cca gga gga ccg ggg atg aac cct gtc ggg aat tcc atg       288
Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
                85                  90                  95
```

```
gca atg gct ttc cag gtc cca ccc aac tca ccc cag ggg agt gtg gcc      336
Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
            100                 105                 110

tgc ccg ccc cct cca gcc tac tgc aac acg cct ccg ccc ccg tac gaa      384
Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
        115                 120                 125

cag gta gtg aag gcc aag tag                                          405
Gln Val Val Lys Ala Lys  *
    130
```

<210> 182
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(134)
<223> Xaa = Any Amino Acid

<400> 182

```
Met Pro Leu Leu Arg Gly Leu Leu Trp Leu Gln Val Leu Cys Ala Gly
 1               5                  10                  15
Pro Leu His Thr Glu Ala Val Val Leu Leu Val Pro Ser Asp Asp Gly
            20                  25                  30
Arg Ala Phe Leu Leu Arg Xaa Gly Phe Phe Ile Arg Arg Arg Met Tyr
        35                  40                  45
Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
    50                  55                  60
Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
65                  70                  75                  80
Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
                85                  90                  95
Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
            100                 105                 110
Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
        115                 120                 125
Gln Val Val Lys Ala Lys
    130
```

<210> 183

<211> 900
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(900)

<221> misc_feature
<222> (1)...(900)
<223> n = A,T,C or G

<400> 183
```
atg gag aga gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc       48
Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val
 1               5                  10                  15

gtc ttc atc ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct       96
Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro
            20                  25                  30

nag gcc tgg gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac      144
Xaa Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His
        35                  40                  45

cca agt cat gta cag ctg aag gta gtt gct gga aac cat gac att ggc      192
Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly
    50                  55                  60

ttc cat tat gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg      240
Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val
65                  70                  75                  80

ttc agc tct gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg      288
Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met
                85                  90                  95

gtc aac agc gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa      336
Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu
            100                 105                 110

aca gaa gca gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga      384
Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg
        115                 120                 125
```

```
gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg        432
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr
    130                 135                 140

tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat        480
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp
145                 150                 155                 160

gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc        528
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile
                165                 170                 175

cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag        576
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys
            180                 185                 190

ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac        624
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His
        195                 200                 205

agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc        672
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val
    210                 215                 220

cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt        720
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly
225                 230                 235                 240

agc atc acg ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt        768
Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg
                245                 250                 255

gag gat gtg gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg        816
Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val
            260                 265                 270

gtc ctc aca ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct        864
Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser
        275                 280                 285

ggt ttg aac ttg ctc gga aag cgt aag aca aga tga                        900
Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg  *
    290                 295
```

<210> 184
<211> 299
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(299)
<223> Xaa = Any Amino Acid

<400> 184
Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val
1 5 10 15
Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro
20 25 30
Xaa Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His
35 40 45
Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly
50 55 60
Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val
65 70 75 80
Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met
85 90 95
Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu
100 105 110
Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg
115 120 125
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr
130 135 140
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp
145 150 155 160
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile
165 170 175
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys
180 185 190
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His
195 200 205
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val
210 215 220
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly
225 230 235 240
Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg

```
                245                 250                 255
Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val
            260                 265                 270
Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser
        275                 280                 285
Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg
    290                 295

<210> 185
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(453)

<400> 185
atg tca gca tgt ttg gca ttg gag cgg gtt gca gct ggc caa ggg ctg      48
Met Ser Ala Cys Leu Ala Leu Glu Arg Val Ala Ala Gly Gln Gly Leu
 1               5                  10                  15

cct act gaa tca ctc ttc tat cgt gct gtt ctt cag gat att att aaa      96
Pro Thr Glu Ser Leu Phe Tyr Arg Ala Val Leu Gln Asp Ile Ile Lys
            20                  25                  30

gat tgt tat ggc atc acc aaa tgt gat cgg cat gtt ggt aaa att tat     144
Asp Cys Tyr Gly Ile Thr Lys Cys Asp Arg His Val Gly Lys Ile Tyr
        35                  40                  45

tcc aaa tgt tct tct ttt ctg gat tat gtc aga cgg tct cta aag aag     192
Ser Lys Cys Ser Ser Phe Leu Asp Tyr Val Arg Arg Ser Leu Lys Lys
    50                  55                  60

ctt gga tta gat gag tcc aag ctg cca gaa aaa att ata atg aac tac     240
Leu Gly Leu Asp Glu Ser Lys Leu Pro Glu Lys Ile Ile Met Asn Tyr
65                  70                  75                  80

tac gag aag tat aag cct cga atg aat gag ctg gaa gct ttt aat atg     288
Tyr Glu Lys Tyr Lys Pro Arg Met Asn Glu Leu Glu Ala Phe Asn Met
                85                  90                  95

ttg aaa gtt gta ctg gct ccc tgt ata gag act ttg att ctt ctg gat     336
Leu Lys Val Val Leu Ala Pro Cys Ile Glu Thr Leu Ile Leu Leu Asp
```

100 105 110

cga ctt tgt tac ctg aaa gag cag gaa gat att gca tgg tct gct ctt 384
Arg Leu Cys Tyr Leu Lys Glu Gln Glu Asp Ile Ala Trp Ser Ala Leu
115 120 125

gtg aag ttg ttt gat ccc gtg aaa tct ccc aga tgt tat gct gtt att 432
Val Lys Leu Phe Asp Pro Val Lys Ser Pro Arg Cys Tyr Ala Val Ile
130 135 140

gcc ctg aag aag cag cag tga 453
Ala Leu Lys Lys Gln Gln *
145 150

<210> 186
<211> 150
<212> PRT
<213> Homo sapiens

<400> 186
Met Ser Ala Cys Leu Ala Leu Glu Arg Val Ala Ala Gly Gln Gly Leu
1 5 10 15
Pro Thr Glu Ser Leu Phe Tyr Arg Ala Val Leu Gln Asp Ile Ile Lys
20 25 30
Asp Cys Tyr Gly Ile Thr Lys Cys Asp Arg His Val Gly Lys Ile Tyr
35 40 45
Ser Lys Cys Ser Ser Phe Leu Asp Tyr Val Arg Arg Ser Leu Lys Lys
50 55 60
Leu Gly Leu Asp Glu Ser Lys Leu Pro Glu Lys Ile Ile Met Asn Tyr
65 70 75 80
Tyr Glu Lys Tyr Lys Pro Arg Met Asn Glu Leu Glu Ala Phe Asn Met
85 90 95
Leu Lys Val Val Leu Ala Pro Cys Ile Glu Thr Leu Ile Leu Leu Asp
100 105 110
Arg Leu Cys Tyr Leu Lys Glu Gln Glu Asp Ile Ala Trp Ser Ala Leu
115 120 125
Val Lys Leu Phe Asp Pro Val Lys Ser Pro Arg Cys Tyr Ala Val Ile
130 135 140
Ala Leu Lys Lys Gln Gln
145 150

<210> 187
<211> 1491

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1491)

<400> 187
atg gcg ctg tgg cgc ggc tcc gcg tac gcg ggc ttc ctg gcg ctg gcc 48
Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
1 5 10 15

gtg ggc tgc gtc ttc ctg ctg gag cca gag ctg cca ggc tcg gcg ctg 96
Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
20 25 30

cgc tct ctc tgg agc tcg ctg tgt ctg ggg ccc gcg cct gcg ccc ccg 144
Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
35 40 45

gga ccc gtc tcc ccc gag ggc cgg ttg gcg gca gcc tgg gac gcg ctt 192
Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
50 55 60

atc gtg cgg cca gtc cgg cgc tgg cgc cgc gtg gca gtg gga gtc aat 240
Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
65 70 75 80

gca tgt gtt gat gtg gtg ctc tca ggg gtg aag ctc ttg cag gca ctt 288
Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
85 90 95

ggc ctt agt cct ggg aat ggg aaa gat cac agc att ctg cat tca agg 336
Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
100 105 110

aat gat ctg gaa gaa gcc ttc att cac ttc atg ggg aag gga gca gct 384
Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala
115 120 125

gct gag cgc ttc ttc agt gat aag gaa act ttt cac gac att gcc cag 432
Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
130 135 140

gtt gcg tca gag ttc cca gga gcc cag cac tat gta gga gga aat gca 480
Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala
145 150 155 160

gct tta att gga cag aaa ttt gca gcc aac tca gat tta aag gtt ctt 528
Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu
165 170 175

ctt tgc ggt cca gtt ggt cca aag cta cat gag ctt ctt gat gac aat 576
Leu Cys Gly Pro Val Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn
180 185 190

gtc ttt gtt cca cca gag tca ttg cag gaa gtg gat gag ttc cac ctc 624
Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu
195 200 205

att tta gag tat caa gca ggg gag gag tgg ggc cag tta aaa gct ccc 672
Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro
210 215 220

cat gcc aac cga ttc atc ttc tct cac gac ctc tcc aac ggg gcc atg 720
His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met
225 230 235 240

aat atg ctg gag gtg ttt gtg tct agc ctg gag gag ttt cag cca gac 768
Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp
245 250 255

ctg gtg gtc ctc tct gga ttg cac atg atg gag gga caa agc aag gag 816
Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu
260 265 270

ctc cag agg aag aga ctc ttg gag gtt gta acc tcc att tct gac atc 864
Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile
275 280 285

ccc act ggt att cca gtt cac cta gag ctg gcc agt atg act aac agg 912
Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg
290 295 300

gag ctc atg agc agc att gtc cat cag gtc ttt ccc gcg gtg act tcc 960
Glu Leu Met Ser Ser Ile Val His Gln Val Phe Pro Ala Val Thr Ser
305 310 315 320

```
ctt ggg ctg aat gaa cag gag ctg tta ttt ctc acc cag tca gcc tct      1008
Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser
                325                 330                 335

gga cct cac tct tct ctc tct tcc tgg aac ggt gtt cct gat gtg ggc      1056
Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly
            340                 345                 350

atg gtc agt gac atc ctc ttc tgg atc ttg aaa gaa cat ggg agg agt      1104
Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser
        355                 360                 365

aaa agc aga gcc tcg gat ctc acc agg atc cat ttc cac acg ctg gtc      1152
Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val
    370                 375                 380

tac cac atc ctg gca act gtg gat gga cac tgg gcc aac cag ctg gca      1200
Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala
385                 390                 395                 400

gcc gtg gct gca gga gct cgt gtg gct ggg aca cag gcc tgc gcc aca      1248
Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr
                405                 410                 415

gaa acc ata gac acc agc cga gtg tct ctg agg gca ccc caa gag ttc      1296
Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe
            420                 425                 430

atg act tcc cat tcg gag gca ggc tcc agg att gta tta aac cca aac      1344
Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn
        435                 440                 445

aag cca gta gta gaa tgg cac aga gag gga ata tcc ttc cac ttc aca      1392
Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr
    450                 455                 460

cca gta ttg gtg tgt aaa gac ccc att cga act gta ggc ctt gga gat      1440
Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp
465                 470                 475                 480

gcc att tca gcc gaa gga ctc ttc tat tcg gaa gta cac cct cac tat      1488
Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr
                485                 490                 495
```

tag 1491
*

<210> 188
<211> 496
<212> PRT
<213> Homo sapiens

<400> 188
Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
1 5 10 15
Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
20 25 30
Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
35 40 45
Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
50 55 60
Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
65 70 75 80
Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
85 90 95
Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
100 105 110
Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala
115 120 125
Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
130 135 140
Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala
145 150 155 160
Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu
165 170 175
Leu Cys Gly Pro Val Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn
180 185 190
Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu
195 200 205
Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro
210 215 220
His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met
225 230 235 240
Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp
245 250 255
Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu

260 265 270
Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile
275 280 285
Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg
290 295 300
Glu Leu Met Ser Ser Ile Val His Gln Val Phe Pro Ala Val Thr Ser
305 310 315 320
Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser
325 330 335
Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly
340 345 350
Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser
355 360 365
Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val
370 375 380
Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala
385 390 395 400
Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr
405 410 415
Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe
420 425 430
Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn
435 440 445
Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr
450 455 460
Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp
465 470 475 480
Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr
485 490 495

<210> 189
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(339)

<400> 189
atg ggg tct cgg ttg tcc cag cct ttt gag tcc tat atc act gcg cct 48
Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
1 5 10 15

ccc ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc 96
Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
20 25 30

gga gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg 144
Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
35 40 45

agc tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac 192
Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
50 55 60

gtg tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt 240
Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
65 70 75 80

cca tgg acc att acg cag atg gtc atc ggc ctc agc att gcc acc tgg 288
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp
85 90 95

ggt atc gtt gtc atg gca gac ccc aaa ggg aag gcc tac cgc gtt gtt 336
Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
100 105 110

tga 339
*

<210> 190
<211> 112
<212> PRT
<213> Homo sapiens

<400> 190
Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
1 5 10 15
Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
20 25 30
Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
35 40 45
Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
50 55 60
Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser

```
65                  70                  75                  80
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp
                85                  90                  95
Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
            100                 105                 110
```

<210> 191
<211> 630
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(630)

<400> 191

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atg gcg gcg gcc atg gca gca tct tcc ctg acg gtc acc tta ggg cgg      48
Met Ala Ala Ala Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg
 1               5                  10                  15

ctg gcg tcc gcg tgc agc cac agc atc ctg aga cct tcg ggg ccc gga      96
Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly
            20                  25                  30

gca gcc tcc ctt tgg tct gct tct cga agg ttc aat tca cag agc act     144
Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr
        35                  40                  45

tca tat cta cca gga tat gtt cct aaa aca tcc ctg agt tca cca cct     192
Ser Tyr Leu Pro Gly Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro
    50                  55                  60

tgg cca gaa gtt gtt ctg cca gac cca gtt gag gag acc aga cac cat     240
Trp Pro Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His
65                  70                  75                  80

gca gag gtc gtg aag aag gtg aat gag atg atc gtc acg ggg cag tat     288
Ala Glu Val Val Lys Lys Val Asn Glu Met Ile Val Thr Gly Gln Tyr
                85                  90                  95

ggc agg ctc ttt gcc gtg gtg cac ttt gcc agc cgc cag tgg aag gtg     336
Gly Arg Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val
            100                 105                 110
```

acc tct gaa gac ctg atc tta att gga aat gaa cta gac ctt gcg tgt 384
Thr Ser Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys
115 120 125

gga gag aga att cga ctg gag aag gtc ctg ctg gtt ggg gca gac aac 432
Gly Glu Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn
130 135 140

ttc acg ctg ctt ggc aag cca ctc ctc gga aag gat ctt gtt cga gta 480
Phe Thr Leu Leu Gly Lys Pro Leu Leu Gly Lys Asp Leu Val Arg Val
145 150 155 160

gaa gcc aca gtc att gaa aag aca gaa tca tgg cca aga atc att atg 528
Glu Ala Thr Val Ile Glu Lys Thr Glu Ser Trp Pro Arg Ile Ile Met
165 170 175

aga ttc agg aaa agg aaa aac ttc aag aag aaa aga atc gtc acg acc 576
Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ile Val Thr Thr
180 185 190

ccg cag act gtc ctc cgg ata aac agc att gag att gct ccg tgt ttg 624
Pro Gln Thr Val Leu Arg Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu
195 200 205

ttg tga 630
Leu *

<210> 192
<211> 209
<212> PRT
<213> Homo sapiens

<400> 192
Met Ala Ala Ala Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg
1 5 10 15
Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly
20 25 30
Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr
35 40 45
Ser Tyr Leu Pro Gly Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro
50 55 60
Trp Pro Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His

65 70 75 80
Ala Glu Val Val Lys Lys Val Asn Glu Met Ile Val Thr Gly Gln Tyr
85 90 95
Gly Arg Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val
100 105 110
Thr Ser Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys
115 120 125
Gly Glu Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn
130 135 140
Phe Thr Leu Leu Gly Lys Pro Leu Leu Gly Lys Asp Leu Val Arg Val
145 150 155 160
Glu Ala Thr Val Ile Glu Lys Thr Glu Ser Trp Pro Arg Ile Ile Met
165 170 175
Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ile Val Thr Thr
180 185 190
Pro Gln Thr Val Leu Arg Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu
195 200 205
Leu

<210> 193
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(351)

<400> 193
atg ggg tct cgg ttg tcc cag cct ttt gag tcc tat atc act gcg cct 48
Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
1 5 10 15

ccc ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc 96
Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
20 25 30

gga gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg 144
Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
35 40 45

agc tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac 192
Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr

```
            50                  55                  60

gtg tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt        240
Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
 65                 70                  75                  80

cca tgg acc att acg cag atg gtc atc ggc ctc agt gag aat caa ggc        288
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Glu Asn Gln Gly
                85                  90                  95

att gcc acc tgg ggt atc gtt gtc atg gca gac ccc aaa ggg aag gcc        336
Ile Ala Thr Trp Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala
            100                 105                 110

tac cgc gtt gtt tga                                                    351
Tyr Arg Val Val  *
        115


<210> 194
<211> 116
<212> PRT
<213> Homo sapiens

<400> 194
Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
 1               5                  10                  15
Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
            20                  25                  30
Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
        35                  40                  45
Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
    50                  55                  60
Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
65                  70                  75                  80
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Glu Asn Gln Gly
                85                  90                  95
Ile Ala Thr Trp Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala
            100                 105                 110
Tyr Arg Val Val
        115

<210> 195
<211> 1047
```

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1047)

<400> 195

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atg cgg ctc ctc ggc tgg tgg caa gta ttg ctg tgg gtg ctg gga ctt      48
Met Arg Leu Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu
 1               5                  10                  15

ccc gtc cgc ggc gtg gag gtt gca gag gaa agt ggt cgc tta tgg tca      96
Pro Val Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser
            20                  25                  30

gag gag cag cct gct cac cct ctc cag gtg ggg gct gtg tac ctg ggt     144
Glu Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
        35                  40                  45

gag gag gag ctc ctg cat gac ccg atg ggc cag gac agg gca gca gaa     192
Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala Glu
    50                  55                  60

gag gcc aat gcg gtg ctg ggg ctg gac acc caa ggc gat cac atg gtg     240
Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His Met Val
65                  70                  75                  80

atg ctg tct gtg att cct ggg gaa gct gag gac aaa gtg agt tca gag     288
Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val Ser Ser Glu
                85                  90                  95

cct agc ggc gtc acc tgt ggt gct gga gga gcg gag gac tca agg tgc     336
Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu Asp Ser Arg Cys
            100                 105                 110

aac gtc cga gag agc ctt ttc tct ctg gat ggc gct gga gca cac ttc     384
Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly Ala Gly Ala His Phe
        115                 120                 125

cct gac aga gaa gag gag tat tac aca gag cca gaa gtg gcg gaa tct     432
Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu Pro Glu Val Ala Glu Ser
    130                 135                 140
```

```
gac gca gcc ccg aca gag gac tcc aat aac act gaa agt ctg aaa tcc      480
Asp Ala Ala Pro Thr Glu Asp Ser Asn Asn Thr Glu Ser Leu Lys Ser
145                 150                 155                 160

cca aag gtg aac tgt gag gag aga aac att aca gga tta gaa aat ttc      528
Pro Lys Val Asn Cys Glu Glu Arg Asn Ile Thr Gly Leu Glu Asn Phe
                165                 170                 175

act ctg aaa att tta aat atg tca cag gac ctt atg gat ttt ctg aac      576
Thr Leu Lys Ile Leu Asn Met Ser Gln Asp Leu Met Asp Phe Leu Asn
            180                 185                 190

cca aac ggt agt gac tgt act cta gtc ctg ttt tac acc ccg tgg tgc      624
Pro Asn Gly Ser Asp Cys Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys
        195                 200                 205

cgc ttt tct gcc agt ttg gcc cct cac ttt aac tct ctg ccc cgg gca      672
Arg Phe Ser Ala Ser Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala
    210                 215                 220

ttt cca gct ctt cac ttt ttg gca ctg gat gca tct cag cac agc agc      720
Phe Pro Ala Leu His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser
225                 230                 235                 240

ctt tct acc agg ttt ggc acc gta gct gtt cct aat att tta tta ttt      768
Leu Ser Thr Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe
                245                 250                 255

caa gga gct aaa cca atg gcc aga ttt aat cat aca gat cga aca ctg      816
Gln Gly Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu
            260                 265                 270

gaa aca ctg aaa atc ttc att ttt aat cag aca ggt ata gaa gcc aag      864
Glu Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys
        275                 280                 285

aag aat gtg gtg gta act caa gcc gac caa ata ggc cct ctt ccc agc      912
Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro Ser
    290                 295                 300

act ttg ata aaa agt gtg gac tgg ttg ctt gta ttt tcc tta ttc ttt      960
Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu Phe Phe
305                 310                 315                 320
```

```
tta att agt ttt att atg tat gct acc att cga act gag agt att cgg      1008
Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu Ser Ile Arg
                325                 330                 335

tgg cta att cca gga caa gag cag gaa cat gtg gag tag                  1047
Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu  *
            340                 345
```

<210> 196
<211> 348
<212> PRT
<213> Homo sapiens

<400> 196

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Met Arg Leu Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu
 1               5                  10                  15
Pro Val Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser
            20                  25                  30
Glu Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
        35                  40                  45
Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala Glu
    50                  55                  60
Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His Met Val
65                  70                  75                  80
Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val Ser Ser Glu
                85                  90                  95
Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu Asp Ser Arg Cys
            100                 105                 110
Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly Ala Gly Ala His Phe
        115                 120                 125
Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu Pro Glu Val Ala Glu Ser
    130                 135                 140
Asp Ala Ala Pro Thr Glu Asp Ser Asn Asn Thr Glu Ser Leu Lys Ser
145                 150                 155                 160
Pro Lys Val Asn Cys Glu Glu Arg Asn Ile Thr Gly Leu Glu Asn Phe
                165                 170                 175
Thr Leu Lys Ile Leu Asn Met Ser Gln Asp Leu Met Asp Phe Leu Asn
            180                 185                 190
Pro Asn Gly Ser Asp Cys Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys
        195                 200                 205
Arg Phe Ser Ala Ser Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala
    210                 215                 220
Phe Pro Ala Leu His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser
```

225 230 235 240
Leu Ser Thr Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe
245 250 255
Gln Gly Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu
260 265 270
Glu Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys
275 280 285
Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro Ser
290 295 300
Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu Phe Phe
305 310 315 320
Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu Ser Ile Arg
325 330 335
Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu
340 345

<210> 197
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(444)

<400> 197
atg gcc ttc cca aag aag aaa ctt cag ggt ctt gtg gct gca acc atc 48
Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile
1 5 10 15

acg cca atg act gag aat gga gaa atc aac ttt tca gta att ggt cag 96
Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
20 25 30

tat gtg gat tat ctt gtg aaa gaa cag gga gtg aag aac att ttt gtg 144
Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
35 40 45

aat ggc aca aca gga gaa ggc ctg tcc ctg agc gtc tca gag cgt cgc 192
Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
50 55 60

cag gtt gca gag gag tgg gtg aca aaa ggg aag gac aag ctg gat cag 240
Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln

```
 65                  70                  75                  80

gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg       288
Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu
                85                  90                  95

gcc caa cat gca gca gaa ata gga gct gat ggc atc gct gtc att gca       336
Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
            100                 105                 110

ccg ttc ttc ctc aag cca tgg acc aaa gat atc ctg att aat ttc cta       384
Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
        115                 120                 125

aag gaa gtg gct gct gcg ccc ctg ccc tgc cat ttt att act atc aca       432
Lys Glu Val Ala Ala Ala Pro Leu Pro Cys His Phe Ile Thr Ile Thr
    130                 135                 140

ttc ctg cct tga                                                       444
Phe Leu Pro  *
145


      <210> 198
      <211> 147
      <212> PRT
      <213> Homo sapiens

      <400> 198
Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile
 1               5                  10                  15
Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
            20                  25                  30
Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
        35                  40                  45
Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
    50                  55                  60
Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
65                  70                  75                  80
Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu
                85                  90                  95
Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
            100                 105                 110
Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
```

```
        115                 120                 125
Lys Glu Val Ala Ala Ala Pro Leu Pro Cys His Phe Ile Thr Ile Thr
    130                 135                 140
Phe Leu Pro
145

      &lt;210&gt; 199
      &lt;211&gt; 705
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapiens

      &lt;220&gt;
      &lt;221&gt; CDS
      &lt;222&gt; (1)...(705)

      &lt;221&gt; misc_feature
      &lt;222&gt; (1)...(705)
      &lt;223&gt; n = A,T,C or G

      &lt;400&gt; 199
atg atg tct caa ggt agt cag ttt ttg tat tca act ttt ggc tat acc      48
Met Met Ser Gln Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr
 1               5                  10                  15

cta ctg gca gcc ata gta gag aga gct tca gga tgt aaa tat ttg gac      96
Leu Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
            20                  25                  30

tat atg cag aaa ata ttc cat gac ttg gat atg ctg acg act gtg cag     144
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val Gln
        35                  40                  45

gaa gaa aac gag cca gtg att tac aat aga gca aga ttt tat gtt tac     192
Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg Phe Tyr Val Tyr
    50                  55                  60

aat aaa aag aaa cgt ctt gtc aac aca cct tac gtg gat aac tcc tat     240
Asn Lys Lys Lys Arg Leu Val Asn Thr Pro Tyr Val Asp Asn Ser Tyr
65                  70                  75                  80

aaa tgg gct ggt ggt gga ttt ctg tct aca gtg ggt gac ctt ctg aaa     288
Lys Trp Ala Gly Gly Gly Phe Leu Ser Thr Val Gly Asp Leu Leu Lys
                85                  90                  95
```

ttt ggg aat gca atg ctt tat ggt tac caa gtt ggg ctg ttt aag aac 336
Phe Gly Asn Ala Met Leu Tyr Gly Tyr Gln Val Gly Leu Phe Lys Asn
100 105 110

tca aat gaa aat ctt tta cct gga tac ctc aaa cca gaa aca atg gtt 384
Ser Asn Glu Asn Leu Leu Pro Gly Tyr Leu Lys Pro Glu Thr Met Val
115 120 125

atg atg tgg acc cca gtc cct aac aca gag atg tct tgg gat aaa gag 432
Met Met Trp Thr Pro Val Pro Asn Thr Glu Met Ser Trp Asp Lys Glu
130 135 140

ggt aaa tat gca atg gcg tgg ggt gtt gtg gaa ang aaa caa acg tat 480
Gly Lys Tyr Ala Met Ala Trp Gly Val Val Glu Xaa Lys Gln Thr Tyr
145 150 155 160

ggt tcg tgt aga aag caa cgg cat tat gct tca cat act gga ggg gca 528
Gly Ser Cys Arg Lys Gln Arg His Tyr Ala Ser His Thr Gly Gly Ala
165 170 175

gtg ggt gcc agt agt gtc ctg ctg gtc ctt cct gaa gaa ctg gat aca 576
Val Gly Ala Ser Ser Val Leu Leu Val Leu Pro Glu Glu Leu Asp Thr
180 185 190

gag act ata aat aac aag gtt ccc cca aga gga atc att gtt tct atc 624
Glu Thr Ile Asn Asn Lys Val Pro Pro Arg Gly Ile Ile Val Ser Ile
195 200 205

ata tgt aac atg caa tct gtt ggc ctc aat agc acc gct ttg aag att 672
Ile Cys Asn Met Gln Ser Val Gly Leu Asn Ser Thr Ala Leu Lys Ile
210 215 220

gcc ctt gaa ttt gat aaa gac aga tca gac tga 705
Ala Leu Glu Phe Asp Lys Asp Arg Ser Asp *
225 230

<210> 200
<211> 234
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT

<222> (1)...(234)
<223> Xaa = Any Amino Acid

<400> 200
Met Met Ser Gln Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr
1 5 10 15
Leu Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
20 25 30
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val Gln
35 40 45
Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg Phe Tyr Val Tyr
50 55 60
Asn Lys Lys Lys Arg Leu Val Asn Thr Pro Tyr Val Asp Asn Ser Tyr
65 70 75 80
Lys Trp Ala Gly Gly Gly Phe Leu Ser Thr Val Gly Asp Leu Leu Lys
85 90 95
Phe Gly Asn Ala Met Leu Tyr Gly Tyr Gln Val Gly Leu Phe Lys Asn
100 105 110
Ser Asn Glu Asn Leu Leu Pro Gly Tyr Leu Lys Pro Glu Thr Met Val
115 120 125
Met Met Trp Thr Pro Val Pro Asn Thr Glu Met Ser Trp Asp Lys Glu
130 135 140
Gly Lys Tyr Ala Met Ala Trp Gly Val Val Glu Xaa Lys Gln Thr Tyr
145 150 155 160
Gly Ser Cys Arg Lys Gln Arg His Tyr Ala Ser His Thr Gly Gly Ala
165 170 175
Val Gly Ala Ser Ser Val Leu Leu Val Leu Pro Glu Glu Leu Asp Thr
180 185 190
Glu Thr Ile Asn Asn Lys Val Pro Pro Arg Gly Ile Ile Val Ser Ile
195 200 205
Ile Cys Asn Met Gln Ser Val Gly Leu Asn Ser Thr Ala Leu Lys Ile
210 215 220
Ala Leu Glu Phe Asp Lys Asp Arg Ser Asp
225 230

<210> 201
<211> 885
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(885)

<221> misc_feature
<222> (1)...(885)
<223> n = A,T,C or G

<400> 201

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atg ctg gct gtg tca gtg ctg gcc gca gtc cgc ggc ggc gac gag gtg      48
Met Leu Ala Val Ser Val Leu Ala Ala Val Arg Gly Gly Asp Glu Val
 1               5                  10                  15

agg cgc gtc cgc gag agc aac gtc ctc cac gag aag tcc aag ggg aag      96
Arg Arg Val Arg Glu Ser Asn Val Leu His Glu Lys Ser Lys Gly Lys
            20                  25                  30

acg cgc gag gga gcc gag gac aag atg acc agc ggc gac gtg ctg tcc     144
Thr Arg Glu Gly Ala Glu Asp Lys Met Thr Ser Gly Asp Val Leu Ser
        35                  40                  45

aac cgc aag atg ttc tac ctg ctc aag acc gcc ttc ccc agc gtc cag     192
Asn Arg Lys Met Phe Tyr Leu Leu Lys Thr Ala Phe Pro Ser Val Gln
    50                  55                  60

att aat act gag gaa cac gtg gat gca gct gat cag gag gtt atc ttg     240
Ile Asn Thr Glu Glu His Val Asp Ala Ala Asp Gln Glu Val Ile Leu
65                  70                  75                  80

tgg gat cat aag att cct gag gat atc cta aag gaa gta act act cct     288
Trp Asp His Lys Ile Pro Glu Asp Ile Leu Lys Glu Val Thr Thr Pro
                85                  90                  95

aaa gag gta cca gca gaa agt gtt act gtc tgg att gac cca ctt gat     336
Lys Glu Val Pro Ala Glu Ser Val Thr Val Trp Ile Asp Pro Leu Asp
            100                 105                 110

gct aca cag gaa tat aca gag gat ctt cga aag tac gtc act act atg     384
Ala Thr Gln Glu Tyr Thr Glu Asp Leu Arg Lys Tyr Val Thr Thr Met
        115                 120                 125

gtg tgt gtg gct gta aat ggt aaa ccc atg cta gga gtt ata cat aag     432
Val Cys Val Ala Val Asn Gly Lys Pro Met Leu Gly Val Ile His Lys
    130                 135                 140

cca ttt tcc gaa tat aca gct tgg gca atg gta gat ggt ggt tca aat     480
Pro Phe Ser Glu Tyr Thr Ala Trp Ala Met Val Asp Gly Gly Ser Asn
145                 150                 155                 160
```

gtg aaa gcc cgc tct tcc tac aat gag aag acc cca agg ntc gtt gtg 528
Val Lys Ala Arg Ser Ser Tyr Asn Glu Lys Thr Pro Arg Xaa Val Val
165 170 175

tct cgt tcc cat tca ggg atg gtc aaa cag gtc gct ctt cag act ttt 576
Ser Arg Ser His Ser Gly Met Val Lys Gln Val Ala Leu Gln Thr Phe
180 185 190

gga aac cag act aca att atc cca gct ggt ggt gct ggt tat aaa gtt 624
Gly Asn Gln Thr Thr Ile Ile Pro Ala Gly Gly Ala Gly Tyr Lys Val
195 200 205

tta gca ctt ttg gat gtg cct gat aag agt caa gaa aaa gct gat tta 672
Leu Ala Leu Leu Asp Val Pro Asp Lys Ser Gln Glu Lys Ala Asp Leu
210 215 220

tac atc cat gtg aca tac atc aaa aag tgg gat ata tgt gct ggt aat 720
Tyr Ile His Val Thr Tyr Ile Lys Lys Trp Asp Ile Cys Ala Gly Asn
225 230 235 240

gcc atc tta aaa gcc cta ggg ggg cat atg act acc ctg agt ggt gaa 768
Ala Ile Leu Lys Ala Leu Gly Gly His Met Thr Thr Leu Ser Gly Glu
245 250 255

gaa atc agt tac act ggt tca gac ggc att gaa ggg gga ctc ctt gct 816
Glu Ile Ser Tyr Thr Gly Ser Asp Gly Ile Glu Gly Gly Leu Leu Ala
260 265 270

agc atc aga atg aac cac cag gcc ctg gtc aga aaa ctc cca gat cta 864
Ser Ile Arg Met Asn His Gln Ala Leu Val Arg Lys Leu Pro Asp Leu
275 280 285

gaa aag aca gga cat aaa tga 885
Glu Lys Thr Gly His Lys *
290

<210> 202
<211> 294
<212> PRT
<213> Homo sapiens

<220>

<221> VARIANT
<222> (1)...(294)
<223> Xaa = Any Amino Acid

<400> 202
Met Leu Ala Val Ser Val Leu Ala Ala Val Arg Gly Gly Asp Glu Val
1   5   10   15
Arg Arg Val Arg Glu Ser Asn Val Leu His Glu Lys Ser Lys Gly Lys
            20   25   30
Thr Arg Glu Gly Ala Glu Asp Lys Met Thr Ser Gly Asp Val Leu Ser
        35   40   45
Asn Arg Lys Met Phe Tyr Leu Leu Lys Thr Ala Phe Pro Ser Val Gln
    50   55   60
Ile Asn Thr Glu Glu His Val Asp Ala Ala Asp Gln Glu Val Ile Leu
65   70   75   80
Trp Asp His Lys Ile Pro Glu Asp Ile Leu Lys Glu Val Thr Thr Pro
                85   90   95
Lys Glu Val Pro Ala Glu Ser Val Thr Val Trp Ile Asp Pro Leu Asp
            100   105   110
Ala Thr Gln Glu Tyr Thr Glu Asp Leu Arg Lys Tyr Val Thr Thr Met
        115   120   125
Val Cys Val Ala Val Asn Gly Lys Pro Met Leu Gly Val Ile His Lys
    130   135   140
Pro Phe Ser Glu Tyr Thr Ala Trp Ala Met Val Asp Gly Gly Ser Asn
145   150   155   160
Val Lys Ala Arg Ser Ser Tyr Asn Glu Lys Thr Pro Arg Xaa Val Val
                165   170   175
Ser Arg Ser His Ser Gly Met Val Lys Gln Val Ala Leu Gln Thr Phe
            180   185   190
Gly Asn Gln Thr Thr Ile Ile Pro Ala Gly Gly Ala Gly Tyr Lys Val
        195   200   205
Leu Ala Leu Leu Asp Val Pro Asp Lys Ser Gln Glu Lys Ala Asp Leu
    210   215   220
Tyr Ile His Val Thr Tyr Ile Lys Lys Trp Asp Ile Cys Ala Gly Asn
225   230   235   240
Ala Ile Leu Lys Ala Leu Gly Gly His Met Thr Thr Leu Ser Gly Glu
                245   250   255
Glu Ile Ser Tyr Thr Gly Ser Asp Gly Ile Glu Gly Gly Leu Leu Ala
            260   265   270
Ser Ile Arg Met Asn His Gln Ala Leu Val Arg Lys Leu Pro Asp Leu
        275   280   285
Glu Lys Thr Gly His Lys
    290

<210> 203
<211> 861
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(861)

<400> 203

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atg gag gaa aaa aga cgg cga gcc cga gtt cag gga gcc tgg gct gcc       48
Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala
 1               5                  10                  15

cct gtt aaa agc cag gcc att gct cag cca gct acc act gct aag agc       96
Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser
            20                  25                  30

cat ctc cac cag aag cct ggc cag acc tgg aag aac aaa gag cat cat      144
His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His
        35                  40                  45

ctc tct gac aga gag ttt gtg ttc aaa gaa cct cag cag gta gta cgt      192
Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg
    50                  55                  60

aga gct cct gag cca cga gtg att gac aga gag ggt gtg tat gaa atc      240
Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile
65                  70                  75                  80

agc ctg tca ccc aca ggt gta tct agg gtc tgt ttg tat cct ggc ttt      288
Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe
                85                  90                  95

gtt gac gtg aaa gaa gct gac tgg ata ttg gaa cag ctt tgt caa gat      336
Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp
            100                 105                 110

gtt ccc tgg aaa cag agg acc ggc atc aga gag gat ata act tat cag      384
Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln
        115                 120                 125

caa cca aga ctt aca gca tgg tat gga gaa ctt cct tac act tat tca      432
Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser
```

130 135 140

aga atc act atg gaa cca aat cct cac tgg cac cct gtg ctg cgc aca 480
Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr
145 150 155 160

cta aag aac cgc att gaa gag aac act ggc cac acc ttc aac tcc tta 528
Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu
165 170 175

ctc tgc aat ctt tat cgc aat gag aag gac agc gtg gac tgg cac agt 576
Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser
180 185 190

gat gat gaa ccc tca cta ggg agg tgc ccc att att gct tca cta agt 624
Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser
195 200 205

ttt ggt gcc aca cgc aca ttt gag atg aga aag aag cca cca cca gaa 672
Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu
210 215 220

gag aat gga gac tac aca tat gtg gaa aga gtg aag ata ccc ttg gat 720
Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp
225 230 235 240

cat ggt acc ttg tta atc atg gaa gga gcg aca caa gct gac tgg cag 768
His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln
245 250 255

cat cga gtg ccc aaa gaa tac cac tct aga gaa ccg aga gtg aac ctg 816
His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu
260 265 270

acc ttt cgg aca gtc tat cca gac cct cga ggg gca ccc tgg tga 861
Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp *
275 280 285

<210> 204
<211> 286
<212> PRT
<213> Homo sapiens

<400> 204

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Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala
1               5                   10                  15
Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser
            20                  25                  30
His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His
        35                  40                  45
Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg
    50                  55                  60
Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile
65                  70                  75                  80
Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe
                85                  90                  95
Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp
            100                 105                 110
Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln
        115                 120                 125
Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser
    130                 135                 140
Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr
145                 150                 155                 160
Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu
                165                 170                 175
Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser
            180                 185                 190
Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser
        195                 200                 205
Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu
    210                 215                 220
Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp
225                 230                 235                 240
His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln
                245                 250                 255
His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu
            260                 265                 270
Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
        275                 280                 285
```

<210> 205
<211> 561
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)...(561)

<400> 205
atg att cac tgg cat tct gag aaa gca act ctt ctt tta aat gct cca 48
Met Ile His Trp His Ser Glu Lys Ala Thr Leu Leu Leu Asn Ala Pro
1 5 10 15

tca ttt tca gat caa ctt cct ggt aca atg gcc acc ctt tct ctg gtg 96
Ser Phe Ser Asp Gln Leu Pro Gly Thr Met Ala Thr Leu Ser Leu Val
20 25 30

aat gag gca cag tat ctg ctg atc aac aca tcc agt att ttg gaa ctt 144
Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser Ile Leu Glu Leu
35 40 45

cac cgg caa cta aac acc agt gat gag aat gga aag gag gaa tta ttc 192
His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys Glu Glu Leu Phe
50 55 60

tca ctg aag gat ctc agc ttg cgt ttt cgt gcc aat att att atc aat 240
Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn Ile Ile Ile Asn
65 70 75 80

gga aaa agg gct ttt gaa gaa gag aaa tgg gat gag att tca att ggc 288
Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu Ile Ser Ile Gly
85 90 95

tct ttg cgt ttc cag gtt ttg ggg cct tgt cac aga tgc cag atg att 336
Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg Cys Gln Met Ile
100 105 110

tgc atc gac cag caa act ggg caa cga aac cag cat gtt ttc caa aaa 384
Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His Val Phe Gln Lys
115 120 125

ctt tct gag agt cgt gaa aca aag gtg aac ttt ggc atg tac ctg atg 432
Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly Met Tyr Leu Met
130 135 140

cat gca tca ttg gat tta tcc tcc cca tgt ttc ctg tct gta gga tct 480
His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu Ser Val Gly Ser
145 150 155 160

```
cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt cat gat tta cct       528
Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly His Asp Leu Pro
                165                 170                 175

gca tct gag aaa cac cag gat gtt acc tcc taa                           561
Ala Ser Glu Lys His Gln Asp Val Thr Ser  *
            180                 185


<210> 206
<211> 186
<212> PRT
<213> Homo sapiens

<400> 206
Met Ile His Trp His Ser Glu Lys Ala Thr Leu Leu Leu Asn Ala Pro
 1               5                  10                  15
Ser Phe Ser Asp Gln Leu Pro Gly Thr Met Ala Thr Leu Ser Leu Val
            20                  25                  30
Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser Ile Leu Glu Leu
        35                  40                  45
His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys Glu Glu Leu Phe
    50                  55                  60
Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn Ile Ile Ile Asn
65                  70                  75                  80
Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu Ile Ser Ile Gly
                85                  90                  95
Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg Cys Gln Met Ile
            100                 105                 110
Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His Val Phe Gln Lys
        115                 120                 125
Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly Met Tyr Leu Met
    130                 135                 140
His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu Ser Val Gly Ser
145                 150                 155                 160
Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly His Asp Leu Pro
                165                 170                 175
Ala Ser Glu Lys His Gln Asp Val Thr Ser
            180                 185

<210> 207
<211> 1272
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> (1)...(1272)

<221> misc_feature
<222> (1)...(1272)
<223> n = A,T,C or G

<400> 207

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atg cac aat tac tgc ttt gtg ttt gct ctg gga tac ctc aca gtg tgc      48
Met His Asn Tyr Cys Phe Val Phe Ala Leu Gly Tyr Leu Thr Val Cys
 1               5                  10                  15

caa gtt act cga gtc tat atc ttt gac tat gga caa tat tct gct gat      96
Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly Gln Tyr Ser Ala Asp
            20                  25                  30

ttt tca ggc cca atg atg atc att act cag aag atc act agt ttg gct     144
Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys Ile Thr Ser Leu Ala
        35                  40                  45

tgc gaa att cat gat ggg atg ttt cgg aag gat gaa gaa ctg act tcc     192
Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp Glu Glu Leu Thr Ser
    50                  55                  60

tca cag agg gat tta gct gta agg cgc atg cca agc tta ctg gag tat     240
Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro Ser Leu Leu Glu Tyr
65                  70                  75                  80

ttg agt tac aac tgt aac ttc atg ggg atc ctg gca ngc cca ntt tgc     288
Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu Ala Xaa Pro Xaa Cys
                85                  90                  95

tct tac aaa gac tac att act ttc att gaa ggc aga tca tac cat atc     336
Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly Arg Ser Tyr His Ile
            100                 105                 110

aca caa tct ggt gaa aat gga aaa gaa gag aca cag tat gaa aga aca     384
Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr Gln Tyr Glu Arg Thr
        115                 120                 125

gag cca tct cca aat act gcg gtt gtt cag aag ctc tta gtt tgt ggg     432
Glu Pro Ser Pro Asn Thr Ala Val Val Gln Lys Leu Leu Val Cys Gly
```

130 135 140

ctg tcc ttg tta ttt cac ttg acc atc tgt aca aca tta cct gtg gag 480
Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr Leu Pro Val Glu
145 150 155 160

tac aac att gat gag cat ttt caa gct aca gct tcg tgg cca aca aag 528
Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser Trp Pro Thr Lys
165 170 175

att atc tat ctg tat atc tct ctt ttg gct gcc aga ccc aaa tac tat 576
Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg Pro Lys Tyr Tyr
180 185 190

ttt gca tgg acg cta gct gat gcc att aat aat gct gca ggc ttt ggt 624
Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala Ala Gly Phe Gly
195 200 205

ttc aga ggg tat gac gaa aat gga gca gct cgc tgg gac tta att tcc 672
Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp Asp Leu Ile Ser
210 215 220

aat ttg aga att caa caa ata gag atg tca aca agt ttc aag atg ttt 720
Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser Phe Lys Met Phe
225 230 235 240

ctt gat aat tgg aat att cag aca gct ctt tgg ctc aaa agg gtg tgt 768
Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Leu Lys Arg Val Cys
245 250 255

tat gaa cga acc tcc ttc agt cca act atc cag acg ttc att ctc tct 816
Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr Phe Ile Leu Ser
260 265 270

gcc att tgg cac ggg gta tac cca gga tat tat cta acg ttt cta aca 864
Ala Ile Trp His Gly Val Tyr Pro Gly Tyr Tyr Leu Thr Phe Leu Thr
275 280 285

ggg gtg tta atg aca tta gca gca aga gct atg aga aat aac ttt aga 912
Gly Val Leu Met Thr Leu Ala Ala Arg Ala Met Arg Asn Asn Phe Arg
290 295 300

cat tat ttc att gaa cct tcc caa ctg aaa tta ttt tat gat gtt ata 960
His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe Tyr Asp Val Ile

305 310 315 320

aca tgg ata gta act caa gta gca ata agt tac aca gtt gtg cca ttt 1008
Thr Trp Ile Val Thr Gln Val Ala Ile Ser Tyr Thr Val Val Pro Phe
325 330 335

gtg ctt ctt tct ata aaa cca tca ctc acg ttt tac agc tcc tgg tat 1056
Val Leu Leu Ser Ile Lys Pro Ser Leu Thr Phe Tyr Ser Ser Trp Tyr
340 345 350

tat tgc ctg cac att ctt ggt atc tta gta tta ttg ttg ttg cca gtg 1104
Tyr Cys Leu His Ile Leu Gly Ile Leu Val Leu Leu Leu Leu Pro Val
355 360 365

aaa aaa act caa aga aga aag aat aca cat gaa aac att cag ctc tca 1152
Lys Lys Thr Gln Arg Arg Lys Asn Thr His Glu Asn Ile Gln Leu Ser
370 375 380

caa tcc aaa aag ttt gat gaa gga gaa aat tct ttg gga cag aac agt 1200
Gln Ser Lys Lys Phe Asp Glu Gly Glu Asn Ser Leu Gly Gln Asn Ser
385 390 395 400

ttt tct aca aca aac aat gtt tgc aat cag aat caa gaa ata gcc tcg 1248
Phe Ser Thr Thr Asn Asn Val Cys Asn Gln Asn Gln Glu Ile Ala Ser
405 410 415

aga cat tca tca cta aag cag tga 1272
Arg His Ser Ser Leu Lys Gln *
420

<210> 208
<211> 423
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(423)
<223> Xaa = Any Amino Acid

<400> 208
Met His Asn Tyr Cys Phe Val Phe Ala Leu Gly Tyr Leu Thr Val Cys
1 5 10 15

```
Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly Gln Tyr Ser Ala Asp
            20                  25                  30
Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys Ile Thr Ser Leu Ala
        35                  40                  45
Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp Glu Glu Leu Thr Ser
    50                  55                  60
Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro Ser Leu Leu Glu Tyr
65                  70                  75                  80
Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu Ala Xaa Pro Xaa Cys
                85                  90                  95
Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly Arg Ser Tyr His Ile
            100                 105                 110
Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr Gln Tyr Glu Arg Thr
        115                 120                 125
Glu Pro Ser Pro Asn Thr Ala Val Val Gln Lys Leu Leu Val Cys Gly
    130                 135                 140
Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr Leu Pro Val Glu
145                 150                 155                 160
Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser Trp Pro Thr Lys
                165                 170                 175
Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg Pro Lys Tyr Tyr
            180                 185                 190
Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala Ala Gly Phe Gly
        195                 200                 205
Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp Asp Leu Ile Ser
    210                 215                 220
Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser Phe Lys Met Phe
225                 230                 235                 240
Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Leu Lys Arg Val Cys
                245                 250                 255
Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr Phe Ile Leu Ser
            260                 265                 270
Ala Ile Trp His Gly Val Tyr Pro Gly Tyr Tyr Leu Thr Phe Leu Thr
        275                 280                 285
Gly Val Leu Met Thr Leu Ala Ala Arg Ala Met Arg Asn Asn Phe Arg
    290                 295                 300
His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe Tyr Asp Val Ile
305                 310                 315                 320
Thr Trp Ile Val Thr Gln Val Ala Ile Ser Tyr Thr Val Val Pro Phe
                325                 330                 335
Val Leu Leu Ser Ile Lys Pro Ser Leu Thr Phe Tyr Ser Ser Trp Tyr
            340                 345                 350
Tyr Cys Leu His Ile Leu Gly Ile Leu Val Leu Leu Leu Leu Pro Val
        355                 360                 365
```

Lys Lys Thr Gln Arg Arg Lys Asn Thr His Glu Asn Ile Gln Leu Ser
370 375 380
Gln Ser Lys Lys Phe Asp Glu Gly Glu Asn Ser Leu Gly Gln Asn Ser
385 390 395 400
Phe Ser Thr Thr Asn Asn Val Cys Asn Gln Asn Gln Glu Ile Ala Ser
405 410 415
Arg His Ser Ser Leu Lys Gln
420

<210> 209
<211> 1413
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1413)

<400> 209
atg tct aga ctg gga gcc ctg ggt ggt gcc cgt gcc ggg ctg gga ctg 48
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
1 5 10 15

ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc 96
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
20 25 30

cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc 144
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
35 40 45

aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg 192
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
50 55 60

ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc 240
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
65 70 75 80

agc ctt cca cgg gaa gga cag gag aag gtg ctg gac cgc ctg gac ttt 288
Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe
85 90 95

gtg ctg acc agc ctt gtg gcg ctg cgg cgg gag gtg gag gag ctg aga 336

```
Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg
            100                 105                 110

agc agc ctg cga ggg ctt gcg ggg gag att gtt ggg gag gtc cga tgc      384
Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys
        115                 120                 125

cac atg gaa gag aac cag aga gtg gct cgg cgg cga agg ttt ccg ttt      432
His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe
    130                 135                 140

gtc cgg gag agg agt gac tcc act ggc tcc agc tct gtc tac ttc acg      480
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
145                 150                 155                 160

gcc tcc tcg gga gcc acg ttc aca gat gct gag agt gaa ggg ggt tac      528
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
                165                 170                 175

aca aca gcc aat gcg gag tct gac aat gag cgg gac tct gac aaa gaa      576
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
            180                 185                 190

agt gag gac ggg gaa gat gaa gtg agc tgt gag act gtg aag atg ggg      624
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
        195                 200                 205

aga aag gat tct ctt gac ttg gag gaa gag gca gct tca ggt gcc tcc      672
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
    210                 215                 220

agt gcc ctg gag gct gga ggt tcc tca ggc ttg gag gat gtg ctg ccc      720
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
225                 230                 235                 240

ctc ctg cag cag gcc gac gag ctg cac agg ggt gat gag caa ggc aag      768
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys
                245                 250                 255

cgg gag ggc ttc cag ctg ctg ctc aac aac aag ctg gtg tat gga agc      816
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser
            260                 265                 270

cgg cag gac ttt ctc tgg cgc ctg gcc cga gcc tac agt gac atg tgt      864
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Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys
275 280 285

gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga 912
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly
290 295 300

aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac 960
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp
305 310 315 320

tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag 1008
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu
325 330 335

agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg 1056
Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val
340 345 350

gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt 1104
Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu
355 360 365

ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa 1152
Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys
370 375 380

aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa 1200
Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu
385 390 395 400

gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt 1248
Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe
405 410 415

tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg 1296
Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly
420 425 430

aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca 1344
Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro
435 440 445

gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg 1392

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu
    450   455   460

gaa gtc att tta cga gac taa   1413
Glu Val Ile Leu Arg Asp *
465   470

<210> 210
<211> 470
<212> PRT
<213> Homo sapiens

<400> 210
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
 1   5   10   15
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
            20   25   30
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
        35   40   45
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
    50   55   60
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
65   70   75   80
Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe
                85   90   95
Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg
            100   105   110
Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys
        115   120   125
His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe
    130   135   140
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
145   150   155   160
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
                165   170   175
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
            180   185   190
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
        195   200   205
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
    210   215   220
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
225   230   235   240

Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys
245 250 255
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser
260 265 270
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys
275 280 285
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly
290 295 300
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp
305 310 315 320
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu
325 330 335
Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val
340 345 350
Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu
355 360 365
Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys
370 375 380
Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu
385 390 395 400
Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe
405 410 415
Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly
420 425 430
Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro
435 440 445
Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu
450 455 460
Glu Val Ile Leu Arg Asp
465 470

<210> 211
<211> 1137
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1137)

<400> 211
atg gac ctc gcg gga ctg ctg aag tct cag ttc ctg tgc cac ctg gtc 48
Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
1 5 10 15

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ttc tgc tac gtc ttt att gcc tca ggg cta atc atc aac acc att cag      96
Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln
            20                  25                  30

ctc ttc act ctc ctc ctc tgg ccc att aac aag cag ctc ttc cgg aag     144
Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys
        35                  40                  45

atc aac tgc aga ctg tcc tat tgc atc tca agc cag ctg gtg atg ctg     192
Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu
    50                  55                  60

ctg gag tgg tgg tcg ggc acg gaa tgc acc atc ttc acg gac ccg cgc     240
Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg
65                  70                  75                  80

gcc tac ctc aag tat ggg aag gaa aat gcc atc gtg gtt ctc aac cac     288
Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His
                85                  90                  95

aag ttt gaa att gac ttt ctg tgt ggc tgg agc ctg tcc gaa cgc ttt     336
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe
            100                 105                 110

ggg ctg tta ggg ggc tcc aag gtc ctg gcc aag aaa gag ctg gcc tat     384
Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr
        115                 120                 125

gtc cca att atc ggc tgg atg tgg tac ttc acc gag atg gtc ttc tgt     432
Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys
    130                 135                 140

tcg cgc aag tgg gag cag gat cgc aag acg gtt gcc acc agt ttg cag     480
Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln
145                 150                 155                 160

cac ctc cgg gac tac ccc gag aag tat ttt ttc ctg att cac tgt gag     528
His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu
                165                 170                 175

ggc aca cgg ttc acg gag aag aag cat gag atc agc atg cag gtg gcc     576
Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala
            180                 185                 190
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cgg gcc aag ggg ctg cct cgc ctc aag cat cac ctg ttg cca cga acc 624
Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr
195 200 205

aag ggc ttc gcc atc acc gtg agg agc ttg aga aat gta gtt tca gct 672
Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala
210 215 220

gta tat gac tgt aca ctc aat ttc aga aat aat gaa aat cca aca ctg 720
Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
225 230 235 240

ctg gga gtc cta aac gga aag aaa tac cat gca gat ttg tat gtt agg 768
Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg
245 250 255

agg atc cca ctg gaa gac atc cct gaa gac gat gac gag tgc tcg gcc 816
Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala
260 265 270

tgg ctg cac aag ctc tac cag gag aag gat gcc ttt cag gag gag tac 864
Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr
275 280 285

tac agg acg ggc acc ttc cca gag acg ccc atg gtg ccc ccc cgg cgg 912
Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg
290 295 300

ccc tgg acc ctc gtg aac tgg ctg ttt tgg gcc tcg ctg gtg ctc tac 960
Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr
305 310 315 320

cct ttc ttc cag ttc ctg gtc agc atg atc agg agc ggg tct tcc ctg 1008
Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu
325 330 335

acg ctg gcc agc ttc atc ctc gtc ttc ttt gtg gcc tct gtg gga gtt 1056
Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val
340 345 350

cga tgg atg att ggt gtg acg gaa att gac aag ggc tct gcc tac ggc 1104
Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly
355 360 365

aac tct gac agc aag cag aaa ctg aat gac tga 1137
Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp *
370 375

<210> 212
<211> 378
<212> PRT
<213> Homo sapiens

<400> 212
Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
1 5 10 15
Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln
20 25 30
Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys
35 40 45
Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu
50 55 60
Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg
65 70 75 80
Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His
85 90 95
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe
100 105 110
Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr
115 120 125
Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys
130 135 140
Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln
145 150 155 160
His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu
165 170 175
Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala
180 185 190
Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr
195 200 205
Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala
210 215 220
Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
225 230 235 240
Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg
245 250 255

Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala
260 265 270
Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr
275 280 285
Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg
290 295 300
Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr
305 310 315 320
Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu
325 330 335
Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val
340 345 350
Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly
355 360 365
Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp
370 375

<210> 213
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(495)

<400> 213
atg tcg gtg aac atg gac gag ctg cgg cac cag gtc atg atc aac cag 48
Met Ser Val Asn Met Asp Glu Leu Arg His Gln Val Met Ile Asn Gln
1 5 10 15

ttc gtg ctg gcc gcg ggc tgc gcg gcc gac cag gcg aag cag ttg ctg 96
Phe Val Leu Ala Ala Gly Cys Ala Ala Asp Gln Ala Lys Gln Leu Leu
20 25 30

cag gcg gcc cac tgg cag ttc gag acc gcg ctg agc acg ttc ttc caa 144
Gln Ala Ala His Trp Gln Phe Glu Thr Ala Leu Ser Thr Phe Phe Gln
35 40 45

gaa acc aac att ccc aac agc cac cac cac cac cag atg atg tgc act 192
Glu Thr Asn Ile Pro Asn Ser His His His His Gln Met Met Cys Thr
50 55 60

ccc agc aac acc cct gcc acg ccg ccc aac ttc ccc gat gcg ctg gcc 240

Pro Ser Asn Thr Pro Ala Thr Pro Pro Asn Phe Pro Asp Ala Leu Ala
65 70 75 80

atg ttc tcc aag ctc cgc gcc tcc gag ggc ctg cag agc agc aac agc 288
Met Phe Ser Lys Leu Arg Ala Ser Glu Gly Leu Gln Ser Ser Asn Ser
85 90 95

ccc atg aca gcc gca gcc tgc tcc cca cct gca aac ttc agc ccc ttc 336
Pro Met Thr Ala Ala Ala Cys Ser Pro Pro Ala Asn Phe Ser Pro Phe
100 105 110

tgg gcc tcg tcc ccg ccc agc cac cag gcg ccc tgg atc ccg ccc tcc 384
Trp Ala Ser Ser Pro Pro Ser His Gln Ala Pro Trp Ile Pro Pro Ser
115 120 125

tcc ccc acc acc ttc cac cac ctc cac cgc cca cag ccc acg tgg ccc 432
Ser Pro Thr Thr Phe His His Leu His Arg Pro Gln Pro Thr Trp Pro
130 135 140

cca gga gca cag cag ggg ggc gcc cag cag aaa gcc atg gcg gcc atg 480
Pro Gly Ala Gln Gln Gly Gly Ala Gln Gln Lys Ala Met Ala Ala Met
145 150 155 160

gac ggc cag aga tga 495
Asp Gly Gln Arg *

<210> 214
<211> 164
<212> PRT
<213> Homo sapiens

<400> 214
Met Ser Val Asn Met Asp Glu Leu Arg His Gln Val Met Ile Asn Gln
1 5 10 15
Phe Val Leu Ala Ala Gly Cys Ala Ala Asp Gln Ala Lys Gln Leu Leu
20 25 30
Gln Ala Ala His Trp Gln Phe Glu Thr Ala Leu Ser Thr Phe Phe Gln
35 40 45
Glu Thr Asn Ile Pro Asn Ser His His His His Gln Met Met Cys Thr
50 55 60
Pro Ser Asn Thr Pro Ala Thr Pro Pro Asn Phe Pro Asp Ala Leu Ala
65 70 75 80

Met Phe Ser Lys Leu Arg Ala Ser Glu Gly Leu Gln Ser Ser Asn Ser
85 90 95
Pro Met Thr Ala Ala Ala Cys Ser Pro Pro Ala Asn Phe Ser Pro Phe
100 105 110
Trp Ala Ser Ser Pro Pro Ser His Gln Ala Pro Trp Ile Pro Pro Ser
115 120 125
Ser Pro Thr Thr Phe His His Leu His Arg Pro Gln Pro Thr Trp Pro
130 135 140
Pro Gly Ala Gln Gln Gly Gly Ala Gln Gln Lys Ala Met Ala Ala Met
145 150 155 160
Asp Gly Gln Arg

<210> 215
<211> 3105
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(3105)

<400> 215
atg gct gcc gct acc ggt gcg gtg gca gcc tcg gcc gcc tcg ggt cag 48
Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
1 5 10 15

gcg gaa ggt aaa aag atc acc gat ctg cgg gtc atc gat ctg aag tcc 96
Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser
20 25 30

gag ctg aag cgg cgg aac tta gac atc acc gga gtc aag acc gtg ctc 144
Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu
35 40 45

atc tcc cga ctc aag cag gct att gaa gag gaa gga ggc gat cca gat 192
Ile Ser Arg Leu Lys Gln Ala Ile Glu Glu Glu Gly Gly Asp Pro Asp
50 55 60

aat att gaa tta act gtt tca act gat act cca aac aag aaa cca act 240
Asn Ile Glu Leu Thr Val Ser Thr Asp Thr Pro Asn Lys Lys Pro Thr
65 70 75 80

aaa ggc aaa ggt aaa aaa cat gaa gca gat gag ttg agt gga gat gct 288

```
Lys Gly Lys Gly Lys Lys His Glu Ala Asp Glu Leu Ser Gly Asp Ala
                85                  90                  95

tct gtg gaa gat gat gct ttt atc aag gac tgt gaa ttg gag aat caa     336
Ser Val Glu Asp Asp Ala Phe Ile Lys Asp Cys Glu Leu Glu Asn Gln
            100                 105                 110

gag gca cat gag caa gat gga aat gat gaa cta aag gac tct gaa gaa     384
Glu Ala His Glu Gln Asp Gly Asn Asp Glu Leu Lys Asp Ser Glu Glu
        115                 120                 125

ttt ggt gaa aat gaa gaa gaa aat gtg cat tcc aag gag tta ctc tct     432
Phe Gly Glu Asn Glu Glu Glu Asn Val His Ser Lys Glu Leu Leu Ser
    130                 135                 140

gca gaa gaa aac aag aga gct cat gaa tta ata gag gca gaa gga ata     480
Ala Glu Glu Asn Lys Arg Ala His Glu Leu Ile Glu Ala Glu Gly Ile
145                 150                 155                 160

gaa gat ata gaa aaa gag gac atc gaa agt cag gaa att gaa gct caa     528
Glu Asp Ile Glu Lys Glu Asp Ile Glu Ser Gln Glu Ile Glu Ala Gln
                165                 170                 175

gaa ggt gaa gat gat acc ttt cta aca gcc caa gat ggt gag gaa gaa     576
Glu Gly Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu
            180                 185                 190

gaa aat gag aaa gat ata gca ggt tct ggt gat ggt aca caa gaa gta     624
Glu Asn Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val
        195                 200                 205

tct aaa cct ctt cct tca gaa ggg agc cta gct gag gct gat cac aca     672
Ser Lys Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr
    210                 215                 220

gct cat gaa gag atg gaa gct cat acg act gtg aaa gaa gct gag gat     720
Ala His Glu Glu Met Glu Ala His Thr Thr Val Lys Glu Ala Glu Asp
225                 230                 235                 240

gac aac atc tcg gtc aca atc cag gct gaa gat gcc atc act ctg gat     768
Asp Asn Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp
                245                 250                 255

ttt gat ggt gat gac ctc cta gaa aca ggt aaa aat gtg aaa att aca     816
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Phe Asp Gly Asp Asp Leu Leu Glu Thr Gly Lys Asn Val Lys Ile Thr
            260                 265                 270

gat tct gaa gca agt aag cca aaa gat ggg cag gac gcc att gca cag      864
Asp Ser Glu Ala Ser Lys Pro Lys Asp Gly Gln Asp Ala Ile Ala Gln
        275                 280                 285

agc ccg gag aag gaa agc aag gat tat gag atg aat gcg aac cat aaa      912
Ser Pro Glu Lys Glu Ser Lys Asp Tyr Glu Met Asn Ala Asn His Lys
    290                 295                 300

gat ggt aag aag gaa gac tgc gtg aag ggt gac cct gtc gag aag gaa      960
Asp Gly Lys Lys Glu Asp Cys Val Lys Gly Asp Pro Val Glu Lys Glu
305                 310                 315                 320

gcc aga gaa agt tct aag aaa gca gaa tct gga gac aaa gaa aag gat     1008
Ala Arg Glu Ser Ser Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp
                325                 330                 335

act ttg aag aaa ggg ccc tcg tct act ggg gcc tct ggt caa gca aag     1056
Thr Leu Lys Lys Gly Pro Ser Ser Thr Gly Ala Ser Gly Gln Ala Lys
            340                 345                 350

agc tct tca aag gaa tct aaa gac agc aag aca tca tct aaa gat gac     1104
Ser Ser Ser Lys Glu Ser Lys Asp Ser Lys Thr Ser Ser Lys Asp Asp
        355                 360                 365

aaa gga agt aca agt agt act agt ggt agc agt gga agc tca act aaa     1152
Lys Gly Ser Thr Ser Ser Thr Ser Gly Ser Ser Gly Ser Ser Thr Lys
    370                 375                 380

aat atc tgg gtt agt gga ctt tca tct aat acc aaa gct gct gat ttg     1200
Asn Ile Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu
385                 390                 395                 400

aag aac ctc ttt ggc aaa tat gga aag gtt ctg agt gca aaa gta gtt     1248
Lys Asn Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val
                405                 410                 415

aca aat gct cga agt cct ggg gca aaa tgc tat ggc att gta act atg     1296
Thr Asn Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met
            420                 425                 430

tct tca agc aca gag gtg tcc agg tgt att gca cat ctt cat cgc act     1344
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Ser Ser Ser Thr Glu Val Ser Arg Cys Ile Ala His Leu His Arg Thr
435 440 445

gag ctg cat gga cag ctg att tct gtt gaa aaa gta aaa ggt gat ccc 1392
Glu Leu His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro
450 455 460

tct aag aaa gaa atg aag aaa gaa aat gat gaa aag agt agt tca aga 1440
Ser Lys Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg
465 470 475 480

agt tct gga gat aaa aaa aat acg agt gat aga agt agc aag aca caa 1488
Ser Ser Gly Asp Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr Gln
485 490 495

gcc tct gtc aaa aaa gaa gag aaa aga tcg tct gag aaa tct gaa aaa 1536
Ala Ser Val Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys
500 505 510

aaa gaa agc aag gat act aag aaa ata gaa ggt aaa gat gag aag aat 1584
Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Gly Lys Asp Glu Lys Asn
515 520 525

gat aat gga gca agt ggc caa aca tca gaa tcg att aaa aaa agt gaa 1632
Asp Asn Gly Ala Ser Gly Gln Thr Ser Glu Ser Ile Lys Lys Ser Glu
530 535 540

gaa aag aag cga ata agt tcc aag agt cca gga cat atg gta ata cta 1680
Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu
545 550 555 560

gac caa act aaa gga gat cat tgt aga cca tca aga aga gga aga tat 1728
Asp Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr
565 570 575

gag aaa att cat gga aga agt aag gaa aag gag aga gct agt cta gat 1776
Glu Lys Ile His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp
580 585 590

aaa aaa aga gat aaa gac tac aga agg aaa gag atc ttg cct ttt gaa 1824
Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu
595 600 605

aag atg aag gaa caa agg ttg aga gaa cat tta gtt cgt ttt gaa agg 1872

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Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg
    610                 615                 620

ctg cga cga gca atg gaa ctt cga aga cga aga gag att gca gag aga      1920
Leu Arg Arg Ala Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg
625                 630                 635                 640

gag cgt cga gag cga gaa cgc att aga ata att cgt gaa cgg gaa gaa      1968
Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu
                645                 650                 655

cgg gaa cgc tta cag aga gag aga gag cgc cta gaa att gaa agg caa      2016
Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln
            660                 665                 670

aaa cta gag aga gag aga atg gaa cgc gaa cgc ttg gaa agg gaa cgc      2064
Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg
        675                 680                 685

att cgt att gaa cag gaa cgt cgt aag gaa gct gaa cgg att gct cga      2112
Ile Arg Ile Glu Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg
    690                 695                 700

gaa aga gag gaa ctc aga agg caa caa cag cag ctt cgt tat gaa caa      2160
Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln
705                 710                 715                 720

gaa aaa agg aat tcc ttg aaa cgc cca cgt gat gta gat cat agg cga      2208
Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg
                725                 730                 735

gat gat cct tac tgg agc gag aat aaa aag ttg tct cta gat aca gat      2256
Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp
            740                 745                 750

gca cga ttt ggc cat gga tcc gac tac tct cgc caa cag aac aga ttt      2304
Ala Arg Phe Gly His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe
        755                 760                 765

aat gac ttt gat cac cga gag agg ggc agg ttt cct gag agt tca gca      2352
Asn Asp Phe Asp His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala
    770                 775                 780

gta cag tct tca tct ttt gaa agg cgg gat cgc ttt gtt ggt caa agt      2400
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Val Gln Ser Ser Ser Phe Glu Arg Arg Asp Arg Phe Val Gly Gln Ser
785 790 795 800

gag ggg aaa aaa gca cga cct act gca cga agg gaa gat cca agc ttc 2448
Glu Gly Lys Lys Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe
805 810 815

gaa aga tat ccc aaa aat ttc agt gac tcc aga aga aat gag cct cca 2496
Glu Arg Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro
820 825 830

cca cca aga aat gaa ctt aga gaa tca gac agg cga gaa gta cga ggg 2544
Pro Pro Arg Asn Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg Gly
835 840 845

gag cga gac gaa agg aga acg gtg att att cat gac agg cct gat atc 2592
Glu Arg Asp Glu Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp Ile
850 855 860

act cat cct aga cat cct cga gag gca ggg ccc aat cct tcc aga ccc 2640
Thr His Pro Arg His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro
865 870 875 880

acc agc tgg aaa agt gaa gga agc atg tcc act gac aaa cgg gaa aca 2688
Thr Ser Trp Lys Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu Thr
885 890 895

aga gtt gaa agg cca gaa cga tct ggg aga gaa gta tca ggg cac agt 2736
Arg Val Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Ser
900 905 910

gtg aga ggc gct ccc cct ggg aat cgt agc agc gct tcg ggg tac ggg 2784
Val Arg Gly Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly
915 920 925

agc aga gag gga gac aga gga gtc atc aca gac cga gga ggt gga tca 2832
Ser Arg Glu Gly Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly Ser
930 935 940

cag cac tat cct gag gag cga cat gtg gtt gaa cgc cat gga cgg gac 2880
Gln His Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp
945 950 955 960

aca agc gga cca agg aaa gag tgg cat ggt cca ccc tct caa ggg cct 2928

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Thr Ser Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro
                965                 970                 975

agc tat cat gat acg agg cga atg ggt gac ggc cgg gca gga gca ggc      2976
Ser Tyr His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly
            980                 985                 990

atg ata acc caa cat tca agt aac gca tcc cca att aat aga att gta      3024
Met Ile Thr Gln His Ser Ser Asn Ala Ser Pro Ile Asn Arg Ile Val
        995                 1000                1005

caa atc agt ggc aat tcc atg cca aga gga agt ggc tcc gga ttt aag      3072
Gln Ile Ser Gly Asn Ser Met Pro Arg Gly Ser Gly Ser Gly Phe Lys
    1010                1015                1020

cca ttt aag ggt gga cct ccg cga cga ttc tga                          3105
Pro Phe Lys Gly Gly Pro Pro Arg Arg Phe  *
1025                1030


      <210> 216
      <211> 1034
      <212> PRT
      <213> Homo sapiens

      <400> 216
Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
 1               5                  10                  15
Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser
            20                  25                  30
Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu
        35                  40                  45
Ile Ser Arg Leu Lys Gln Ala Ile Glu Glu Glu Gly Gly Asp Pro Asp
    50                  55                  60
Asn Ile Glu Leu Thr Val Ser Thr Asp Thr Pro Asn Lys Lys Pro Thr
65                  70                  75                  80
Lys Gly Lys Gly Lys Lys His Glu Ala Asp Glu Leu Ser Gly Asp Ala
                85                  90                  95
Ser Val Glu Asp Asp Ala Phe Ile Lys Asp Cys Glu Leu Glu Asn Gln
            100                 105                 110
Glu Ala His Glu Gln Asp Gly Asn Asp Glu Leu Lys Asp Ser Glu Glu
        115                 120                 125
Phe Gly Glu Asn Glu Glu Glu Asn Val His Ser Lys Glu Leu Leu Ser
    130                 135                 140
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Ala Glu Glu Asn Lys Arg Ala His Glu Leu Ile Glu Ala Glu Gly Ile
145 150 155 160
Glu Asp Ile Glu Lys Glu Asp Ile Glu Ser Gln Glu Ile Glu Ala Gln
165 170 175
Glu Gly Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu
180 185 190
Glu Asn Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val
195 200 205
Ser Lys Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr
210 215 220
Ala His Glu Glu Met Glu Ala His Thr Thr Val Lys Glu Ala Glu Asp
225 230 235 240
Asp Asn Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp
245 250 255
Phe Asp Gly Asp Asp Leu Leu Glu Thr Gly Lys Asn Val Lys Ile Thr
260 265 270
Asp Ser Glu Ala Ser Lys Pro Lys Asp Gly Gln Asp Ala Ile Ala Gln
275 280 285
Ser Pro Glu Lys Glu Ser Lys Asp Tyr Glu Met Asn Ala Asn His Lys
290 295 300
Asp Gly Lys Lys Glu Asp Cys Val Lys Gly Asp Pro Val Glu Lys Glu
305 310 315 320
Ala Arg Glu Ser Ser Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp
325 330 335
Thr Leu Lys Lys Gly Pro Ser Ser Thr Gly Ala Ser Gly Gln Ala Lys
340 345 350
Ser Ser Ser Lys Glu Ser Lys Asp Ser Lys Thr Ser Ser Lys Asp Asp
355 360 365
Lys Gly Ser Thr Ser Ser Thr Ser Gly Ser Ser Gly Ser Ser Thr Lys
370 375 380
Asn Ile Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu
385 390 395 400
Lys Asn Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val
405 410 415
Thr Asn Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met
420 425 430
Ser Ser Ser Thr Glu Val Ser Arg Cys Ile Ala His Leu His Arg Thr
435 440 445
Glu Leu His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro
450 455 460
Ser Lys Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg
465 470 475 480
Ser Ser Gly Asp Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr Gln
485 490 495

Ala Ser Val Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys
500 505 510

Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Gly Lys Asp Glu Lys Asn
515 520 525

Asp Asn Gly Ala Ser Gly Gln Thr Ser Glu Ser Ile Lys Lys Ser Glu
530 535 540

Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu
545 550 555 560

Asp Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr
565 570 575

Glu Lys Ile His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp
580 585 590

Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu
595 600 605

Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg
610 615 620

Leu Arg Arg Ala Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg
625 630 635 640

Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu
645 650 655

Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln
660 665 670

Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg
675 680 685

Ile Arg Ile Glu Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg
690 695 700

Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln
705 710 715 720

Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg
725 730 735

Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp
740 745 750

Ala Arg Phe Gly His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe
755 760 765

Asn Asp Phe Asp His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala
770 775 780

Val Gln Ser Ser Ser Phe Glu Arg Arg Asp Arg Phe Val Gly Gln Ser
785 790 795 800

Glu Gly Lys Lys Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe
805 810 815

Glu Arg Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro
820 825 830

Pro Pro Arg Asn Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg Gly
835 840 845

Glu Arg Asp Glu Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp Ile
    850   855   860
Thr His Pro Arg His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro
865   870   875   880
Thr Ser Trp Lys Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu Thr
                885   890   895
Arg Val Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Ser
            900   905   910
Val Arg Gly Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly
        915   920   925
Ser Arg Glu Gly Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly Ser
    930   935   940
Gln His Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp
945   950   955   960
Thr Ser Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro
                965   970   975
Ser Tyr His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly
            980   985   990
Met Ile Thr Gln His Ser Ser Asn Ala Ser Pro Ile Asn Arg Ile Val
        995   1000   1005
Gln Ile Ser Gly Asn Ser Met Pro Arg Gly Ser Gly Ser Gly Phe Lys
    1010   1015   1020
Pro Phe Lys Gly Gly Pro Pro Arg Arg Phe
1025   1030

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<211> 1428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1428)

<400> 217
atg cct cac agg aag aaa aag ccc ttt ata gag aag aag aaa gct gtg 48
Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu Lys Lys Lys Ala Val
 1   5   10   15

tct ttt cac ttg gtc cac cgg agc caa cga gat cct tta gca gca gat 96
Ser Phe His Leu Val His Arg Ser Gln Arg Asp Pro Leu Ala Ala Asp
            20   25   30

gag agt gca ccc cag agg gtt cta ttg ccc aca caa aaa ata gac aat 144

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Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr Gln Lys Ile Asp Asn
        35                  40                  45

gaa gaa agg cga gca gaa cag agg aag tat gga gtg ttc ttt gat gac      192
Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly Val Phe Phe Asp Asp
    50                  55                  60

gac tat gac tac ctg cag cac ctg aag gaa cca tct ggg cct tca gag      240
Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro Ser Gly Pro Ser Glu
65                  70                  75                  80

ctt att ccc tca agt acc ttc agt gca cac aac agg aga gag gag aaa      288
Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn Arg Arg Glu Glu Lys
                85                  90                  95

gaa gaa acg cta gta att cca agc act gga att aag ttg cct tca tca      336
Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser
            100                 105                 110

gtg ttt gct tca gag ttt gag gaa gat gtt gga ttg tta aat aaa gca      384
Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala
        115                 120                 125

gct cca gtt tca gga cct cga ctg gat ttt gat cct gac att gtt gca      432
Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala
    130                 135                 140

gct ctt gat gat gat ttt gac ttt gat gat cca gat aat ctg ctt gag      480
Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu
145                 150                 155                 160

gat gac ttt att ctt cag gcc aat aag gca aca gga gag gaa gag gga      528
Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly
                165                 170                 175

atg gat ata cag aaa tct gag aat gaa gat gac agc gag tgg gaa gat      576
Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp
            180                 185                 190

gtg gat gat gag aag gga gat agc aat gat gac tat gac tct gca ggc      624
Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly
        195                 200                 205

cta ttg tca gat gaa gac tgt atg tct gtg ccc gga aaa act cac aga      672
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Leu Leu Ser Asp Glu Asp Cys Met Ser Val Pro Gly Lys Thr His Arg
210 215 220

gct ata gca gat cac ttg ttc tgg agt gag gaa aca aag agt cgc ttc 720
Ala Ile Ala Asp His Leu Phe Trp Ser Glu Glu Thr Lys Ser Arg Phe
225 230 235 240

acg gag tat tcg atg act tcc tca gtc atg agg aga aat gaa cag ctg 768
Thr Glu Tyr Ser Met Thr Ser Ser Val Met Arg Arg Asn Glu Gln Leu
245 250 255

acc cta cat gat gag agg ttt gag aag ttt tat gag caa tat gat gat 816
Thr Leu His Asp Glu Arg Phe Glu Lys Phe Tyr Glu Gln Tyr Asp Asp
260 265 270

gat gaa att gga gct ctg gat aat gca gaa ttg gaa ggt tct att caa 864
Asp Glu Ile Gly Ala Leu Asp Asn Ala Glu Leu Glu Gly Ser Ile Gln
275 280 285

gtg gac agc aat cgc tta cag gaa gtt ttg aat gac tac tat aaa gag 912
Val Asp Ser Asn Arg Leu Gln Glu Val Leu Asn Asp Tyr Tyr Lys Glu
290 295 300

aag gca gag aat tgt gta aaa ttg aat acc ctt gaa ccc ttg gag gat 960
Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu Glu Pro Leu Glu Asp
305 310 315 320

caa gac ctg cca atg aat gag ctt gat gag tct gag gag gaa gaa atg 1008
Gln Asp Leu Pro Met Asn Glu Leu Asp Glu Ser Glu Glu Glu Glu Met
325 330 335

att act gta gtc ctt gaa gaa gcc aaa gag aag tgg gat tgt gaa tct 1056
Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys Trp Asp Cys Glu Ser
340 345 350

att tgt agt aca tac tca aat tta tat aac cat cca cag ctt atc aag 1104
Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His Pro Gln Leu Ile Lys
355 360 365

tat caa cca aag ccc aaa caa att cga ata tct tct aaa aca gga ata 1152
Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser Ser Lys Thr Gly Ile
370 375 380

cct ctc aat gtc tta cca aag aaa gga ctc aca gca aag caa act gaa 1200

Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
385 390 395 400

aga ata cag atg att aat ggc agt gat ctt cct aaa gta tca act cag 1248
Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
405 410 415

cca cgt tct aaa aat gaa agc aaa gaa gat aaa aga gca aga aag caa 1296
Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
420 425 430

gct ata aaa gaa gag cgc aag gaa cga aga gtg gag aag aaa gct aac 1344
Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
435 440 445

aaa tta gca ttt aaa ctg gag aaa aga agg caa gaa aaa gag ctg ctg 1392
Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
450 455 460

aac ttg aag aag aat gtt gag ggt cta aag cta tag 1428
Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu *
465 470 475

<210> 218
<211> 475
<212> PRT
<213> Homo sapiens

<400> 218
Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu Lys Lys Lys Ala Val
1 5 10 15
Ser Phe His Leu Val His Arg Ser Gln Arg Asp Pro Leu Ala Ala Asp
20 25 30
Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr Gln Lys Ile Asp Asn
35 40 45
Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly Val Phe Phe Asp Asp
50 55 60
Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro Ser Gly Pro Ser Glu
65 70 75 80
Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn Arg Arg Glu Glu Lys
85 90 95
Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser
100 105 110

Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala
115 120 125
Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala
130 135 140
Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu
145 150 155 160
Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly
165 170 175
Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp
180 185 190
Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly
195 200 205
Leu Leu Ser Asp Glu Asp Cys Met Ser Val Pro Gly Lys Thr His Arg
210 215 220
Ala Ile Ala Asp His Leu Phe Trp Ser Glu Glu Thr Lys Ser Arg Phe
225 230 235 240
Thr Glu Tyr Ser Met Thr Ser Ser Val Met Arg Arg Asn Glu Gln Leu
245 250 255
Thr Leu His Asp Glu Arg Phe Glu Lys Phe Tyr Glu Gln Tyr Asp Asp
260 265 270
Asp Glu Ile Gly Ala Leu Asp Asn Ala Glu Leu Glu Gly Ser Ile Gln
275 280 285
Val Asp Ser Asn Arg Leu Gln Glu Val Leu Asn Asp Tyr Tyr Lys Glu
290 295 300
Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu Glu Pro Leu Glu Asp
305 310 315 320
Gln Asp Leu Pro Met Asn Glu Leu Asp Glu Ser Glu Glu Glu Glu Met
325 330 335
Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys Trp Asp Cys Glu Ser
340 345 350
Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His Pro Gln Leu Ile Lys
355 360 365
Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser Ser Lys Thr Gly Ile
370 375 380
Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
385 390 395 400
Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
405 410 415
Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
420 425 430
Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
435 440 445
Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
450 455 460

Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu
465 470 475

<210> 219
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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<400> 219
atg gcg ttc tcc gcc tgc ttt ggc ggc atc atc ttc aac atc ctc gtg 48
Met Ala Phe Ser Ala Cys Phe Gly Gly Ile Ile Phe Asn Ile Leu Val
1 5 10 15

ggt gtg ggg ctg ggc tgc ctg ctc cag atc tcc cga agc cac aca gaa 96
Gly Val Gly Leu Gly Cys Leu Leu Gln Ile Ser Arg Ser His Thr Glu
20 25 30

gtg aag ctg gag cca gac gga ctg ctg gtg tgg gtc ctg gca ggc gcc 144
Val Lys Leu Glu Pro Asp Gly Leu Leu Val Trp Val Leu Ala Gly Ala
35 40 45

ctg ggg ctc agc ctc gtc ttc tcc ctg gtc tca gtc cca ttg cag tgc 192
Leu Gly Leu Ser Leu Val Phe Ser Leu Val Ser Val Pro Leu Gln Cys
50 55 60

ttc cag ctc agc aga gtc tat ggc ttc tgc ctg ctc ctc ttc tac ctg 240
Phe Gln Leu Ser Arg Val Tyr Gly Phe Cys Leu Leu Leu Phe Tyr Leu
65 70 75 80

aac ttc ctt gtc gtg gcc ctc ctc act gaa ttt gga gtg att cac ctg 288
Asn Phe Leu Val Val Ala Leu Leu Thr Glu Phe Gly Val Ile His Leu
85 90 95

aaa agc atg tga 300
Lys Ser Met *

<210> 220
<211> 99

<212> PRT
<213> Homo sapiens

<400> 220
Met Ala Phe Ser Ala Cys Phe Gly Gly Ile Ile Phe Asn Ile Leu Val
1 5 10 15
Gly Val Gly Leu Gly Cys Leu Leu Gln Ile Ser Arg Ser His Thr Glu
20 25 30
Val Lys Leu Glu Pro Asp Gly Leu Leu Val Trp Val Leu Ala Gly Ala
35 40 45
Leu Gly Leu Ser Leu Val Phe Ser Leu Val Ser Val Pro Leu Gln Cys
50 55 60
Phe Gln Leu Ser Arg Val Tyr Gly Phe Cys Leu Leu Leu Phe Tyr Leu
65 70 75 80
Asn Phe Leu Val Val Ala Leu Leu Thr Glu Phe Gly Val Ile His Leu
85 90 95
Lys Ser Met

<210> 221
<211> 1113
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1113)

<400> 221
atg agt gcc tct gcg gcc acc ggg gtc ttc gtg ctg tcc ctc tcg gcc 48
Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
1 5 10 15

atc ccg gtc acc tat gtc ttc aac cac ctg gcg gcc cag cat gat tcc 96
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
20 25 30

tgg act att gta ggg gtt gct gcc ctc atc ctg ttc ctg gta gca ctg 144
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
35 40 45

ctg gct cgt gtc ctc gtc aaa aga aaa cca ccc cgg gac cca ctg ttc 192
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
50 55 60

tat gtg tat gca gtt ttt gga ttt acc agc gtg gtg aac ctc atc ata 240
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
65 70 75 80

gga ctg gag caa gat gga atc att gac ggg ttc atg aca cac tac ttg 288
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
85 90 95

aga gag ggt gaa ccg tat ctg aac acc gca tat ggg cac atg atc tgc 336
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
100 105 110

tac tgg gat ggc tct gct cat tat ctg atg tac ctg gtg atg gtg gca 384
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
115 120 125

gcc ata gca tgg gag gaa act tat aga acc att ggc cta tat tgg gtt 432
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
130 135 140

gga tct att att atg agt gtt gtt gtt ttt gtg cca gga aac att gta 480
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
145 150 155 160

ggg aag tat gga aca cga att tgc cct gct ttt ttc tta agc ata cca 528
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
165 170 175

tat act tgt ctt cct gtc tgg gct ggt ttc aga atc tat aat cag cca 576
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
180 185 190

tca gaa aat tat aat tac ccc tca aag gtt att caa gaa gcc caa gcg 624
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
195 200 205

aaa gac ctg ctg aga aga cca ttt gat tta atg ttg gtt gtg tgt ctc 672
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
210 215 220

ctc ctg gca act gga ttt tgc ctg ttc aga ggt ttg att gct ttg gat 720
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
225 230 235 240

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tgc cca tct gag ctc tgc cga tta tat acg caa ttt caa gag ccc tat        768
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
                245                 250                 255

cta aag gat cct gct gct tat cct aaa att cag atg ctg gca tat atg        816
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
            260                 265                 270

ttc tat tct gtt cct tac ttt gtg act gca ctg tat ggc tta gtg gtt        864
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
        275                 280                 285

cct gga tgt tcc tgg atg cct gac atc aca ttg ata cat gct gga ggt        912
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
    290                 295                 300

ctg gct cag gct cag ttt tct cac att ggt gca tct ctt cat gct aga        960
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
305                 310                 315                 320

act gct tat gtc tac aga gtc cct gaa gaa gca aaa atc ctt ttt tta       1008
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
                325                 330                 335

gca tta aac ata gca tat gga gtt ctt cct cag ctc ttg gcc tat cgt       1056
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
            340                 345                 350

tgt atc tac aaa cca gag ttc ttc ata aaa aca aag gca gaa gaa aaa       1104
Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
        355                 360                 365

gtg gaa taa                                                           1113
Val Glu  *
    370
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<210> 222
<211> 370
<212> PRT
<213> Homo sapiens

<400> 222

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Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
 1               5                  10                  15
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
            20                  25                  30
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
        35                  40                  45
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
    50                  55                  60
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
65                  70                  75                  80
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
                85                  90                  95
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
            100                 105                 110
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
        115                 120                 125
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
    130                 135                 140
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
145                 150                 155                 160
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
                165                 170                 175
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
            180                 185                 190
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
        195                 200                 205
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
    210                 215                 220
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
225                 230                 235                 240
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
                245                 250                 255
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
            260                 265                 270
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
        275                 280                 285
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
    290                 295                 300
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
305                 310                 315                 320
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
                325                 330                 335
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
            340                 345                 350
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Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
        355                 360                 365
Val Glu
    370
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<210> 223
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(357)

<400> 223

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atg gag cgt ctc ggt gtg ctg tgg acg ctg ctg gtg tcc cgc tgg ttc      48
Met Glu Arg Leu Gly Val Leu Trp Thr Leu Leu Val Ser Arg Trp Phe
 1               5                  10                  15

atc tgc ctg ttt gtg gac atc ttg ccc gtg gag aca gtg ctt cgg atc      96
Ile Cys Leu Phe Val Asp Ile Leu Pro Val Glu Thr Val Leu Arg Ile
            20                  25                  30

tgg gac tgt ttg ttt aac gaa ggc tcg aag att atc ttc cgg gtg gcc     144
Trp Asp Cys Leu Phe Asn Glu Gly Ser Lys Ile Ile Phe Arg Val Ala
        35                  40                  45

ctg acc tta att aag cag cac cag gag ttg att ttg gaa gcc acc agc     192
Leu Thr Leu Ile Lys Gln His Gln Glu Leu Ile Leu Glu Ala Thr Ser
    50                  55                  60

gtt cca gac att tgc gat aag ttt aag cag ata acc aaa ggg agt ttc     240
Val Pro Asp Ile Cys Asp Lys Phe Lys Gln Ile Thr Lys Gly Ser Phe
65                  70                  75                  80

gtg atg gag tgt cac acg ttt atg cag aaa ata ttt tca gaa cct gga     288
Val Met Glu Cys His Thr Phe Met Gln Lys Ile Phe Ser Glu Pro Gly
                85                  90                  95

agc tta tcc atg gcc acc gtc gcc aag ctc cgc gag agc tgc agg gcc     336
Ser Leu Ser Met Ala Thr Val Ala Lys Leu Arg Glu Ser Cys Arg Ala
            100                 105                 110

cgg ctg ctg gca cag ggg tga                                         357
```

Arg Leu Leu Ala Gln Gly *
115

<210> 224
<211> 118
<212> PRT
<213> Homo sapiens

<400> 224
Met Glu Arg Leu Gly Val Leu Trp Thr Leu Leu Val Ser Arg Trp Phe
1 5 10 15
Ile Cys Leu Phe Val Asp Ile Leu Pro Val Glu Thr Val Leu Arg Ile
20 25 30
Trp Asp Cys Leu Phe Asn Glu Gly Ser Lys Ile Ile Phe Arg Val Ala
35 40 45
Leu Thr Leu Ile Lys Gln His Gln Glu Leu Ile Leu Glu Ala Thr Ser
50 55 60
Val Pro Asp Ile Cys Asp Lys Phe Lys Gln Ile Thr Lys Gly Ser Phe
65 70 75 80
Val Met Glu Cys His Thr Phe Met Gln Lys Ile Phe Ser Glu Pro Gly
85 90 95
Ser Leu Ser Met Ala Thr Val Ala Lys Leu Arg Glu Ser Cys Arg Ala
100 105 110
Arg Leu Leu Ala Gln Gly
115

<210> 225
<211> 1764
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1764)

<400> 225
atg agg ccg cga ggt ctc ccg ccg ctc ctg gtg gtg ctc ctg ggc tgc 48
Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
1 5 10 15

tgg gcc tcc gtg agc gcc cag acc gat gcc acc ccg gcg gtg acg aca 96
Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
20 25 30

```
gag ggc ctc aac tcc acc gag gca gcc ctg gcc acc ttc gga act ttc      144
Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe
        35                  40                  45

ccg tcg acc agg ccc ccc ggg act ccc agg gct cca ggg ccc tcc tcc      192
Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser
    50                  55                  60

ggc ccc agg cct acc cca gtc acg gac gtt gct gtt ctc tgt gtc tgt      240
Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys
65                  70                  75                  80

gac tta tcc cca gca cag tgt gac atc aac tgc tgc tgt gat ccc gac      288
Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp
                85                  90                  95

tgc agc tcc gtg gat ttc agt gtc ttt tct gcc tgc tca gtt cca gtt      336
Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val
            100                 105                 110

gtc acg ggc gac agc cag ttt tgt agt caa aaa gca gtc atc tat tca      384
Val Thr Gly Asp Ser Gln Phe Cys Ser Gln Lys Ala Val Ile Tyr Ser
        115                 120                 125

ttg aat ttt aca gca aac cca cct caa aga gta ttt gaa ctt gtt gac      432
Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg Val Phe Glu Leu Val Asp
    130                 135                 140

cag att aat cca tct att ttc tgc att cat att aca aac tat aaa cct      480
Gln Ile Asn Pro Ser Ile Phe Cys Ile His Ile Thr Asn Tyr Lys Pro
145                 150                 155                 160

gca tta tcc ttt att aat cca gaa gta cct gat gaa aac aat ttt gat      528
Ala Leu Ser Phe Ile Asn Pro Glu Val Pro Asp Glu Asn Asn Phe Asp
                165                 170                 175

aca ttg atg aaa aca tct gat ggt ttt aca ttg aat gct gaa tca tat      576
Thr Leu Met Lys Thr Ser Asp Gly Phe Thr Leu Asn Ala Glu Ser Tyr
            180                 185                 190

gtt tcc ttc aca acc aaa ctg gat att cct act gct gct aaa tat gag      624
Val Ser Phe Thr Thr Lys Leu Asp Ile Pro Thr Ala Ala Lys Tyr Glu
        195                 200                 205
```

```
tat ggg gtt cct ctg cag act tca gat tcg ttt ctg aga ttt cct tcg       672
Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser Phe Leu Arg Phe Pro Ser
    210                 215                 220

tcc ctg aca tca tct ctg tgc act gat aat aac cct gca gcg ttt ctg       720
Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn Asn Pro Ala Ala Phe Leu
225                 230                 235                 240

gtg aac cag gct gtt aag tgc acc aga aaa ata aat tta gaa cag tgt       768
Val Asn Gln Ala Val Lys Cys Thr Arg Lys Ile Asn Leu Glu Gln Cys
                245                 250                 255

gaa gaa att gaa gcc ctc agc atg gct ttt tac agc agc ccg gaa att       816
Glu Glu Ile Glu Ala Leu Ser Met Ala Phe Tyr Ser Ser Pro Glu Ile
            260                 265                 270

ctg agg gta cct gat tca aga aaa aag gtc cct atc act gtt cag tcc       864
Leu Arg Val Pro Asp Ser Arg Lys Lys Val Pro Ile Thr Val Gln Ser
        275                 280                 285

atc gtc att cag tct cta aat aaa acg ctc acc cga cgg gag gac act       912
Ile Val Ile Gln Ser Leu Asn Lys Thr Leu Thr Arg Arg Glu Asp Thr
    290                 295                 300

gat gtg ctg cag ccg act ctc gtc aac gct gga cac ttt agc ctt tgc       960
Asp Val Leu Gln Pro Thr Leu Val Asn Ala Gly His Phe Ser Leu Cys
305                 310                 315                 320

gtg aat gtt gtt ctt gag gta aag tac agc ctc aca tac aca gat gca      1008
Val Asn Val Val Leu Glu Val Lys Tyr Ser Leu Thr Tyr Thr Asp Ala
                325                 330                 335

ggt gaa gtc acc aaa gct gat ctc tca ttc gtt ctg ggg aca gtt agc      1056
Gly Glu Val Thr Lys Ala Asp Leu Ser Phe Val Leu Gly Thr Val Ser
            340                 345                 350

agc gta gtg gtc cca ctg cag caa aag ttt gaa att cat ttt ctt cag      1104
Ser Val Val Val Pro Leu Gln Gln Lys Phe Glu Ile His Phe Leu Gln
        355                 360                 365

gaa aat acc cag cca gtc cct ctc agt gga aac cct ggt tat gtc gtg      1152
Glu Asn Thr Gln Pro Val Pro Leu Ser Gly Asn Pro Gly Tyr Val Val
    370                 375                 380
```

```
ggg ctc cca tta gct gct gga ttc cag cct cat aag ggg tct ggg att      1200
Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro His Lys Gly Ser Gly Ile
385                 390                 395                 400

att cag acc aca aat aga tat gga cag ctt act att ctt cat agc aca      1248
Ile Gln Thr Thr Asn Arg Tyr Gly Gln Leu Thr Ile Leu His Ser Thr
                405                 410                 415

act gag caa gac tgc tta gca ctg gag ggg gtc cgg acc cca gta tta      1296
Thr Glu Gln Asp Cys Leu Ala Leu Glu Gly Val Arg Thr Pro Val Leu
            420                 425                 430

ttt ggt tac act atg caa tct ggc tgt aaa cta aga ctg act gga gct      1344
Phe Gly Tyr Thr Met Gln Ser Gly Cys Lys Leu Arg Leu Thr Gly Ala
        435                 440                 445

ctc ccg tgt cag ctc gta gca cag aag gtg aag agc ctg ctg tgg ggc      1392
Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys Ser Leu Leu Trp Gly
    450                 455                 460

cag ggc ttc cca gat tac gtg gcc cct ttt gga aat tcc cag gcc cag      1440
Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly Asn Ser Gln Ala Gln
465                 470                 475                 480

gac atg ctg gac tgg gtg ccc atc cac ttc atc acc cag tca ttc aac      1488
Asp Met Leu Asp Trp Val Pro Ile His Phe Ile Thr Gln Ser Phe Asn
                485                 490                 495

agg aag gat tcc tgc cag ctc cca ggg gct ttg gtt ata gaa gtg aag      1536
Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu Val Ile Glu Val Lys
            500                 505                 510

tgg act aaa tac gga tcc ctg ctg aat cca cag gcc aaa ata gtc aat      1584
Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln Ala Lys Ile Val Asn
        515                 520                 525

gta act gca aat cta att tca tcc tcc ttt cct gag gcc aac tca gga      1632
Val Thr Ala Asn Leu Ile Ser Ser Ser Phe Pro Glu Ala Asn Ser Gly
    530                 535                 540

aat gaa agg acg att ctt att tcc act gcg gtt act ttt gtg gat gtg      1680
Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val Thr Phe Val Asp Val
545                 550                 555                 560
```

tct gca cct gca gag gca ggc ttc aga gct cca cca gcc atc aat gcc 1728
Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro Pro Ala Ile Asn Ala
565 570 575

agg ctg ccc ttt aac ttc ttc ttc ccg ttt gtt tga 1764
Arg Leu Pro Phe Asn Phe Phe Phe Pro Phe Val *
580 585

<210> 226
<211> 587
<212> PRT
<213> Homo sapiens

<400> 226
Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
1 5 10 15
Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
20 25 30
Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe
35 40 45
Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser
50 55 60
Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys
65 70 75 80
Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp
85 90 95
Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val
100 105 110
Val Thr Gly Asp Ser Gln Phe Cys Ser Gln Lys Ala Val Ile Tyr Ser
115 120 125
Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg Val Phe Glu Leu Val Asp
130 135 140
Gln Ile Asn Pro Ser Ile Phe Cys Ile His Ile Thr Asn Tyr Lys Pro
145 150 155 160
Ala Leu Ser Phe Ile Asn Pro Glu Val Pro Asp Glu Asn Asn Phe Asp
165 170 175
Thr Leu Met Lys Thr Ser Asp Gly Phe Thr Leu Asn Ala Glu Ser Tyr
180 185 190
Val Ser Phe Thr Thr Lys Leu Asp Ile Pro Thr Ala Ala Lys Tyr Glu
195 200 205
Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser Phe Leu Arg Phe Pro Ser
210 215 220

Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn Asn Pro Ala Ala Phe Leu
225 230 235 240
Val Asn Gln Ala Val Lys Cys Thr Arg Lys Ile Asn Leu Glu Gln Cys
245 250 255
Glu Glu Ile Glu Ala Leu Ser Met Ala Phe Tyr Ser Ser Pro Glu Ile
260 265 270
Leu Arg Val Pro Asp Ser Arg Lys Lys Val Pro Ile Thr Val Gln Ser
275 280 285
Ile Val Ile Gln Ser Leu Asn Lys Thr Leu Thr Arg Arg Glu Asp Thr
290 295 300
Asp Val Leu Gln Pro Thr Leu Val Asn Ala Gly His Phe Ser Leu Cys
305 310 315 320
Val Asn Val Val Leu Glu Val Lys Tyr Ser Leu Thr Tyr Thr Asp Ala
325 330 335
Gly Glu Val Thr Lys Ala Asp Leu Ser Phe Val Leu Gly Thr Val Ser
340 345 350
Ser Val Val Val Pro Leu Gln Gln Lys Phe Glu Ile His Phe Leu Gln
355 360 365
Glu Asn Thr Gln Pro Val Pro Leu Ser Gly Asn Pro Gly Tyr Val Val
370 375 380
Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro His Lys Gly Ser Gly Ile
385 390 395 400
Ile Gln Thr Thr Asn Arg Tyr Gly Gln Leu Thr Ile Leu His Ser Thr
405 410 415
Thr Glu Gln Asp Cys Leu Ala Leu Glu Gly Val Arg Thr Pro Val Leu
420 425 430
Phe Gly Tyr Thr Met Gln Ser Gly Cys Lys Leu Arg Leu Thr Gly Ala
435 440 445
Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys Ser Leu Leu Trp Gly
450 455 460
Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly Asn Ser Gln Ala Gln
465 470 475 480
Asp Met Leu Asp Trp Val Pro Ile His Phe Ile Thr Gln Ser Phe Asn
485 490 495
Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu Val Ile Glu Val Lys
500 505 510
Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln Ala Lys Ile Val Asn
515 520 525
Val Thr Ala Asn Leu Ile Ser Ser Ser Phe Pro Glu Ala Asn Ser Gly
530 535 540
Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val Thr Phe Val Asp Val
545 550 555 560
Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro Pro Ala Ile Asn Ala
565 570 575

```
Arg Leu Pro Phe Asn Phe Phe Phe Pro Phe Val
            580                 585

      <210> 227
      <211> 963
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(963)

      <400> 227
atg gcc ggc ctg gcg gcg cgg ttg gtc ctg cta gct ggg gca gcg gcg      48
Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala Ala
 1               5                  10                  15

ctg gcg agc ggc tcc cag ggc gac cgt gag ccg gtg tac cgc gac tgc      96
Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys
            20                  25                  30

gta ctg cag tgc gaa gag cag aac tgc tct ggg ggc gct ctg aat cac     144
Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala Leu Asn His
        35                  40                  45

ttc cgc tcc cgc cag cca atc tac atg agt cta gca ggc tgg acc tgt     192
Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys
    50                  55                  60

cgg gac gac tgt aag tat gag tgt atg tgg gtc acc gtt ggg ctc tac     240
Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr
65                  70                  75                  80

ctc cag gaa ggt cac aaa gtg cct cag ttc cat ggc aag tgg ccc ttc     288
Leu Gln Glu Gly His Lys Val Pro Gln Phe His Gly Lys Trp Pro Phe
                85                  90                  95

tcc cgg ttc ctg ttc ttt caa gag ccg gca tcg gcc gtg gcc tcg ttt     336
Ser Arg Phe Leu Phe Phe Gln Glu Pro Ala Ser Ala Val Ala Ser Phe
            100                 105                 110

ctc aat ggc ctg gcc agc ctg gtg atg ctc tgc cgc tac cgc acc ttc     384
Leu Asn Gly Leu Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe
        115                 120                 125
```

gtg cca gcc tcc tcc ccc atg tac cac acc tgt gtg gcc ttc gcc tgg 432
Val Pro Ala Ser Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp
130 135 140

gtg tcc ctc aat gca tgg ttc tgg tcc aca gtc ttc cac acc agg gac 480
Val Ser Leu Asn Ala Trp Phe Trp Ser Thr Val Phe His Thr Arg Asp
145 150 155 160

act gac ctc aca gag aaa atg gac tac ttc tgt gcc tcc act gtc atc 528
Thr Asp Leu Thr Glu Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile
165 170 175

cta cac tca atc tac ctg tgc tgc gtc agg acc gtg ggg ctg cag cac 576
Leu His Ser Ile Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His
180 185 190

cca gct gtg gtc agt gcc ttc cgg gct ctc ctg ctg ctc atg ctg acc 624
Pro Ala Val Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr
195 200 205

gtg cac gtc tcc tac ctg agc ctc atc cgc ttc gac tat ggc tac aac 672
Val His Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn
210 215 220

ctg gtg gcc aac gtg gct att ggc ctg gtc aac gtg gtg tgg tgg ctg 720
Leu Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu
225 230 235 240

gcc tgg tgc ctg tgg aac cag cgg cgg ctg cct cac gtg cgc aag tgc 768
Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys Cys
245 250 255

gtg gtg gtg gtc ttg ctg ctg cag ggg ctg tcc ctg ctc gag ctg ctt 816
Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu Leu Leu
260 265 270

gac ttc cca ccg ctc ttc tgg gtc ctg gat gcc cat gcc atc tgg cac 864
Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala Ile Trp His
275 280 285

atc agc acc atc cct gtc cac gtc ctc ttt ttc agc ttt ctg gaa gat 912
Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser Phe Leu Glu Asp
290 295 300

gac agc ctg tac ctg ctg aag gaa tca gag gac aag ttc aag ctg gac 960
Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp Lys Phe Lys Leu Asp
305 310 315 320

tga 963
*

<210> 228
<211> 320
<212> PRT
<213> Homo sapiens

<400> 228
Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala Ala
1 5 10 15
Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys
20 25 30
Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala Leu Asn His
35 40 45
Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys
50 55 60
Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr
65 70 75 80
Leu Gln Glu Gly His Lys Val Pro Gln Phe His Gly Lys Trp Pro Phe
85 90 95
Ser Arg Phe Leu Phe Phe Gln Glu Pro Ala Ser Ala Val Ala Ser Phe
100 105 110
Leu Asn Gly Leu Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe
115 120 125
Val Pro Ala Ser Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp
130 135 140
Val Ser Leu Asn Ala Trp Phe Trp Ser Thr Val Phe His Thr Arg Asp
145 150 155 160
Thr Asp Leu Thr Glu Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile
165 170 175
Leu His Ser Ile Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His
180 185 190
Pro Ala Val Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr
195 200 205
Val His Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn
210 215 220

```
Leu Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu
225                 230                 235                 240
Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys Cys
                245                 250                 255
Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu Leu Leu
            260                 265                 270
Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala Ile Trp His
        275                 280                 285
Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser Phe Leu Glu Asp
    290                 295                 300
Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp Lys Phe Lys Leu Asp
305                 310                 315                 320

      <210> 229
      <211> 657
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(657)

      <221> misc_feature
      <222> (1)...(657)
      <223> n = A,T,C or G

      <400> 229
atg gcg cgg aag aag gtg cgt ccg cgg ctg atc gcg gan ctg gcc cgc      48
Met Ala Arg Lys Lys Val Arg Pro Arg Leu Ile Ala Xaa Leu Ala Arg
 1               5                  10                  15

cgc gtg cgc gcc ctg cgg gag caa ctg aac agg ccg cgc gac tcc cag      96
Arg Val Arg Ala Leu Arg Glu Gln Leu Asn Arg Pro Arg Asp Ser Gln
            20                  25                  30

ctc tac gcg gtg gac tac gag acc ttg acg cgg ccg ttc tct gga cgc     144
Leu Tyr Ala Val Asp Tyr Glu Thr Leu Thr Arg Pro Phe Ser Gly Arg
        35                  40                  45

cgg ctg ccg gtc cgg gcc tgg gcc gac gtg cgc cgc gag anc cgc ctc     192
Arg Leu Pro Val Arg Ala Trp Ala Asp Val Arg Arg Glu Xaa Arg Leu
    50                  55                  60

ttg cag ctg ctc ggc cgc ctc ccg ctc ttc ggc ctg ggc cgc ctg gtc     240
```

```
Leu Gln Leu Leu Gly Arg Leu Pro Leu Phe Gly Leu Gly Arg Leu Val
 65                 70                  75                  80

acg cgc aag tcc tgg ctg tgg cag cac gac gag ccg tgc tac tgg cgc      288
Thr Arg Lys Ser Trp Leu Trp Gln His Asp Glu Pro Cys Tyr Trp Arg
                85                  90                  95

ctc acg cgg gtg cgg ccc gac tac acg gcg cag aac ttg gac cac ggg      336
Leu Thr Arg Val Arg Pro Asp Tyr Thr Ala Gln Asn Leu Asp His Gly
            100                 105                 110

aag gcc tgg ggc atc ctg acc ttc aaa ggg aag act gag agc gag gcg      384
Lys Ala Trp Gly Ile Leu Thr Phe Lys Gly Lys Thr Glu Ser Glu Ala
        115                 120                 125

cgg gag atc gaa cac gtc atg tac cat gac tgg cgg ctg gtg ccc aag      432
Arg Glu Ile Glu His Val Met Tyr His Asp Trp Arg Leu Val Pro Lys
    130                 135                 140

cac gag gag gag gcc ttc acc gcg ttc acg ccg gcg ccg gaa gac agc      480
His Glu Glu Glu Ala Phe Thr Ala Phe Thr Pro Ala Pro Glu Asp Ser
145                 150                 155                 160

ctg gcc tcc gtg ccg tac ccg cct ctc ctc cgg gcc atg att atc gca      528
Leu Ala Ser Val Pro Tyr Pro Pro Leu Leu Arg Ala Met Ile Ile Ala
                165                 170                 175

gaa cga cag aaa aat gga gac aca agc acc gag gag ccc atg ctg aat      576
Glu Arg Gln Lys Asn Gly Asp Thr Ser Thr Glu Glu Pro Met Leu Asn
            180                 185                 190

gtg cag agg ata cgc atg gaa ccc tgg gat tac cct gca aaa cag gaa      624
Val Gln Arg Ile Arg Met Glu Pro Trp Asp Tyr Pro Ala Lys Gln Glu
        195                 200                 205

gac aaa gga agg gcc aag ggc acc ccc gtc tag                          657
Asp Lys Gly Arg Ala Lys Gly Thr Pro Val  *
    210                 215
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<210> 230
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(218)
<223> Xaa = Any Amino Acid

<400> 230
Met Ala Arg Lys Lys Val Arg Pro Arg Leu Ile Ala Xaa Leu Ala Arg
1 5 10 15
Arg Val Arg Ala Leu Arg Glu Gln Leu Asn Arg Pro Arg Asp Ser Gln
20 25 30
Leu Tyr Ala Val Asp Tyr Glu Thr Leu Thr Arg Pro Phe Ser Gly Arg
35 40 45
Arg Leu Pro Val Arg Ala Trp Ala Asp Val Arg Arg Glu Xaa Arg Leu
50 55 60
Leu Gln Leu Leu Gly Arg Leu Pro Leu Phe Gly Leu Gly Arg Leu Val
65 70 75 80
Thr Arg Lys Ser Trp Leu Trp Gln His Asp Glu Pro Cys Tyr Trp Arg
85 90 95
Leu Thr Arg Val Arg Pro Asp Tyr Thr Ala Gln Asn Leu Asp His Gly
100 105 110
Lys Ala Trp Gly Ile Leu Thr Phe Lys Gly Lys Thr Glu Ser Glu Ala
115 120 125
Arg Glu Ile Glu His Val Met Tyr His Asp Trp Arg Leu Val Pro Lys
130 135 140
His Glu Glu Glu Ala Phe Thr Ala Phe Thr Pro Ala Pro Glu Asp Ser
145 150 155 160
Leu Ala Ser Val Pro Tyr Pro Pro Leu Leu Arg Ala Met Ile Ile Ala
165 170 175
Glu Arg Gln Lys Asn Gly Asp Thr Ser Thr Glu Glu Pro Met Leu Asn
180 185 190
Val Gln Arg Ile Arg Met Glu Pro Trp Asp Tyr Pro Ala Lys Gln Glu
195 200 205
Asp Lys Gly Arg Ala Lys Gly Thr Pro Val
210 215

<210> 231
<211> 1116
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1116)

<221> misc_feature
<222> (1)...(1116)
<223> n = A,T,C or G

<400> 231

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atg tct gtg gcc cac tgt ttc tcc atc aaa ggc caa ggc act gtg atg        48
Met Ser Val Ala His Cys Phe Ser Ile Lys Gly Gln Gly Thr Val Met
 1               5                  10                  15

aca ggg acc atc ctt tca ggc tcc atc agc ctc ggt gac agt gtg gag        96
Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val Glu
            20                  25                  30

atc cct gcc ctc aag gtg gtg aag aag gtg aag tcc atg cag atg ttc       144
Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met Phe
        35                  40                  45

cac atg ccc atc act tca gcc atg caa gga gac cgg ctg ggc atc tgc       192
His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile Cys
    50                  55                  60

gtc acc cag ttt gac cct aag ctg ctg gag cgc ggg ttg gtg tgt gcc       240
Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys Ala
65                  70                  75                  80

ccc gag tcc ctg cac act gtc cat gcg gcc ctc atc tct gtg gaa aag       288
Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu Lys
                85                  90                  95

ata ccg tat ttc cgg ggg ccc ctg caa acc aag gcc aag ttc cac att       336
Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His Ile
            100                 105                 110

aca gtg ggc cat gaa aca gtc atg ggc cgg ttg atg ttc ttc agt cct       384
Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser Pro
        115                 120                 125

gct cca gat aac ttt gac cag gag cct ata ctg gac tct ttc aac ttc       432
Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn Phe
    130                 135                 140

tct caa gaa tac ctt ttc cag gag cag tac ctg tcc aag gat ttg aca       480
Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu Thr
```

145 150 155 160

cca gca gtg aca gac aat gat gag gcc gac aag aag gcc ggc cag gcc 528
Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln Ala
165 170 175

aca gag ggc cat tgt cct cgg cag cag tgg gcc ctg gtg gag ttt gag 576
Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe Glu
180 185 190

aag ccc gtc acc tgc cct cgg ctg tgc ctg gtg att ggc tcc agg cta 624
Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg Leu
195 200 205

gat gcg gac att cac acc aac acg tgc cgg cta gcc ttc cat ggc atc 672
Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly Ile
210 215 220

ctg ctc cac ggg cta gag gac agg aac tac gcc gac agc ttc ctg ccc 720
Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu Pro
225 230 235 240

agg ctg aag gtg tac aag ctg aag cac aag cat ggc ctt gtg gag cgg 768
Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu Arg
245 250 255

gcg atg gat gac tac agt gtg atc ggc cgc tcc ctg ttc aaa aag gaa 816
Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys Glu
260 265 270

acc aac atc cag ctc ttc gtg ggg ctc aag gtg cac ttg tcc act ggg 864
Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr Gly
275 280 285

gaa ctg ggc atc atc gac agt gcc ttc ggc cag agc ggc aag ttc aag 912
Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe Lys
290 295 300

atc cac atc cca ggt ggc ctc agc ccc gag tcc aag aag atc ctg aca 960
Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu Thr
305 310 315 320

ccc gcc ctc aag aag cgg gcc cgg gct ggc cgt ggg gag gcc acc agg 1008
Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr Arg

325 330 335

cag gag gag agc gcc gag cgg agn agg ccc tca cag cat gtg gtg ctc 1056
Gln Glu Glu Ser Ala Glu Arg Xaa Arg Pro Ser Gln His Val Val Leu
340 345 350

agc ctg act ttc aag cgt tat gtc ttc gac acc cac aag cgc atg gtt 1104
Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met Val
355 360 365

cag tct ccc tga 1116
Gln Ser Pro *
370

<210> 232
<211> 371
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(371)
<223> Xaa = Any Amino Acid

<400> 232
Met Ser Val Ala His Cys Phe Ser Ile Lys Gly Gln Gly Thr Val Met
1 5 10 15
Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val Glu
20 25 30
Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met Phe
35 40 45
His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile Cys
50 55 60
Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys Ala
65 70 75 80
Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu Lys
85 90 95
Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His Ile
100 105 110
Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser Pro
115 120 125
Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn Phe
130 135 140

```
Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu Thr
145                 150                 155                 160
Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln Ala
                165                 170                 175
Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe Glu
            180                 185                 190
Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg Leu
        195                 200                 205
Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly Ile
    210                 215                 220
Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu Pro
225                 230                 235                 240
Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu Arg
                245                 250                 255
Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys Glu
            260                 265                 270
Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr Gly
        275                 280                 285
Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe Lys
    290                 295                 300
Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu Thr
305                 310                 315                 320
Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr Arg
                325                 330                 335
Gln Glu Glu Ser Ala Glu Arg Xaa Arg Pro Ser Gln His Val Val Leu
            340                 345                 350
Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met Val
        355                 360                 365
Gln Ser Pro
    370
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<210> 233
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1275)

<221> misc_feature
<222> (1)...(1275)
<223> n = A,T,C or G

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     <400> 233
atg gcg gca gtg gca acc tgc ggt agt gtt gcc gcg agt act ggg tct      48
Met Ala Ala Val Ala Thr Cys Gly Ser Val Ala Ala Ser Thr Gly Ser
 1               5                  10                  15

gca gtg gcg aca gca gnc aag agc aac gtc acc agt ttc cag agg agg      96
Ala Val Ala Thr Ala Xaa Lys Ser Asn Val Thr Ser Phe Gln Arg Arg
            20                  25                  30

ggt cct aga gcc agc gtg acc aac gac agc ggc cct cga ctg gtg tcc     144
Gly Pro Arg Ala Ser Val Thr Asn Asp Ser Gly Pro Arg Leu Val Ser
        35                  40                  45

att gcg ggc acg cga ccg tcg gtg cgg aat gga cag ctg ctg gta tca     192
Ile Ala Gly Thr Arg Pro Ser Val Arg Asn Gly Gln Leu Leu Val Ser
    50                  55                  60

acc ggg ctc cca gcc cta gac cag ctc tta ggt gga ggt tta gcc gtt     240
Thr Gly Leu Pro Ala Leu Asp Gln Leu Leu Gly Gly Gly Leu Ala Val
65                  70                  75                  80

gga aca gtt ctt cta att gag gag gat aaa tat aat att tac tca cct     288
Gly Thr Val Leu Leu Ile Glu Glu Asp Lys Tyr Asn Ile Tyr Ser Pro
                85                  90                  95

ttg ctc ttc aag tat ttc ctg gca gaa gga att gtc aat ggg cat act     336
Leu Leu Phe Lys Tyr Phe Leu Ala Glu Gly Ile Val Asn Gly His Thr
            100                 105                 110

ttg ttg gtt gca tct gct aaa gag gat cct gcc aac att tta cag gaa     384
Leu Leu Val Ala Ser Ala Lys Glu Asp Pro Ala Asn Ile Leu Gln Glu
        115                 120                 125

ctt cca gca cca tta ctt gat gat aaa tgt aaa aag gaa ttt gat gaa     432
Leu Pro Ala Pro Leu Leu Asp Asp Lys Cys Lys Lys Glu Phe Asp Glu
    130                 135                 140

gat gta tac aat cat aaa aca cca gaa tct aat att aag atg aaa ata     480
Asp Val Tyr Asn His Lys Thr Pro Glu Ser Asn Ile Lys Met Lys Ile
145                 150                 155                 160

gct tgg cgt tac cag tta tta ccc aag atg gag att gga cca gta tca     528
Ala Trp Arg Tyr Gln Leu Leu Pro Lys Met Glu Ile Gly Pro Val Ser
                165                 170                 175
```

```
tct tca aga ttt ggt cac tat tat gat gca tca aaa aga atg cca caa        576
Ser Ser Arg Phe Gly His Tyr Tyr Asp Ala Ser Lys Arg Met Pro Gln
            180                 185                 190

gaa cta att gag gct tca aat tgg cat gga ttt ttt ctt cca gag aaa        624
Glu Leu Ile Glu Ala Ser Asn Trp His Gly Phe Phe Leu Pro Glu Lys
        195                 200                 205

ata tct tca act ctc aaa gta gaa ccc tgt tct ttg acc cct ggc tac        672
Ile Ser Ser Thr Leu Lys Val Glu Pro Cys Ser Leu Thr Pro Gly Tyr
    210                 215                 220

aca aag ctg ctt cag ttt atc cag aac atc att tat gag gaa gga ttt        720
Thr Lys Leu Leu Gln Phe Ile Gln Asn Ile Ile Tyr Glu Glu Gly Phe
225                 230                 235                 240

gat gga tcc aat cct cag aaa aaa cag aga aac att tta aga ata gga        768
Asp Gly Ser Asn Pro Gln Lys Lys Gln Arg Asn Ile Leu Arg Ile Gly
                245                 250                 255

att cag aat ctt ggc tca cct tta tgg gga gac gat att tgc tgt gca        816
Ile Gln Asn Leu Gly Ser Pro Leu Trp Gly Asp Asp Ile Cys Cys Ala
            260                 265                 270

gaa aat ggt ggc aac agt cac agc ctt acc aag ttc ctc tat gtt ctc        864
Glu Asn Gly Gly Asn Ser His Ser Leu Thr Lys Phe Leu Tyr Val Leu
        275                 280                 285

cgt ggt ctt ctg aga acc tct ctt tca gcc tgc atc atc aca atg cca        912
Arg Gly Leu Leu Arg Thr Ser Leu Ser Ala Cys Ile Ile Thr Met Pro
    290                 295                 300

aca cat ctg atc cag aat aaa gcc att att gcc cgt gtc aca acc ttg        960
Thr His Leu Ile Gln Asn Lys Ala Ile Ile Ala Arg Val Thr Thr Leu
305                 310                 315                 320

tca gat gta gta gtt ggt ctg gaa tca ttt att ggt tct gag aga gaa       1008
Ser Asp Val Val Val Gly Leu Glu Ser Phe Ile Gly Ser Glu Arg Glu
                325                 330                 335

act aac cca ttg tat aag gat tat cat gga ttg att cat ata cgg cag       1056
Thr Asn Pro Leu Tyr Lys Asp Tyr His Gly Leu Ile His Ile Arg Gln
            340                 345                 350
```

att cct cgg ctt aat aac ttg atc tgt gat gaa tca gat gtc aaa gac 1104
Ile Pro Arg Leu Asn Asn Leu Ile Cys Asp Glu Ser Asp Val Lys Asp
355 360 365

tta gct ttt aaa tta aaa agg aag cta ttc acc att gag cga ctg cat 1152
Leu Ala Phe Lys Leu Lys Arg Lys Leu Phe Thr Ile Glu Arg Leu His
370 375 380

ttg cct cca gac ttg tca gac aca gtg agc cgc tca agc aaa atg gat 1200
Leu Pro Pro Asp Leu Ser Asp Thr Val Ser Arg Ser Ser Lys Met Asp
385 390 395 400

ctg gca gaa tcc gcc aag cgg ctg ggc cca ggc tgt ggc atg atg gcc 1248
Leu Ala Glu Ser Ala Lys Arg Leu Gly Pro Gly Cys Gly Met Met Ala
405 410 415

gga ggc aag aag cac ctg gac ttc tag 1275
Gly Gly Lys Lys His Leu Asp Phe *
420

<210> 234
<211> 424
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(424)
<223> Xaa = Any Amino Acid

<400> 234
Met Ala Ala Val Ala Thr Cys Gly Ser Val Ala Ala Ser Thr Gly Ser
1 5 10 15
Ala Val Ala Thr Ala Xaa Lys Ser Asn Val Thr Ser Phe Gln Arg Arg
20 25 30
Gly Pro Arg Ala Ser Val Thr Asn Asp Ser Gly Pro Arg Leu Val Ser
35 40 45
Ile Ala Gly Thr Arg Pro Ser Val Arg Asn Gly Gln Leu Leu Val Ser
50 55 60
Thr Gly Leu Pro Ala Leu Asp Gln Leu Leu Gly Gly Gly Leu Ala Val
65 70 75 80
Gly Thr Val Leu Leu Ile Glu Glu Asp Lys Tyr Asn Ile Tyr Ser Pro

85 90 95
Leu Leu Phe Lys Tyr Phe Leu Ala Glu Gly Ile Val Asn Gly His Thr
100 105 110
Leu Leu Val Ala Ser Ala Lys Glu Asp Pro Ala Asn Ile Leu Gln Glu
115 120 125
Leu Pro Ala Pro Leu Leu Asp Asp Lys Cys Lys Lys Glu Phe Asp Glu
130 135 140
Asp Val Tyr Asn His Lys Thr Pro Glu Ser Asn Ile Lys Met Lys Ile
145 150 155 160
Ala Trp Arg Tyr Gln Leu Leu Pro Lys Met Glu Ile Gly Pro Val Ser
165 170 175
Ser Ser Arg Phe Gly His Tyr Tyr Asp Ala Ser Lys Arg Met Pro Gln
180 185 190
Glu Leu Ile Glu Ala Ser Asn Trp His Gly Phe Phe Leu Pro Glu Lys
195 200 205
Ile Ser Ser Thr Leu Lys Val Glu Pro Cys Ser Leu Thr Pro Gly Tyr
210 215 220
Thr Lys Leu Leu Gln Phe Ile Gln Asn Ile Ile Tyr Glu Glu Gly Phe
225 230 235 240
Asp Gly Ser Asn Pro Gln Lys Lys Gln Arg Asn Ile Leu Arg Ile Gly
245 250 255
Ile Gln Asn Leu Gly Ser Pro Leu Trp Gly Asp Asp Ile Cys Cys Ala
260 265 270
Glu Asn Gly Gly Asn Ser His Ser Leu Thr Lys Phe Leu Tyr Val Leu
275 280 285
Arg Gly Leu Leu Arg Thr Ser Leu Ser Ala Cys Ile Ile Thr Met Pro
290 295 300
Thr His Leu Ile Gln Asn Lys Ala Ile Ile Ala Arg Val Thr Thr Leu
305 310 315 320
Ser Asp Val Val Val Gly Leu Glu Ser Phe Ile Gly Ser Glu Arg Glu
325 330 335
Thr Asn Pro Leu Tyr Lys Asp Tyr His Gly Leu Ile His Ile Arg Gln
340 345 350
Ile Pro Arg Leu Asn Asn Leu Ile Cys Asp Glu Ser Asp Val Lys Asp
355 360 365
Leu Ala Phe Lys Leu Lys Arg Lys Leu Phe Thr Ile Glu Arg Leu His
370 375 380
Leu Pro Pro Asp Leu Ser Asp Thr Val Ser Arg Ser Ser Lys Met Asp
385 390 395 400
Leu Ala Glu Ser Ala Lys Arg Leu Gly Pro Gly Cys Gly Met Met Ala
405 410 415
Gly Gly Lys Lys His Leu Asp Phe
420

<210> 235
<211> 1188
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1188)

<400> 235
atg gag gag ctc cca ggc tat gaa gag acc ctg acc cgc ctg gct gcc 48
Met Glu Glu Leu Pro Gly Tyr Glu Glu Thr Leu Thr Arg Leu Ala Ala
1 5 10 15

att ctc gcc aaa cac ttt gcc gac gca cgc att gtg ggc act gac atc 96
Ile Leu Ala Lys His Phe Ala Asp Ala Arg Ile Val Gly Thr Asp Ile
20 25 30

cga gac tca ctg atg cag gcc ctg gcc agc tac gtg tgc tac cca cac 144
Arg Asp Ser Leu Met Gln Ala Leu Ala Ser Tyr Val Cys Tyr Pro His
35 40 45

tcc ctg cgg gct gtg gag cga atc ccc gag gag cag cgt atc gcc atg 192
Ser Leu Arg Ala Val Glu Arg Ile Pro Glu Glu Gln Arg Ile Ala Met
50 55 60

gtg agg aac ctc ctg gcg ccc tat gag cag cgg ccc tgg gcc cag acc 240
Val Arg Asn Leu Leu Ala Pro Tyr Glu Gln Arg Pro Trp Ala Gln Thr
65 70 75 80

aac tgg atc ctg gtg cgg ctc tgg agg ggc tgt ggc ttc ggg tac cgc 288
Asn Trp Ile Leu Val Arg Leu Trp Arg Gly Cys Gly Phe Gly Tyr Arg
85 90 95

tat aca cgg ctg cca cat ctg ctg aaa acc aaa ctt gag gac gcc aat 336
Tyr Thr Arg Leu Pro His Leu Leu Lys Thr Lys Leu Glu Asp Ala Asn
100 105 110

ttg ccc agc ctc cag aag ccc tgc cct tcc acc ctg ctg cag cag cac 384
Leu Pro Ser Leu Gln Lys Pro Cys Pro Ser Thr Leu Leu Gln Gln His
115 120 125

atg gcg gac ctc cta cag cag ggt cct gat gtg gca ccc agc ttc ctc 432
Met Ala Asp Leu Leu Gln Gln Gly Pro Asp Val Ala Pro Ser Phe Leu

130 135 140

aac agc gtc ctc aat cag ctc aac tgg gcc ttc tct gaa ttc att ggc 480
Asn Ser Val Leu Asn Gln Leu Asn Trp Ala Phe Ser Glu Phe Ile Gly
145 150 155 160

atg atc caa gag atc cag cag gct gct gag cgc ctg gag cgg aac ttt 528
Met Ile Gln Glu Ile Gln Gln Ala Ala Glu Arg Leu Glu Arg Asn Phe
165 170 175

gtg gac agc cgg cag ctc aag gta tgt gcc acc tgc ttt gac ctc tcg 576
Val Asp Ser Arg Gln Leu Lys Val Cys Ala Thr Cys Phe Asp Leu Ser
180 185 190

gtc agc ctg ctg cgt gtc ttg gag atg act atc aca ctg gtg cct gag 624
Val Ser Leu Leu Arg Val Leu Glu Met Thr Ile Thr Leu Val Pro Glu
195 200 205

ata ttc ctt gac tgg acc cgg cct acc tct gag atg ctg ctg cgg cgt 672
Ile Phe Leu Asp Trp Thr Arg Pro Thr Ser Glu Met Leu Leu Arg Arg
210 215 220

ctt gca cag ctg cta aac cag gtg ctg aac cgg gtg aca gct gag agg 720
Leu Ala Gln Leu Leu Asn Gln Val Leu Asn Arg Val Thr Ala Glu Arg
225 230 235 240

aac ctg ttt gat cgt gtg gtc acc cta cgg ctg cct ggc cta gag agc 768
Asn Leu Phe Asp Arg Val Val Thr Leu Arg Leu Pro Gly Leu Glu Ser
245 250 255

gtg gac cac tat ccc att ctg gtg gca gtg acg ggc atc ctg gtg cag 816
Val Asp His Tyr Pro Ile Leu Val Ala Val Thr Gly Ile Leu Val Gln
260 265 270

ctc ctg gtg cgt ggc cca gcc tca gag aga gag caa gcc aca tca gtg 864
Leu Leu Val Arg Gly Pro Ala Ser Glu Arg Glu Gln Ala Thr Ser Val
275 280 285

ctc ctg gca gat ccc tgc ttc cag cta cgc tca ata tgc tat ctc ctg 912
Leu Leu Ala Asp Pro Cys Phe Gln Leu Arg Ser Ile Cys Tyr Leu Leu
290 295 300

gga cag cca gag ccc cca gca cct ggc act gct ctg cca gcc cct gac 960
Gly Gln Pro Glu Pro Pro Ala Pro Gly Thr Ala Leu Pro Ala Pro Asp

```
305                 310                 315                 320

cgg aag cgc ttc tcc ctg cag agc tat gcg gat tat atc agt gcc gat      1008
Arg Lys Arg Phe Ser Leu Gln Ser Tyr Ala Asp Tyr Ile Ser Ala Asp
                325                 330                 335

gag ctg gcc caa gtg gaa cag atg ctg gcg cac ctg acc tct gca tct      1056
Glu Leu Ala Gln Val Glu Gln Met Leu Ala His Leu Thr Ser Ala Ser
            340                 345                 350

gcc cag gca gca gct gcc tcc ctg ccc acc agt gag gag gac tct gcc      1104
Ala Gln Ala Ala Ala Ala Ser Leu Pro Thr Ser Glu Glu Asp Ser Ala
        355                 360                 365

cca tct gct atg ccc acc cca tct ctg ctg tgt tcc agc cct gtg gcc      1152
Pro Ser Ala Met Pro Thr Pro Ser Leu Leu Cys Ser Ser Pro Val Ala
    370                 375                 380

aca agt cct gca aag cct gta tca acc agc acc tga                      1188
Thr Ser Pro Ala Lys Pro Val Ser Thr Ser Thr  *
385                 390                 395


      &lt;210&gt; 236
      &lt;211&gt; 395
      &lt;212&gt; PRT
      &lt;213&gt; Homo sapiens

      &lt;400&gt; 236
Met Glu Glu Leu Pro Gly Tyr Glu Glu Thr Leu Thr Arg Leu Ala Ala
 1               5                  10                  15
Ile Leu Ala Lys His Phe Ala Asp Ala Arg Ile Val Gly Thr Asp Ile
            20                  25                  30
Arg Asp Ser Leu Met Gln Ala Leu Ala Ser Tyr Val Cys Tyr Pro His
        35                  40                  45
Ser Leu Arg Ala Val Glu Arg Ile Pro Glu Glu Gln Arg Ile Ala Met
    50                  55                  60
Val Arg Asn Leu Leu Ala Pro Tyr Glu Gln Arg Pro Trp Ala Gln Thr
65                  70                  75                  80
Asn Trp Ile Leu Val Arg Leu Trp Arg Gly Cys Gly Phe Gly Tyr Arg
                85                  90                  95
Tyr Thr Arg Leu Pro His Leu Leu Lys Thr Lys Leu Glu Asp Ala Asn
            100                 105                 110
Leu Pro Ser Leu Gln Lys Pro Cys Pro Ser Thr Leu Leu Gln Gln His
```

```
        115                 120                 125
Met Ala Asp Leu Leu Gln Gln Gly Pro Asp Val Ala Pro Ser Phe Leu
    130                 135                 140
Asn Ser Val Leu Asn Gln Leu Asn Trp Ala Phe Ser Glu Phe Ile Gly
145                 150                 155                 160
Met Ile Gln Glu Ile Gln Gln Ala Ala Glu Arg Leu Glu Arg Asn Phe
                165                 170                 175
Val Asp Ser Arg Gln Leu Lys Val Cys Ala Thr Cys Phe Asp Leu Ser
            180                 185                 190
Val Ser Leu Leu Arg Val Leu Glu Met Thr Ile Thr Leu Val Pro Glu
        195                 200                 205
Ile Phe Leu Asp Trp Thr Arg Pro Thr Ser Glu Met Leu Leu Arg Arg
    210                 215                 220
Leu Ala Gln Leu Leu Asn Gln Val Leu Asn Arg Val Thr Ala Glu Arg
225                 230                 235                 240
Asn Leu Phe Asp Arg Val Val Thr Leu Arg Leu Pro Gly Leu Glu Ser
                245                 250                 255
Val Asp His Tyr Pro Ile Leu Val Ala Val Thr Gly Ile Leu Val Gln
            260                 265                 270
Leu Leu Val Arg Gly Pro Ala Ser Glu Arg Glu Gln Ala Thr Ser Val
        275                 280                 285
Leu Leu Ala Asp Pro Cys Phe Gln Leu Arg Ser Ile Cys Tyr Leu Leu
    290                 295                 300
Gly Gln Pro Glu Pro Pro Ala Pro Gly Thr Ala Leu Pro Ala Pro Asp
305                 310                 315                 320
Arg Lys Arg Phe Ser Leu Gln Ser Tyr Ala Asp Tyr Ile Ser Ala Asp
                325                 330                 335
Glu Leu Ala Gln Val Glu Gln Met Leu Ala His Leu Thr Ser Ala Ser
            340                 345                 350
Ala Gln Ala Ala Ala Ala Ser Leu Pro Thr Ser Glu Glu Asp Ser Ala
        355                 360                 365
Pro Ser Ala Met Pro Thr Pro Ser Leu Leu Cys Ser Ser Pro Val Ala
    370                 375                 380
Thr Ser Pro Ala Lys Pro Val Ser Thr Ser Thr
385                 390                 395
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<210> 237
<211> 1278
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1278)

<221> misc_feature
<222> (1)...(1278)
<223> n = A,T,C or G

<400> 237

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atg gat gac ttg caa aag ttg gga gtc ata ttg cac agt gct att tca      48
Met Asp Asp Leu Gln Lys Leu Gly Val Ile Leu His Ser Ala Ile Ser
 1               5                  10                  15

gtc cca ata agt tca gat gca tcc cct ttt att ctt cca tct tat acc      96
Val Pro Ile Ser Ser Asp Ala Ser Pro Phe Ile Leu Pro Ser Tyr Thr
            20                  25                  30

gaa gca gtt ttg aca agt tta cag gaa gct gta ctt aca gct tta gat     144
Glu Ala Val Leu Thr Ser Leu Gln Glu Ala Val Leu Thr Ala Leu Asp
        35                  40                  45

gtt ctc caa aag gcc att tgt gta gga cca gaa aac atg cag ata atg     192
Val Leu Gln Lys Ala Ile Cys Val Gly Pro Glu Asn Met Gln Ile Met
    50                  55                  60

tat cca gct ata ttt gac cag ttg ttg gca ttt gta gaa ttt tcc tgt     240
Tyr Pro Ala Ile Phe Asp Gln Leu Leu Ala Phe Val Glu Phe Ser Cys
65                  70                  75                  80

aaa cct cca cag tat gga cag ctn gaa aca aag cac att gca aat gca     288
Lys Pro Pro Gln Tyr Gly Gln Xaa Glu Thr Lys His Ile Ala Asn Ala
                85                  90                  95

aaa tat aat cag atc caa cta ttt gca ccg gcg gaa tgg gta gcc ttg     336
Lys Tyr Asn Gln Ile Gln Leu Phe Ala Pro Ala Glu Trp Val Ala Leu
            100                 105                 110

aat tat gtg ccg ttt gct gaa agg tct tta gaa gta gtt gtg gat tta     384
Asn Tyr Val Pro Phe Ala Glu Arg Ser Leu Glu Val Val Val Asp Leu
        115                 120                 125

tac caa aaa aca gcg tgt cac aaa gca gtg gtg aat gag aaa gtg ctc     432
Tyr Gln Lys Thr Ala Cys His Lys Ala Val Val Asn Glu Lys Val Leu
    130                 135                 140

cag aat att att aag act ctt agg gtt cct ctc agt ttg aag tat tcc     480
Gln Asn Ile Ile Lys Thr Leu Arg Val Pro Leu Ser Leu Lys Tyr Ser
```

```
145                 150                 155                 160

tgc cct tct gaa agc aca tgg aaa cta gca gta tcc tct ctc ctc aga      528
Cys Pro Ser Glu Ser Thr Trp Lys Leu Ala Val Ser Ser Leu Leu Arg
                165                 170                 175

gtt ctt tct att ggg cta cct gtt gcc cgg cag cat gct tct tct gga      576
Val Leu Ser Ile Gly Leu Pro Val Ala Arg Gln His Ala Ser Ser Gly
            180                 185                 190

aaa ttt gac agt atg tgg cca gaa cta gcc aat act ttt gaa gat ttt      624
Lys Phe Asp Ser Met Trp Pro Glu Leu Ala Asn Thr Phe Glu Asp Phe
        195                 200                 205

ctc ttt act aaa agc ata cct cca gat aat ctc tct att caa gag ttt      672
Leu Phe Thr Lys Ser Ile Pro Pro Asp Asn Leu Ser Ile Gln Glu Phe
    210                 215                 220

caa aga aat gaa aat att gat gtc gag gta gtt caa ctt atc agc aat      720
Gln Arg Asn Glu Asn Ile Asp Val Glu Val Val Gln Leu Ile Ser Asn
225                 230                 235                 240

gag ata cta cct tat gcc aat ttt att cct aag gaa ttt gtt ggt caa      768
Glu Ile Leu Pro Tyr Ala Asn Phe Ile Pro Lys Glu Phe Val Gly Gln
                245                 250                 255

ata atg aca atg ctt aac aag ggc tca ata cat tct cag tca tct tca      816
Ile Met Thr Met Leu Asn Lys Gly Ser Ile His Ser Gln Ser Ser Ser
            260                 265                 270

ttt aca gaa gca gag att gat att cgt ttg aga gag gaa ttt tct aaa      864
Phe Thr Glu Ala Glu Ile Asp Ile Arg Leu Arg Glu Glu Phe Ser Lys
        275                 280                 285

atg tgt ttt gaa aca tta ctc cag ttt tcc ttc agt aat aaa gtc aca      912
Met Cys Phe Glu Thr Leu Leu Gln Phe Ser Phe Ser Asn Lys Val Thr
    290                 295                 300

aca cct caa gaa ggc tac atc tca cga atg gca ctc tca gtg ctt tta      960
Thr Pro Gln Glu Gly Tyr Ile Ser Arg Met Ala Leu Ser Val Leu Leu
305                 310                 315                 320

aag agg tcc caa gat gta cta cat cgc tat ata gag gat gaa aga tta     1008
Lys Arg Ser Gln Asp Val Leu His Arg Tyr Ile Glu Asp Glu Arg Leu
```

325 330 335

agt ggt aaa tgc cct ctt cca agg caa caa gta aca gaa att ata ttt 1056
Ser Gly Lys Cys Pro Leu Pro Arg Gln Gln Val Thr Glu Ile Ile Phe
340 345 350

gtt tta aaa gca gtc agt act ctt att gat tca ctt aag aaa act cag 1104
Val Leu Lys Ala Val Ser Thr Leu Ile Asp Ser Leu Lys Lys Thr Gln
355 360 365

cct gag aat gtt gat gga aat acc tgg gca caa gta att gcc tta tac 1152
Pro Glu Asn Val Asp Gly Asn Thr Trp Ala Gln Val Ile Ala Leu Tyr
370 375 380

cca act tta gta gaa tgc atc acc tgt tct tct tca gaa gtc tgt tct 1200
Pro Thr Leu Val Glu Cys Ile Thr Cys Ser Ser Ser Glu Val Cys Ser
385 390 395 400

gca ctt aaa gag gca cta gtt cct ttt aag gat ttc atg cag cca cca 1248
Ala Leu Lys Glu Ala Leu Val Pro Phe Lys Asp Phe Met Gln Pro Pro
405 410 415

gca tcc aga gtt caa aat gga gaa tct tga 1278
Ala Ser Arg Val Gln Asn Gly Glu Ser *
420 425

<210> 238
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(425)
<223> Xaa = Any Amino Acid

<400> 238
Met Asp Asp Leu Gln Lys Leu Gly Val Ile Leu His Ser Ala Ile Ser
1 5 10 15
Val Pro Ile Ser Ser Asp Ala Ser Pro Phe Ile Leu Pro Ser Tyr Thr
20 25 30
Glu Ala Val Leu Thr Ser Leu Gln Glu Ala Val Leu Thr Ala Leu Asp
35 40 45

Val Leu Gln Lys Ala Ile Cys Val Gly Pro Glu Asn Met Gln Ile Met
50 55 60
Tyr Pro Ala Ile Phe Asp Gln Leu Leu Ala Phe Val Glu Phe Ser Cys
65 70 75 80
Lys Pro Pro Gln Tyr Gly Gln Xaa Glu Thr Lys His Ile Ala Asn Ala
85 90 95
Lys Tyr Asn Gln Ile Gln Leu Phe Ala Pro Ala Glu Trp Val Ala Leu
100 105 110
Asn Tyr Val Pro Phe Ala Glu Arg Ser Leu Glu Val Val Val Asp Leu
115 120 125
Tyr Gln Lys Thr Ala Cys His Lys Ala Val Val Asn Glu Lys Val Leu
130 135 140
Gln Asn Ile Ile Lys Thr Leu Arg Val Pro Leu Ser Leu Lys Tyr Ser
145 150 155 160
Cys Pro Ser Glu Ser Thr Trp Lys Leu Ala Val Ser Ser Leu Leu Arg
165 170 175
Val Leu Ser Ile Gly Leu Pro Val Ala Arg Gln His Ala Ser Ser Gly
180 185 190
Lys Phe Asp Ser Met Trp Pro Glu Leu Ala Asn Thr Phe Glu Asp Phe
195 200 205
Leu Phe Thr Lys Ser Ile Pro Pro Asp Asn Leu Ser Ile Gln Glu Phe
210 215 220
Gln Arg Asn Glu Asn Ile Asp Val Glu Val Val Gln Leu Ile Ser Asn
225 230 235 240
Glu Ile Leu Pro Tyr Ala Asn Phe Ile Pro Lys Glu Phe Val Gly Gln
245 250 255
Ile Met Thr Met Leu Asn Lys Gly Ser Ile His Ser Gln Ser Ser Ser
260 265 270
Phe Thr Glu Ala Glu Ile Asp Ile Arg Leu Arg Glu Glu Phe Ser Lys
275 280 285
Met Cys Phe Glu Thr Leu Leu Gln Phe Ser Phe Ser Asn Lys Val Thr
290 295 300
Thr Pro Gln Glu Gly Tyr Ile Ser Arg Met Ala Leu Ser Val Leu Leu
305 310 315 320
Lys Arg Ser Gln Asp Val Leu His Arg Tyr Ile Glu Asp Glu Arg Leu
325 330 335
Ser Gly Lys Cys Pro Leu Pro Arg Gln Gln Val Thr Glu Ile Ile Phe
340 345 350
Val Leu Lys Ala Val Ser Thr Leu Ile Asp Ser Leu Lys Lys Thr Gln
355 360 365
Pro Glu Asn Val Asp Gly Asn Thr Trp Ala Gln Val Ile Ala Leu Tyr
370 375 380
Pro Thr Leu Val Glu Cys Ile Thr Cys Ser Ser Ser Glu Val Cys Ser
385 390 395 400

```
Ala Leu Lys Glu Ala Leu Val Pro Phe Lys Asp Phe Met Gln Pro Pro
                405                 410                 415
Ala Ser Arg Val Gln Asn Gly Glu Ser
            420                 425

      <210> 239
      <211> 1053
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(1053)

      <400> 239
atg gat ttg aag gct ctc ctt tct tcc ttg aat gac ttt gca tcc ctc      48
Met Asp Leu Lys Ala Leu Leu Ser Ser Leu Asn Asp Phe Ala Ser Leu
 1               5                  10                  15

tcg ttt gct gag agt tgg gac aat gtt gga tta ctg gtg gaa cca agc      96
Ser Phe Ala Glu Ser Trp Asp Asn Val Gly Leu Leu Val Glu Pro Ser
            20                  25                  30

cca cca cat act gta aat aca ctc ttc ctg acc aat gac ctg act gag     144
Pro Pro His Thr Val Asn Thr Leu Phe Leu Thr Asn Asp Leu Thr Glu
        35                  40                  45

gaa gtg atg gag gag gtg ctg caa aag aag gca gac ctc att ctc tcc     192
Glu Val Met Glu Glu Val Leu Gln Lys Lys Ala Asp Leu Ile Leu Ser
    50                  55                  60

tac cat ccg cct atc ttc cga ccc atg aag cgc ata acc tgg aac aca     240
Tyr His Pro Pro Ile Phe Arg Pro Met Lys Arg Ile Thr Trp Asn Thr
 65                  70                  75                  80

tgg aag gag cgc ctg gtg atc cgg gct ctg gag aac aga gtc ggt atc     288
Trp Lys Glu Arg Leu Val Ile Arg Ala Leu Glu Asn Arg Val Gly Ile
                85                  90                  95

tac tct cct cat aca gcc tat gat gct gcg ccc cag ggc gtc aac aac     336
Tyr Ser Pro His Thr Ala Tyr Asp Ala Ala Pro Gln Gly Val Asn Asn
            100                 105                 110

tgg ttg gct aaa ggg ctt gga gct tgt acc tcc agg ccc ata cat cct     384
```

```
Trp Leu Ala Lys Gly Leu Gly Ala Cys Thr Ser Arg Pro Ile His Pro
        115                 120                 125

tcc aaa gct ccc aac tac cct aca gag gga aac cac cga gta gaa ttc      432
Ser Lys Ala Pro Asn Tyr Pro Thr Glu Gly Asn His Arg Val Glu Phe
    130                 135                 140

aac gtt aac tac acc caa gac ctg gac aaa gtc atg tct gca gtg aaa      480
Asn Val Asn Tyr Thr Gln Asp Leu Asp Lys Val Met Ser Ala Val Lys
145                 150                 155                 160

gga att gac ggt gtt tct gtc act tct ttt tct gct agg act ggt aat      528
Gly Ile Asp Gly Val Ser Val Thr Ser Phe Ser Ala Arg Thr Gly Asn
                165                 170                 175

gag gaa caa aca cgg att aat ctg aat tgt act cag aag gct ttg atg      576
Glu Glu Gln Thr Arg Ile Asn Leu Asn Cys Thr Gln Lys Ala Leu Met
            180                 185                 190

cag gtg gta gat ttt ctt tcc cgg aac aaa caa ctt tat cag aag acg      624
Gln Val Val Asp Phe Leu Ser Arg Asn Lys Gln Leu Tyr Gln Lys Thr
        195                 200                 205

gaa att ctg tca ctg gag aag cct ttg ctt cta cat act gga atg gga      672
Glu Ile Leu Ser Leu Glu Lys Pro Leu Leu Leu His Thr Gly Met Gly
    210                 215                 220

cgg tta tgc aca ctg gat gaa tct gtc tcc ctg gca acc atg att gat      720
Arg Leu Cys Thr Leu Asp Glu Ser Val Ser Leu Ala Thr Met Ile Asp
225                 230                 235                 240

cga ata aaa aga cac cta aaa cta tct cat att cgc tta gcc ctt ggg      768
Arg Ile Lys Arg His Leu Lys Leu Ser His Ile Arg Leu Ala Leu Gly
                245                 250                 255

gtg ggg aga acc tta gag tct caa gtc aaa gtc gtg gcc ctg tgt gct      816
Val Gly Arg Thr Leu Glu Ser Gln Val Lys Val Val Ala Leu Cys Ala
            260                 265                 270

ggt tct ggg agc agc gtt ctg cag ggt gtt gag gct gac ctt tac ctc      864
Gly Ser Gly Ser Ser Val Leu Gln Gly Val Glu Ala Asp Leu Tyr Leu
        275                 280                 285

aca ggt gag atg tcc cat cat gat act ttg gat gct gct tcc caa gga      912
```

```
Thr Gly Glu Met Ser His His Asp Thr Leu Asp Ala Ala Ser Gln Gly
    290                 295                 300

ata aat gtc atc ctc tgt gaa cac agc aac act gaa cga ggc ttt ctt      960
Ile Asn Val Ile Leu Cys Glu His Ser Asn Thr Glu Arg Gly Phe Leu
305                 310                 315                 320

tct gac ctt cga gat atg ctg gat tct cac ttg gag aat aag ata aat     1008
Ser Asp Leu Arg Asp Met Leu Asp Ser His Leu Glu Asn Lys Ile Asn
                325                 330                 335

att atc cta tca gag act gac agg gac cct ctt cag gtg gta taa         1053
Ile Ile Leu Ser Glu Thr Asp Arg Asp Pro Leu Gln Val Val  *
            340                 345                 350


      <210> 240
      <211> 350
      <212> PRT
      <213> Homo sapiens

      <400> 240
Met Asp Leu Lys Ala Leu Leu Ser Ser Leu Asn Asp Phe Ala Ser Leu
 1               5                  10                  15
Ser Phe Ala Glu Ser Trp Asp Asn Val Gly Leu Leu Val Glu Pro Ser
            20                  25                  30
Pro Pro His Thr Val Asn Thr Leu Phe Leu Thr Asn Asp Leu Thr Glu
        35                  40                  45
Glu Val Met Glu Glu Val Leu Gln Lys Lys Ala Asp Leu Ile Leu Ser
    50                  55                  60
Tyr His Pro Pro Ile Phe Arg Pro Met Lys Arg Ile Thr Trp Asn Thr
65                  70                  75                  80
Trp Lys Glu Arg Leu Val Ile Arg Ala Leu Glu Asn Arg Val Gly Ile
                85                  90                  95
Tyr Ser Pro His Thr Ala Tyr Asp Ala Ala Pro Gln Gly Val Asn Asn
            100                 105                 110
Trp Leu Ala Lys Gly Leu Gly Ala Cys Thr Ser Arg Pro Ile His Pro
        115                 120                 125
Ser Lys Ala Pro Asn Tyr Pro Thr Glu Gly Asn His Arg Val Glu Phe
    130                 135                 140
Asn Val Asn Tyr Thr Gln Asp Leu Asp Lys Val Met Ser Ala Val Lys
145                 150                 155                 160
Gly Ile Asp Gly Val Ser Val Thr Ser Phe Ser Ala Arg Thr Gly Asn
                165                 170                 175
```

```
Glu Glu Gln Thr Arg Ile Asn Leu Asn Cys Thr Gln Lys Ala Leu Met
                180                 185                 190
Gln Val Val Asp Phe Leu Ser Arg Asn Lys Gln Leu Tyr Gln Lys Thr
            195                 200                 205
Glu Ile Leu Ser Leu Glu Lys Pro Leu Leu Leu His Thr Gly Met Gly
        210                 215                 220
Arg Leu Cys Thr Leu Asp Glu Ser Val Ser Leu Ala Thr Met Ile Asp
225                 230                 235                 240
Arg Ile Lys Arg His Leu Lys Leu Ser His Ile Arg Leu Ala Leu Gly
                245                 250                 255
Val Gly Arg Thr Leu Glu Ser Gln Val Lys Val Val Ala Leu Cys Ala
                260                 265                 270
Gly Ser Gly Ser Ser Val Leu Gln Gly Val Glu Ala Asp Leu Tyr Leu
            275                 280                 285
Thr Gly Glu Met Ser His His Asp Thr Leu Asp Ala Ala Ser Gln Gly
        290                 295                 300
Ile Asn Val Ile Leu Cys Glu His Ser Asn Thr Glu Arg Gly Phe Leu
305                 310                 315                 320
Ser Asp Leu Arg Asp Met Leu Asp Ser His Leu Glu Asn Lys Ile Asn
                325                 330                 335
Ile Ile Leu Ser Glu Thr Asp Arg Asp Pro Leu Gln Val Val
                340                 345                 350

      <210> 241
      <211> 933
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(933)

      <400> 241
atg ggc gga gaa ttt tgt gtg gct gct atc ttc gga aca tcc agg tca      48
Met Gly Gly Glu Phe Cys Val Ala Ala Ile Phe Gly Thr Ser Arg Ser
 1               5                  10                  15

tgg ttt gca aat aat gca ggt ctg aaa aga gaa aaa gat cag tcc aaa      96
Trp Phe Ala Asn Asn Ala Gly Leu Lys Arg Glu Lys Asp Gln Ser Lys
                20                  25                  30

caa gtt gta gtt gag tcc ctg tac att atc agt tgc tat ggc acc tta     144
Gln Val Val Val Glu Ser Leu Tyr Ile Ile Ser Cys Tyr Gly Thr Leu
            35                  40                  45
```

gtg gaa cac atg atg gag ccg cga ccc ctc agc act gca ccc aag att 192
Val Glu His Met Met Glu Pro Arg Pro Leu Ser Thr Ala Pro Lys Ile
50 55 60

agt gac gac aca cca ctg gaa atg atg aca tcg cct cga gcc agc tgg 240
Ser Asp Asp Thr Pro Leu Glu Met Met Thr Ser Pro Arg Ala Ser Trp
65 70 75 80

act ctg gtt aga acc cct caa tgg aat gaa ttg cag cca ccg ttt aat 288
Thr Leu Val Arg Thr Pro Gln Trp Asn Glu Leu Gln Pro Pro Phe Asn
85 90 95

gca aac cac cct ctg ctc ctc gct gca gat gca gta cag tat tat cag 336
Ala Asn His Pro Leu Leu Leu Ala Ala Asp Ala Val Gln Tyr Tyr Gln
100 105 110

ttc ctg ctt gct ggc ctg gtt ccc cct gga agt cct ggg ccc att act 384
Phe Leu Leu Ala Gly Leu Val Pro Pro Gly Ser Pro Gly Pro Ile Thr
115 120 125

cga cat ggg tct tac gac agt tta gct tct gac cat agt gga cag gaa 432
Arg His Gly Ser Tyr Asp Ser Leu Ala Ser Asp His Ser Gly Gln Glu
130 135 140

gat gaa gaa tgg ctt tcc cag gtt gaa att gta aca cac act gga ccc 480
Asp Glu Glu Trp Leu Ser Gln Val Glu Ile Val Thr His Thr Gly Pro
145 150 155 160

cat aga cgt ctg tgg atg ggt cca cag ttc cag ttc aaa acc atc cat 528
His Arg Arg Leu Trp Met Gly Pro Gln Phe Gln Phe Lys Thr Ile His
165 170 175

ccc tca ggc caa acc aca gtt atc tca tcc agt tca tct gtg ttg cag 576
Pro Ser Gly Gln Thr Thr Val Ile Ser Ser Ser Ser Ser Val Leu Gln
180 185 190

tct cat ggt ccg agt gac acg cca cag cct ctt ttg gat ttt gat aca 624
Ser His Gly Pro Ser Asp Thr Pro Gln Pro Leu Leu Asp Phe Asp Thr
195 200 205

gat gat ctt gat ctc aac agt ctc agg atc cag cca gtc cgc tct gac 672
Asp Asp Leu Asp Leu Asn Ser Leu Arg Ile Gln Pro Val Arg Ser Asp
210 215 220

ccc gtc agc atg cca ggg tca tcc cgt cca gtc tct gat cga agg gga 720
Pro Val Ser Met Pro Gly Ser Ser Arg Pro Val Ser Asp Arg Arg Gly
225 230 235 240

gtt tcc aca gtg att gat gct gcc tca ggt acc ttt gac agg agc gtg 768
Val Ser Thr Val Ile Asp Ala Ala Ser Gly Thr Phe Asp Arg Ser Val
245 250 255

acc ctg ctg gag gtg tgc ggg agc tgg cct gag ggc ttc ggg ctg cgg 816
Thr Leu Leu Glu Val Cys Gly Ser Trp Pro Glu Gly Phe Gly Leu Arg
260 265 270

cac atg tcc tcc atg gag cac acg gag gag ggc tcc ggg agc gac ttg 864
His Met Ser Ser Met Glu His Thr Glu Glu Gly Ser Gly Ser Asp Leu
275 280 285

ccg acg cca tgg ccg agt cac cta gcc ggg acg tcg tgg gat ccg gaa 912
Pro Thr Pro Trp Pro Ser His Leu Ala Gly Thr Ser Trp Asp Pro Glu
290 295 300

cag aca cag ccc ttg acg tag 933
Gln Thr Gln Pro Leu Thr *
305 310

<210> 242
<211> 310
<212> PRT
<213> Homo sapiens

<400> 242
Met Gly Gly Glu Phe Cys Val Ala Ala Ile Phe Gly Thr Ser Arg Ser
1 5 10 15
Trp Phe Ala Asn Asn Ala Gly Leu Lys Arg Glu Lys Asp Gln Ser Lys
20 25 30
Gln Val Val Val Glu Ser Leu Tyr Ile Ile Ser Cys Tyr Gly Thr Leu
35 40 45
Val Glu His Met Met Glu Pro Arg Pro Leu Ser Thr Ala Pro Lys Ile
50 55 60
Ser Asp Asp Thr Pro Leu Glu Met Met Thr Ser Pro Arg Ala Ser Trp
65 70 75 80
Thr Leu Val Arg Thr Pro Gln Trp Asn Glu Leu Gln Pro Pro Phe Asn
85 90 95

Ala Asn His Pro Leu Leu Leu Ala Ala Asp Ala Val Gln Tyr Tyr Gln
100 105 110
Phe Leu Leu Ala Gly Leu Val Pro Pro Gly Ser Pro Gly Pro Ile Thr
115 120 125
Arg His Gly Ser Tyr Asp Ser Leu Ala Ser Asp His Ser Gly Gln Glu
130 135 140
Asp Glu Glu Trp Leu Ser Gln Val Glu Ile Val Thr His Thr Gly Pro
145 150 155 160
His Arg Arg Leu Trp Met Gly Pro Gln Phe Gln Phe Lys Thr Ile His
165 170 175
Pro Ser Gly Gln Thr Thr Val Ile Ser Ser Ser Ser Ser Val Leu Gln
180 185 190
Ser His Gly Pro Ser Asp Thr Pro Gln Pro Leu Leu Asp Phe Asp Thr
195 200 205
Asp Asp Leu Asp Leu Asn Ser Leu Arg Ile Gln Pro Val Arg Ser Asp
210 215 220
Pro Val Ser Met Pro Gly Ser Ser Arg Pro Val Ser Asp Arg Arg Gly
225 230 235 240
Val Ser Thr Val Ile Asp Ala Ala Ser Gly Thr Phe Asp Arg Ser Val
245 250 255
Thr Leu Leu Glu Val Cys Gly Ser Trp Pro Glu Gly Phe Gly Leu Arg
260 265 270
His Met Ser Ser Met Glu His Thr Glu Glu Gly Ser Gly Ser Asp Leu
275 280 285
Pro Thr Pro Trp Pro Ser His Leu Ala Gly Thr Ser Trp Asp Pro Glu
290 295 300
Gln Thr Gln Pro Leu Thr
305 310

<210> 243
<211> 465
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(465)

<221> misc_feature
<222> (1)...(465)
<223> n = A,T,C or G

<400> 243
atg tnc tct ggg gcg agg aca cgg ctt ntg gct nct ggc nct gct gtc 48

Met Xaa Ser Gly Ala Arg Thr Arg Leu Xaa Ala Xaa Gly Xaa Ala Val
1 5 10 15

tca ctg gcc nct ttg ttg aat aag gcg gct gat aaa gga agc agg aag 96
Ser Leu Ala Xaa Leu Leu Asn Lys Ala Ala Asp Lys Gly Ser Arg Lys
20 25 30

cgc tat gaa cca tca gac aag gac agg cag agc cct cct cca gcc aag 144
Arg Tyr Glu Pro Ser Asp Lys Asp Arg Gln Ser Pro Pro Pro Ala Lys
35 40 45

cgg ccc aac aca tcc cca gac cga ggt tct cgg gac cgg aag tca ggt 192
Arg Pro Asn Thr Ser Pro Asp Arg Gly Ser Arg Asp Arg Lys Ser Gly
50 55 60

ggg aga ctg ggc tcc ccg aag cca gag cgg cag aga ggc cag aac tcc 240
Gly Arg Leu Gly Ser Pro Lys Pro Glu Arg Gln Arg Gly Gln Asn Ser
65 70 75 80

aaa gcc cct gca gcc ccg gct gac agg aag cgc can ntg tca ccc cag 288
Lys Ala Pro Ala Ala Pro Ala Asp Arg Lys Arg Xaa Xaa Ser Pro Gln
85 90 95

tcc aag agc tcc agc aag gtc acg agc gtg ccc ggc aaa gcc tcg gat 336
Ser Lys Ser Ser Ser Lys Val Thr Ser Val Pro Gly Lys Ala Ser Asp
100 105 110

ccc ggc gcc gcc agc acc aaa tca ggg aag gcc agc acg ctg tct cgg 384
Pro Gly Ala Ala Ser Thr Lys Ser Gly Lys Ala Ser Thr Leu Ser Arg
115 120 125

cgg gag gag ctg ctg aaa cag ctg aag gcc gtg gag gat gct att gca 432
Arg Glu Glu Leu Leu Lys Gln Leu Lys Ala Val Glu Asp Ala Ile Ala
130 135 140

cgc aag cgg gcc aag atc ccc ggg aaa gca tag 465
Arg Lys Arg Ala Lys Ile Pro Gly Lys Ala *
145 150

<210> 244
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(154)
<223> Xaa = Any Amino Acid

<400> 244
Met Xaa Ser Gly Ala Arg Thr Arg Leu Xaa Ala Xaa Gly Xaa Ala Val
1 5 10 15
Ser Leu Ala Xaa Leu Leu Asn Lys Ala Ala Asp Lys Gly Ser Arg Lys
20 25 30
Arg Tyr Glu Pro Ser Asp Lys Asp Arg Gln Ser Pro Pro Pro Ala Lys
35 40 45
Arg Pro Asn Thr Ser Pro Asp Arg Gly Ser Arg Asp Arg Lys Ser Gly
50 55 60
Gly Arg Leu Gly Ser Pro Lys Pro Glu Arg Gln Arg Gly Gln Asn Ser
65 70 75 80
Lys Ala Pro Ala Ala Pro Ala Asp Arg Lys Arg Xaa Xaa Ser Pro Gln
85 90 95
Ser Lys Ser Ser Ser Lys Val Thr Ser Val Pro Gly Lys Ala Ser Asp
100 105 110
Pro Gly Ala Ala Ser Thr Lys Ser Gly Lys Ala Ser Thr Leu Ser Arg
115 120 125
Arg Glu Glu Leu Leu Lys Gln Leu Lys Ala Val Glu Asp Ala Ile Ala
130 135 140
Arg Lys Arg Ala Lys Ile Pro Gly Lys Ala
145 150

<210> 245
<211> 1839
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1839)

<400> 245
atg gcg gcg gcg ggc cgg ctc ccg agc tcc tgg gcc ctc ttc tcg ccg 48
Met Ala Ala Ala Gly Arg Leu Pro Ser Ser Trp Ala Leu Phe Ser Pro
1 5 10 15

ctc ctc gca ggg ctt gca cta ctg gga gtc ggg ccg gtc cca gcg cgg 96
Leu Leu Ala Gly Leu Ala Leu Leu Gly Val Gly Pro Val Pro Ala Arg

20 25 30

gcg ctg cac aac gtc acg gcc gag ctc ttt ggg gcc gag gcc tgg ggc 144
Ala Leu His Asn Val Thr Ala Glu Leu Phe Gly Ala Glu Ala Trp Gly
35 40 45

acc ctt gcg gct ttc ggg gac ctc aac tcc gac aag cag acg gat ctc 192
Thr Leu Ala Ala Phe Gly Asp Leu Asn Ser Asp Lys Gln Thr Asp Leu
50 55 60

ttc gtg ctg cgg gaa aga aat gac tta atc gtc ttt ttg gca gac cag 240
Phe Val Leu Arg Glu Arg Asn Asp Leu Ile Val Phe Leu Ala Asp Gln
65 70 75 80

aat gca ccc tat ttt aaa ccc aaa gta aag gta tct ttc aag aat cac 288
Asn Ala Pro Tyr Phe Lys Pro Lys Val Lys Val Ser Phe Lys Asn His
85 90 95

agt gca ttg ata aca agt gta gtc cct ggg gat tat gat gga gat tct 336
Ser Ala Leu Ile Thr Ser Val Val Pro Gly Asp Tyr Asp Gly Asp Ser
100 105 110

caa atg gat gtc ctt ctg aca tat ctt ccc aaa aat tat gcc aag agt 384
Gln Met Asp Val Leu Leu Thr Tyr Leu Pro Lys Asn Tyr Ala Lys Ser
115 120 125

gaa tta gga gct gtt atc ttc tgg gga caa aat caa aca tta gat cct 432
Glu Leu Gly Ala Val Ile Phe Trp Gly Gln Asn Gln Thr Leu Asp Pro
130 135 140

aac aat atg acc ata ctc aat agg act ttt caa gat gag cca cta att 480
Asn Asn Met Thr Ile Leu Asn Arg Thr Phe Gln Asp Glu Pro Leu Ile
145 150 155 160

atg gat ttc aat ggt gat cta att cct gat att ttt ggt atc aca aat 528
Met Asp Phe Asn Gly Asp Leu Ile Pro Asp Ile Phe Gly Ile Thr Asn
165 170 175

gaa tcc aac cag cca cag ata cta tta gga ggg aat tta tca tgg cat 576
Glu Ser Asn Gln Pro Gln Ile Leu Leu Gly Gly Asn Leu Ser Trp His
180 185 190

cca gca ttg acc act aca agt aaa atg cga att cca cat tct cat gca 624
Pro Ala Leu Thr Thr Thr Ser Lys Met Arg Ile Pro His Ser His Ala

195 200 205

tttt att gat ctg act gaa gat ttt aca gca gat tta ttc ctg acg aca 672
Phe Ile Asp Leu Thr Glu Asp Phe Thr Ala Asp Leu Phe Leu Thr Thr
210 215 220

ttg aat gcc acc act agt acc ttc cag ttt gaa ata tgg gaa aat ttg 720
Leu Asn Ala Thr Thr Ser Thr Phe Gln Phe Glu Ile Trp Glu Asn Leu
225 230 235 240

gat gga aac ttc tct gtc agt act ata ttg gaa aaa cct caa aat atg 768
Asp Gly Asn Phe Ser Val Ser Thr Ile Leu Glu Lys Pro Gln Asn Met
245 250 255

atg gtg gtt gga cag tca gca ttt gca gac ttt gat gga gat gga cac 816
Met Val Val Gly Gln Ser Ala Phe Ala Asp Phe Asp Gly Asp Gly His
260 265 270

atg gat cat tta ctg cca ggc tgt gaa gat aaa aat tgc caa aag agt 864
Met Asp His Leu Leu Pro Gly Cys Glu Asp Lys Asn Cys Gln Lys Ser
275 280 285

acc atc tac tta gtg aga tct ggg atg aag cag tgg gtt cca gtc cta 912
Thr Ile Tyr Leu Val Arg Ser Gly Met Lys Gln Trp Val Pro Val Leu
290 295 300

caa gat ttc agc aat aag ggc aca ctc tgg ggc ttt gtg cca ttt gtg 960
Gln Asp Phe Ser Asn Lys Gly Thr Leu Trp Gly Phe Val Pro Phe Val
305 310 315 320

gat gaa cag caa cca act gaa ata cca att cca att acc ctt cat att 1008
Asp Glu Gln Gln Pro Thr Glu Ile Pro Ile Pro Ile Thr Leu His Ile
325 330 335

gga gac tac aat atg gat ggc tat cca gac gct ctg gtc ata cta aag 1056
Gly Asp Tyr Asn Met Asp Gly Tyr Pro Asp Ala Leu Val Ile Leu Lys
340 345 350

aac aca tct gga agc aac cag cag gcc ttt tta ctg gag aac gtc cct 1104
Asn Thr Ser Gly Ser Asn Gln Gln Ala Phe Leu Leu Glu Asn Val Pro
355 360 365

tgt aat aat gca agc tgt gaa gag gcg cgt cga atg ttt aaa gtc tac 1152
Cys Asn Asn Ala Ser Cys Glu Glu Ala Arg Arg Met Phe Lys Val Tyr

370 375 380

tgg gag ctg aca gac cta aat caa att aag gat gcc atg gtt gcc acc 1200
Trp Glu Leu Thr Asp Leu Asn Gln Ile Lys Asp Ala Met Val Ala Thr
385 390 395 400

ttc ttt gac att tac gaa gat gga atc ttg gac att gta gtg cta agt 1248
Phe Phe Asp Ile Tyr Glu Asp Gly Ile Leu Asp Ile Val Val Leu Ser
405 410 415

aaa gga tat aca aag aat gat ttt gcc att cat aca cta aaa aat aac 1296
Lys Gly Tyr Thr Lys Asn Asp Phe Ala Ile His Thr Leu Lys Asn Asn
420 425 430

ttt gaa gca gat gct tat ttt gtt aaa gtt att gtt ctt agt ggt ctg 1344
Phe Glu Ala Asp Ala Tyr Phe Val Lys Val Ile Val Leu Ser Gly Leu
435 440 445

tgt tct aat gac tgt cct cgt aag ata aca ccc ttt gga gtg aat caa 1392
Cys Ser Asn Asp Cys Pro Arg Lys Ile Thr Pro Phe Gly Val Asn Gln
450 455 460

cct gga cct tat atc atg tat aca act gta gat gca aat ggg tat ctg 1440
Pro Gly Pro Tyr Ile Met Tyr Thr Thr Val Asp Ala Asn Gly Tyr Leu
465 470 475 480

aaa aat gga tca gct ggc caa ctc agc caa tcc gca cat tta gct ctc 1488
Lys Asn Gly Ser Ala Gly Gln Leu Ser Gln Ser Ala His Leu Ala Leu
485 490 495

caa cta cca tac aac gtg ctt ggt tta ggt cgg agc gca aat ttt ctt 1536
Gln Leu Pro Tyr Asn Val Leu Gly Leu Gly Arg Ser Ala Asn Phe Leu
500 505 510

gac cat ctc tac gtt ggt att ccc cgt cca tct gga gaa aaa tct ata 1584
Asp His Leu Tyr Val Gly Ile Pro Arg Pro Ser Gly Glu Lys Ser Ile
515 520 525

cga aaa caa gag tgg act gca atc att cca aat tcc cag cta att gtc 1632
Arg Lys Gln Glu Trp Thr Ala Ile Ile Pro Asn Ser Gln Leu Ile Val
530 535 540

att cca tac cct cac aat gtc cct cga agt tgg agt gcc aaa ctg tat 1680
Ile Pro Tyr Pro His Asn Val Pro Arg Ser Trp Ser Ala Lys Leu Tyr

545 550 555 560

ctt aca cca agt aat att gtt ctg ctt act gct ata gct ctc atc ggt 1728
Leu Thr Pro Ser Asn Ile Val Leu Leu Thr Ala Ile Ala Leu Ile Gly
565 570 575

gtc tgt gtt ttc atc ttg gca ata att ggc att tta cat tgg cag gaa 1776
Val Cys Val Phe Ile Leu Ala Ile Ile Gly Ile Leu His Trp Gln Glu
580 585 590

aag aaa gca gat gat aga gaa aaa cga caa gaa gcc cac cgg ttt cat 1824
Lys Lys Ala Asp Asp Arg Glu Lys Arg Gln Glu Ala His Arg Phe His
595 600 605

ttt gat gct atg tga 1839
Phe Asp Ala Met *
610

<210> 246
<211> 612
<212> PRT
<213> Homo sapiens

<400> 246
Met Ala Ala Ala Gly Arg Leu Pro Ser Ser Trp Ala Leu Phe Ser Pro
1 5 10 15
Leu Leu Ala Gly Leu Ala Leu Leu Gly Val Gly Pro Val Pro Ala Arg
20 25 30
Ala Leu His Asn Val Thr Ala Glu Leu Phe Gly Ala Glu Ala Trp Gly
35 40 45
Thr Leu Ala Ala Phe Gly Asp Leu Asn Ser Asp Lys Gln Thr Asp Leu
50 55 60
Phe Val Leu Arg Glu Arg Asn Asp Leu Ile Val Phe Leu Ala Asp Gln
65 70 75 80
Asn Ala Pro Tyr Phe Lys Pro Lys Val Lys Val Ser Phe Lys Asn His
85 90 95
Ser Ala Leu Ile Thr Ser Val Val Pro Gly Asp Tyr Asp Gly Asp Ser
100 105 110
Gln Met Asp Val Leu Leu Thr Tyr Leu Pro Lys Asn Tyr Ala Lys Ser
115 120 125
Glu Leu Gly Ala Val Ile Phe Trp Gly Gln Asn Gln Thr Leu Asp Pro
130 135 140
Asn Asn Met Thr Ile Leu Asn Arg Thr Phe Gln Asp Glu Pro Leu Ile

145 150 155 160
Met Asp Phe Asn Gly Asp Leu Ile Pro Asp Ile Phe Gly Ile Thr Asn
165 170 175
Glu Ser Asn Gln Pro Gln Ile Leu Leu Gly Gly Asn Leu Ser Trp His
180 185 190
Pro Ala Leu Thr Thr Thr Ser Lys Met Arg Ile Pro His Ser His Ala
195 200 205
Phe Ile Asp Leu Thr Glu Asp Phe Thr Ala Asp Leu Phe Leu Thr Thr
210 215 220
Leu Asn Ala Thr Thr Ser Thr Phe Gln Phe Glu Ile Trp Glu Asn Leu
225 230 235 240
Asp Gly Asn Phe Ser Val Ser Thr Ile Leu Glu Lys Pro Gln Asn Met
245 250 255
Met Val Val Gly Gln Ser Ala Phe Ala Asp Phe Asp Gly Asp Gly His
260 265 270
Met Asp His Leu Leu Pro Gly Cys Glu Asp Lys Asn Cys Gln Lys Ser
275 280 285
Thr Ile Tyr Leu Val Arg Ser Gly Met Lys Gln Trp Val Pro Val Leu
290 295 300
Gln Asp Phe Ser Asn Lys Gly Thr Leu Trp Gly Phe Val Pro Phe Val
305 310 315 320
Asp Glu Gln Gln Pro Thr Glu Ile Pro Ile Pro Ile Thr Leu His Ile
325 330 335
Gly Asp Tyr Asn Met Asp Gly Tyr Pro Asp Ala Leu Val Ile Leu Lys
340 345 350
Asn Thr Ser Gly Ser Asn Gln Gln Ala Phe Leu Leu Glu Asn Val Pro
355 360 365
Cys Asn Asn Ala Ser Cys Glu Glu Ala Arg Arg Met Phe Lys Val Tyr
370 375 380
Trp Glu Leu Thr Asp Leu Asn Gln Ile Lys Asp Ala Met Val Ala Thr
385 390 395 400
Phe Phe Asp Ile Tyr Glu Asp Gly Ile Leu Asp Ile Val Val Leu Ser
405 410 415
Lys Gly Tyr Thr Lys Asn Asp Phe Ala Ile His Thr Leu Lys Asn Asn
420 425 430
Phe Glu Ala Asp Ala Tyr Phe Val Lys Val Ile Val Leu Ser Gly Leu
435 440 445
Cys Ser Asn Asp Cys Pro Arg Lys Ile Thr Pro Phe Gly Val Asn Gln
450 455 460
Pro Gly Pro Tyr Ile Met Tyr Thr Thr Val Asp Ala Asn Gly Tyr Leu
465 470 475 480
Lys Asn Gly Ser Ala Gly Gln Leu Ser Gln Ser Ala His Leu Ala Leu
485 490 495
Gln Leu Pro Tyr Asn Val Leu Gly Leu Gly Arg Ser Ala Asn Phe Leu

```
            500                 505                 510
Asp His Leu Tyr Val Gly Ile Pro Arg Pro Ser Gly Glu Lys Ser Ile
        515                 520                 525
Arg Lys Gln Glu Trp Thr Ala Ile Ile Pro Asn Ser Gln Leu Ile Val
    530                 535                 540
Ile Pro Tyr Pro His Asn Val Pro Arg Ser Trp Ser Ala Lys Leu Tyr
545                 550                 555                 560
Leu Thr Pro Ser Asn Ile Val Leu Leu Thr Ala Ile Ala Leu Ile Gly
                565                 570                 575
Val Cys Val Phe Ile Leu Ala Ile Ile Gly Ile Leu His Trp Gln Glu
            580                 585                 590
Lys Lys Ala Asp Asp Arg Glu Lys Arg Gln Glu Ala His Arg Phe His
        595                 600                 605
Phe Asp Ala Met
    610

      <210> 247
      <211> 462
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(462)

      <400> 247
atg ggc cgg ctc cca ttg ctc cgg cgc gtt ctc aag ggc ttg cag ctg       48
Met Gly Arg Leu Pro Leu Leu Arg Arg Val Leu Lys Gly Leu Gln Leu
 1               5                  10                  15

ttg ctg tct ctg ctg gcc ttc atc tgt gaa gaa gtt gta tca caa tgt       96
Leu Leu Ser Leu Leu Ala Phe Ile Cys Glu Glu Val Val Ser Gln Cys
            20                  25                  30

act tta tgt gga gga ctt tat ttt ttt gag ttt gta agc tgc agt gcc      144
Thr Leu Cys Gly Gly Leu Tyr Phe Phe Glu Phe Val Ser Cys Ser Ala
        35                  40                  45

ttt ctt ctg agt ctc ctt ata ctg att gtg tat tgc act cca ttt tat      192
Phe Leu Leu Ser Leu Leu Ile Leu Ile Val Tyr Cys Thr Pro Phe Tyr
     50                  55                  60

gag aga gtt gat acc aca aaa gta aaa tca tcg gat ttt tat att act      240
Glu Arg Val Asp Thr Thr Lys Val Lys Ser Ser Asp Phe Tyr Ile Thr
```

65 70 75 80

ttg gga aca gga tgt gtg ttt ttg ttg gca tcc atc att ttt gtt tcc 288
Leu Gly Thr Gly Cys Val Phe Leu Leu Ala Ser Ile Ile Phe Val Ser
85 90 95

aca cat gac agg act tca gct gag att gct gca att gtg ttt gga ttt 336
Thr His Asp Arg Thr Ser Ala Glu Ile Ala Ala Ile Val Phe Gly Phe
100 105 110

ata gca agt ttt atg ttc cta ctt gac ttt atc act atg ctg tat gaa 384
Ile Ala Ser Phe Met Phe Leu Leu Asp Phe Ile Thr Met Leu Tyr Glu
115 120 125

aaa cga cag gag tcc cag ctg aga aaa cct gaa aat acc act agg gct 432
Lys Arg Gln Glu Ser Gln Leu Arg Lys Pro Glu Asn Thr Thr Arg Ala
130 135 140

gaa gcc ctc act gag cca ctt aat gcc taa 462
Glu Ala Leu Thr Glu Pro Leu Asn Ala *
145 150

<210> 248
<211> 153
<212> PRT
<213> Homo sapiens

<400> 248
Met Gly Arg Leu Pro Leu Leu Arg Arg Val Leu Lys Gly Leu Gln Leu
1 5 10 15
Leu Leu Ser Leu Leu Ala Phe Ile Cys Glu Glu Val Val Ser Gln Cys
20 25 30
Thr Leu Cys Gly Gly Leu Tyr Phe Phe Glu Phe Val Ser Cys Ser Ala
35 40 45
Phe Leu Leu Ser Leu Leu Ile Leu Ile Val Tyr Cys Thr Pro Phe Tyr
50 55 60
Glu Arg Val Asp Thr Thr Lys Val Lys Ser Ser Asp Phe Tyr Ile Thr
65 70 75 80
Leu Gly Thr Gly Cys Val Phe Leu Leu Ala Ser Ile Ile Phe Val Ser
85 90 95
Thr His Asp Arg Thr Ser Ala Glu Ile Ala Ala Ile Val Phe Gly Phe
100 105 110
Ile Ala Ser Phe Met Phe Leu Leu Asp Phe Ile Thr Met Leu Tyr Glu

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        115                 120                 125
Lys Arg Gln Glu Ser Gln Leu Arg Lys Pro Glu Asn Thr Thr Arg Ala
    130                 135                 140
Glu Ala Leu Thr Glu Pro Leu Asn Ala
145                 150

      <210> 249
      <211> 1071
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(1071)

      <221> misc_feature
      <222> (1)...(1071)
      <223> n = A,T,C or G

      <400> 249
atg aca ggg acc atc ctt tca ggc tcc atc agc ctc ggt gac agt gtg      48
Met Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val
 1               5                  10                  15

gag atc cct gcc ctc aag gtg gtg aag aag gtg aag tcc atg cag atg      96
Glu Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met
            20                  25                  30

ttc cac atg ccc atc act tca gcc atg caa gga gac cgg ctg ggc atc     144
Phe His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile
        35                  40                  45

tgc gtc acc cag ttt gac cct aag ctg ctg gag cgc ggg ttg gtg tgt     192
Cys Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys
    50                  55                  60

gcc ccc gag tcc ctg cac act gtc cat gcg gcc ctc atc tct gtg gaa     240
Ala Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu
 65                  70                  75                  80

aag ata ccg tat ttc cgg ggg ccc ctg caa acc aag gcc aag ttc cac     288
Lys Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His
                85                  90                  95
```

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att aca gtg ggc cat gaa aca gtc atg ggc cgg ttg atg ttc ttc agt      336
Ile Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser
            100                 105                 110

cct gct cca gat aac ttt gac cag gag cct ata ctg gac tct ttc aac      384
Pro Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn
        115                 120                 125

ttc tct caa gaa tac ctt ttc cag gag cag tac ctg tcc aag gat ttg      432
Phe Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu
    130                 135                 140

aca cca gca gtg aca gac aat gat gag gcc gac aag aag gcc ggc cag      480
Thr Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln
145                 150                 155                 160

gcc aca gag ggc cat tgt cct cgg cag cag tgg gcc ctg gtg gag ttt      528
Ala Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe
                165                 170                 175

gag aag ccc gtc acc tgc cct cgg ctg tgc ctg gtg att ggc tcc agg      576
Glu Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg
            180                 185                 190

cta gat gcg gac att cac acc aac acg tgc cgg cta gcc ttc cat ggc      624
Leu Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly
        195                 200                 205

atc ctg ctc cac ggg cta gag gac agg aac tac gcc gac agc ttc ctg      672
Ile Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu
    210                 215                 220

ccc agg ctg aag gtg tac aag ctg aag cac aag cat ggc ctt gtg gag      720
Pro Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu
225                 230                 235                 240

cgg gcg atg gat gac tac agt gtg atc ggc cgc tcc ctg ttc aaa aag      768
Arg Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys
                245                 250                 255

gaa acc aac atc cag ctc ttc gtg ggg ctc aag gtg cac ttg tcc act      816
Glu Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr
            260                 265                 270
```

```
ggg gaa ctg ggc atc atc gac agt gcc ttc ggc cag agc ggc aag ttc      864
Gly Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe
        275                 280                 285

aag atc cac atc cca ggt ggc ctc agc ccc gag tcc aag aag atc ctg      912
Lys Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu
    290                 295                 300

aca ccc gcc ctc aag aag cgg gcc cgg gct ggc cgt ggg gag gcc acc      960
Thr Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr
305                 310                 315                 320

agg cag gag gag agc gcc gag cgg agn ngg ccc tca cag cat gtg gtg     1008
Arg Gln Glu Glu Ser Ala Glu Arg Xaa Xaa Pro Ser Gln His Val Val
                325                 330                 335

ctc agc ctg act ttc aag cgt tat gtc ttc gac acc cac aag cgc atg     1056
Leu Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met
            340                 345                 350

gtt cag tct ccc tga                                                 1071
Val Gln Ser Pro  *
        355
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<210> 250
<211> 356
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(356)
<223> Xaa = Any Amino Acid

<400> 250

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Met Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val
 1               5                  10                  15
Glu Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met
            20                  25                  30
Phe His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile
        35                  40                  45
Cys Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys
    50                  55                  60
```

Ala Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu
65 70 75 80
Lys Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His
85 90 95
Ile Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser
100 105 110
Pro Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn
115 120 125
Phe Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu
130 135 140
Thr Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln
145 150 155 160
Ala Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe
165 170 175
Glu Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg
180 185 190
Leu Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly
195 200 205
Ile Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu
210 215 220
Pro Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu
225 230 235 240
Arg Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys
245 250 255
Glu Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr
260 265 270
Gly Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe
275 280 285
Lys Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu
290 295 300
Thr Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr
305 310 315 320
Arg Gln Glu Glu Ser Ala Glu Arg Xaa Xaa Pro Ser Gln His Val Val
325 330 335
Leu Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met
340 345 350
Val Gln Ser Pro
355

<210> 251
<211> 567
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(567)

<400> 251
atg gct gcc tct gcc ttt gct ggt gca gtg aga gca gct tca gga atc 48
Met Ala Ala Ser Ala Phe Ala Gly Ala Val Arg Ala Ala Ser Gly Ile
1 5 10 15

cta cgg tcc ctg aat att ttg gca tct tca acc tac cgc aac tgt gtc 96
Leu Arg Ser Leu Asn Ile Leu Ala Ser Ser Thr Tyr Arg Asn Cys Val
20 25 30

aag aat gcc tct ctt att tct gca ttg tcc act gga cgt ttt agt cat 144
Lys Asn Ala Ser Leu Ile Ser Ala Leu Ser Thr Gly Arg Phe Ser His
35 40 45

att cag aca cca gtt gtt tcc tcc act ccc aga ctt acc aca tct gag 192
Ile Gln Thr Pro Val Val Ser Ser Thr Pro Arg Leu Thr Thr Ser Glu
50 55 60

aga aac ctg aca tgt ggg cat acc tca gtg atc ctt aat aga atg gcc 240
Arg Asn Leu Thr Cys Gly His Thr Ser Val Ile Leu Asn Arg Met Ala
65 70 75 80

ccc gtg ctt cca agt gtc ctg aag ctg cca gtc aga tct cta aca tac 288
Pro Val Leu Pro Ser Val Leu Lys Leu Pro Val Arg Ser Leu Thr Tyr
85 90 95

ttc agt gca aga aaa ggc aag aga aag acc gtg aaa gct gtc atc gat 336
Phe Ser Ala Arg Lys Gly Lys Arg Lys Thr Val Lys Ala Val Ile Asp
100 105 110

agg ttt ctt cga ctt cat tgt ggc ctt tgg gtg agg aga aag gct ggc 384
Arg Phe Leu Arg Leu His Cys Gly Leu Trp Val Arg Arg Lys Ala Gly
115 120 125

tat aag aaa aaa tta tgg aaa aag aca cct gca agg aag aag cga ttg 432
Tyr Lys Lys Lys Leu Trp Lys Lys Thr Pro Ala Arg Lys Lys Arg Leu
130 135 140

agg gaa ttt gta ttc tgc aat aaa acc cag agt aaa ctc tta gat aaa 480
Arg Glu Phe Val Phe Cys Asn Lys Thr Gln Ser Lys Leu Leu Asp Lys
145 150 155 160

atg acg acg tcc ttc tgg aag agg cga aac tgg tac gtt gat gat cct 528
Met Thr Thr Ser Phe Trp Lys Arg Arg Asn Trp Tyr Val Asp Asp Pro
165 170 175

tat cag aag tat cat gat cga aca aac ctg aaa gta tag 567
Tyr Gln Lys Tyr His Asp Arg Thr Asn Leu Lys Val *
180 185

<210> 252
<211> 188
<212> PRT
<213> Homo sapiens

<400> 252
Met Ala Ala Ser Ala Phe Ala Gly Ala Val Arg Ala Ala Ser Gly Ile
1 5 10 15
Leu Arg Ser Leu Asn Ile Leu Ala Ser Ser Thr Tyr Arg Asn Cys Val
20 25 30
Lys Asn Ala Ser Leu Ile Ser Ala Leu Ser Thr Gly Arg Phe Ser His
35 40 45
Ile Gln Thr Pro Val Val Ser Ser Thr Pro Arg Leu Thr Thr Ser Glu
50 55 60
Arg Asn Leu Thr Cys Gly His Thr Ser Val Ile Leu Asn Arg Met Ala
65 70 75 80
Pro Val Leu Pro Ser Val Leu Lys Leu Pro Val Arg Ser Leu Thr Tyr
85 90 95
Phe Ser Ala Arg Lys Gly Lys Arg Lys Thr Val Lys Ala Val Ile Asp
100 105 110
Arg Phe Leu Arg Leu His Cys Gly Leu Trp Val Arg Arg Lys Ala Gly
115 120 125
Tyr Lys Lys Lys Leu Trp Lys Lys Thr Pro Ala Arg Lys Lys Arg Leu
130 135 140
Arg Glu Phe Val Phe Cys Asn Lys Thr Gln Ser Lys Leu Leu Asp Lys
145 150 155 160
Met Thr Thr Ser Phe Trp Lys Arg Arg Asn Trp Tyr Val Asp Asp Pro
165 170 175
Tyr Gln Lys Tyr His Asp Arg Thr Asn Leu Lys Val
180 185

<210> 253
<211> 453
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(453)

<400> 253

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atg gac ttc cac ata ctg atc gtc atc ggt tgt gtg gtc agc gcc tcg       48
Met Asp Phe His Ile Leu Ile Val Ile Gly Cys Val Val Ser Ala Ser
 1               5                  10                  15

ctg ctc tcg ttc ctg ttc atc aac aag atc ttc cgg cgc aag act ttt       96
Leu Leu Ser Phe Leu Phe Ile Asn Lys Ile Phe Arg Arg Lys Thr Phe
            20                  25                  30

gag gag gtg gta gcc gag aag cgt gcc ctg agc gcc aat ctc tac aag      144
Glu Glu Val Val Ala Glu Lys Arg Ala Leu Ser Ala Asn Leu Tyr Lys
        35                  40                  45

gcg gcc ggt ggt gcc gct acc aag aag ccc aag aag aag gaa ctt aag      192
Ala Ala Gly Gly Ala Ala Thr Lys Lys Pro Lys Lys Lys Glu Leu Lys
    50                  55                  60

cgc gaa aag aag caa cgt cag cgg gaa cag cag agg gat gtg aac aac      240
Arg Glu Lys Lys Gln Arg Gln Arg Glu Gln Gln Arg Asp Val Asn Asn
65                  70                  75                  80

gag ccg gaa cca gag gaa gcc gaa gac tac tcc gat ggt cag tcg gag      288
Glu Pro Glu Pro Glu Glu Ala Glu Asp Tyr Ser Asp Gly Gln Ser Glu
                85                  90                  95

ggt cag ggc tcc gtg gct ggc gag gaa ccc ggt ctc tcc aag cag cat      336
Gly Gln Gly Ser Val Ala Gly Glu Glu Pro Gly Leu Ser Lys Gln His
            100                 105                 110

gtt gaa ttt gaa ccc gat gca gag gtc ctc act gat cag cga cga ccc      384
Val Glu Phe Glu Pro Asp Ala Glu Val Leu Thr Asp Gln Arg Arg Pro
        115                 120                 125

agt agc gtg gct gag aag gag aac caa cct tct ggg gct ggc aaa aag      432
Ser Ser Val Ala Glu Lys Glu Asn Gln Pro Ser Gly Ala Gly Lys Lys
    130                 135                 140

gga aag aag gat aaa cgt taa                                          453
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Gly Lys Lys Asp Lys Arg *
145 150

<210> 254
<211> 150
<212> PRT
<213> Homo sapiens

<400> 254
Met Asp Phe His Ile Leu Ile Val Ile Gly Cys Val Val Ser Ala Ser
1 5 10 15
Leu Leu Ser Phe Leu Phe Ile Asn Lys Ile Phe Arg Arg Lys Thr Phe
20 25 30
Glu Glu Val Val Ala Glu Lys Arg Ala Leu Ser Ala Asn Leu Tyr Lys
35 40 45
Ala Ala Gly Gly Ala Ala Thr Lys Lys Pro Lys Lys Lys Glu Leu Lys
50 55 60
Arg Glu Lys Lys Gln Arg Gln Arg Glu Gln Gln Arg Asp Val Asn Asn
65 70 75 80
Glu Pro Glu Pro Glu Glu Ala Glu Asp Tyr Ser Asp Gly Gln Ser Glu
85 90 95
Gly Gln Gly Ser Val Ala Gly Glu Glu Pro Gly Leu Ser Lys Gln His
100 105 110
Val Glu Phe Glu Pro Asp Ala Glu Val Leu Thr Asp Gln Arg Arg Pro
115 120 125
Ser Ser Val Ala Glu Lys Glu Asn Gln Pro Ser Gly Ala Gly Lys Lys
130 135 140
Gly Lys Lys Asp Lys Arg
145 150

<210> 255
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(489)

<400> 255
atg gca ttt ctc tca ccc ttg gtt ctc att tgc cat cca acc cat ttt 48
Met Ala Phe Leu Ser Pro Leu Val Leu Ile Cys His Pro Thr His Phe
1 5 10 15

```
ctt gac cca aag ctt atg aaa gaa gaa caa atg tca cag gcc cag ctc      96
Leu Asp Pro Lys Leu Met Lys Glu Glu Gln Met Ser Gln Ala Gln Leu
            20                  25                  30

ttc acc aga agc ttt gat gat ggc ctg ggc ttt gaa tac gtg atg ttc     144
Phe Thr Arg Ser Phe Asp Asp Gly Leu Gly Phe Glu Tyr Val Met Phe
        35                  40                  45

tac aat gac att gag aaa agg atg gtt tgc tta ttt caa gga ggc cct     192
Tyr Asn Asp Ile Glu Lys Arg Met Val Cys Leu Phe Gln Gly Gly Pro
    50                  55                  60

tac ctg gaa gga cca cct gga ttc att cat gga ggt gcc att gca acc     240
Tyr Leu Glu Gly Pro Pro Gly Phe Ile His Gly Gly Ala Ile Ala Thr
65                  70                  75                  80

atg att gat gct act gtt ggt atg tgt gca atg atg gct ggg gga atc     288
Met Ile Asp Ala Thr Val Gly Met Cys Ala Met Met Ala Gly Gly Ile
                85                  90                  95

gtc atg act gcc aat ctc aac atc aat tat aaa aga cct atc cct ctt     336
Val Met Thr Ala Asn Leu Asn Ile Asn Tyr Lys Arg Pro Ile Pro Leu
            100                 105                 110

tgt tct gtt gtt atg ata aat agc caa ctt gat aaa gtt gaa gga agg     384
Cys Ser Val Val Met Ile Asn Ser Gln Leu Asp Lys Val Glu Gly Arg
        115                 120                 125

aaa ttt ttt gtt tcc tgt aat gtt cag agt gtt gat gag aag acc cta     432
Lys Phe Phe Val Ser Cys Asn Val Gln Ser Val Asp Glu Lys Thr Leu
    130                 135                 140

tac tca gag gcg aca agc tta ttt ata aag ctg aat cct gct aaa agt     480
Tyr Ser Glu Ala Thr Ser Leu Phe Ile Lys Leu Asn Pro Ala Lys Ser
145                 150                 155                 160

ctg aca taa                                                         489
Leu Thr  *
```

<210> 256
<211> 162

<212> PRT
<213> Homo sapiens

<400> 256
Met Ala Phe Leu Ser Pro Leu Val Leu Ile Cys His Pro Thr His Phe
1 5 10 15
Leu Asp Pro Lys Leu Met Lys Glu Glu Gln Met Ser Gln Ala Gln Leu
20 25 30
Phe Thr Arg Ser Phe Asp Asp Gly Leu Gly Phe Glu Tyr Val Met Phe
35 40 45
Tyr Asn Asp Ile Glu Lys Arg Met Val Cys Leu Phe Gln Gly Gly Pro
50 55 60
Tyr Leu Glu Gly Pro Pro Gly Phe Ile His Gly Gly Ala Ile Ala Thr
65 70 75 80
Met Ile Asp Ala Thr Val Gly Met Cys Ala Met Met Ala Gly Gly Ile
85 90 95
Val Met Thr Ala Asn Leu Asn Ile Asn Tyr Lys Arg Pro Ile Pro Leu
100 105 110
Cys Ser Val Val Met Ile Asn Ser Gln Leu Asp Lys Val Glu Gly Arg
115 120 125
Lys Phe Phe Val Ser Cys Asn Val Gln Ser Val Asp Glu Lys Thr Leu
130 135 140
Tyr Ser Glu Ala Thr Ser Leu Phe Ile Lys Leu Asn Pro Ala Lys Ser
145 150 155 160
Leu Thr

<210> 257
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(480)

<400> 257
atg tgt ctt ttg gca gtc agt cca gat ggg aat tgg cta gct gca tca 48
Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp Leu Ala Ala Ser
1 5 10 15

ggt acc agt gct gga gtc cat gtc tac aac gta aaa cag cta aag ctt 96
Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys Gln Leu Lys Leu
20 25 30

cac tgc acg gtg cct gct tac aat ttc cca gtg act gct atg gct att 144
His Cys Thr Val Pro Ala Tyr Asn Phe Pro Val Thr Ala Met Ala Ile
35 40 45

gcc ccc aat acc aac aac ctt gtc atc gct cat tcg gac cag cag gta 192
Ala Pro Asn Thr Asn Asn Leu Val Ile Ala His Ser Asp Gln Gln Val
50 55 60

ttt gag tac agc atc cca gac aaa cag tat aca gat tgg agc cgg act 240
Phe Glu Tyr Ser Ile Pro Asp Lys Gln Tyr Thr Asp Trp Ser Arg Thr
65 70 75 80

gtc cag aag cag ggc ttt cac cac ctt tgg ctc caa agg gat act cct 288
Val Gln Lys Gln Gly Phe His His Leu Trp Leu Gln Arg Asp Thr Pro
85 90 95

atc aca cac atc agt ttt cat ccc aag aga ccg atg cac atc ctt ctc 336
Ile Thr His Ile Ser Phe His Pro Lys Arg Pro Met His Ile Leu Leu
100 105 110

cat gat gcc tac atg ttc tgc atc att gac aag tca ttg ccc ctt cca 384
His Asp Ala Tyr Met Phe Cys Ile Ile Asp Lys Ser Leu Pro Leu Pro
115 120 125

aat gac aaa acc tta ctc tac aat cca ttt cct ccc acg aat gac atc 432
Asn Asp Lys Thr Leu Leu Tyr Asn Pro Phe Pro Pro Thr Asn Asp Ile
130 135 140

att gct cag ctc cca cca ccc att aaa aag aag aaa ttt gga acc taa 480
Ile Ala Gln Leu Pro Pro Pro Ile Lys Lys Lys Lys Phe Gly Thr *
145 150 155

<210> 258
<211> 159
<212> PRT
<213> Homo sapiens

<400> 258
Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp Leu Ala Ala Ser
1 5 10 15
Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys Gln Leu Lys Leu
20 25 30

```
His Cys Thr Val Pro Ala Tyr Asn Phe Pro Val Thr Ala Met Ala Ile
        35                  40                  45
Ala Pro Asn Thr Asn Asn Leu Val Ile Ala His Ser Asp Gln Gln Val
    50                  55                  60
Phe Glu Tyr Ser Ile Pro Asp Lys Gln Tyr Thr Asp Trp Ser Arg Thr
65                  70                  75                  80
Val Gln Lys Gln Gly Phe His His Leu Trp Leu Gln Arg Asp Thr Pro
                85                  90                  95
Ile Thr His Ile Ser Phe His Pro Lys Arg Pro Met His Ile Leu Leu
            100                 105                 110
His Asp Ala Tyr Met Phe Cys Ile Ile Asp Lys Ser Leu Pro Leu Pro
        115                 120                 125
Asn Asp Lys Thr Leu Leu Tyr Asn Pro Phe Pro Pro Thr Asn Asp Ile
    130                 135                 140
Ile Ala Gln Leu Pro Pro Pro Ile Lys Lys Lys Lys Phe Gly Thr
145                 150                 155

      <210> 259
      <211> 627
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(627)

      <400> 259
atg gcg tcc tct ttg ctt gcg ggc gag cga ttg gtg cgt gct ttg ggc      48
Met Ala Ser Ser Leu Leu Ala Gly Glu Arg Leu Val Arg Ala Leu Gly
 1               5                  10                  15

ccc ggc ggg gag ctg gag cca gag cgg cta ccc cga aag ctg cgg gcc      96
Pro Gly Gly Glu Leu Glu Pro Glu Arg Leu Pro Arg Lys Leu Arg Ala
            20                  25                  30

gag ctt gag gcc gcg ctg ggg aag aag cac aag ggc ggt gat agc tcc     144
Glu Leu Glu Ala Ala Leu Gly Lys Lys His Lys Gly Gly Asp Ser Ser
        35                  40                  45

agt ggc ccc caa cgc ttg gtt tct ttc cgt ctc atc cgg gat ctg cac     192
Ser Gly Pro Gln Arg Leu Val Ser Phe Arg Leu Ile Arg Asp Leu His
    50                  55                  60

cag cat ctg aga gaa agg gat tcc aaa cta tac ctc cat gag ctc cta     240
```

```
Gln His Leu Arg Glu Arg Asp Ser Lys Leu Tyr Leu His Glu Leu Leu
 65                  70                  75                  80

gaa ggc agt gaa atc tat ctc cca gag gtt gtg aag cct cca cgg aac       288
Glu Gly Ser Glu Ile Tyr Leu Pro Glu Val Val Lys Pro Pro Arg Asn
                 85                  90                  95

cca gaa cta gtt gcc cgg ctg gag aag att aag ata cag ctg gcc aat       336
Pro Glu Leu Val Ala Arg Leu Glu Lys Ile Lys Ile Gln Leu Ala Asn
            100                 105                 110

gag gaa tat aaa cgg atc acc cgc aac gtc act tgt cag gat aca aga       384
Glu Glu Tyr Lys Arg Ile Thr Arg Asn Val Thr Cys Gln Asp Thr Arg
        115                 120                 125

cat ggt ggg act ctc agc gac ctg gga aag caa gtg aga tca ttg aag       432
His Gly Gly Thr Leu Ser Asp Leu Gly Lys Gln Val Arg Ser Leu Lys
    130                 135                 140

gct ctg gtc atc acc atc ttc aat ttc att gtc acg gtg gtt gct gcc       480
Ala Leu Val Ile Thr Ile Phe Asn Phe Ile Val Thr Val Val Ala Ala
145                 150                 155                 160

ttc gtc tgc act tac ctt gga agc caa tat atc ttc aca gaa atg gcc       528
Phe Val Cys Thr Tyr Leu Gly Ser Gln Tyr Ile Phe Thr Glu Met Ala
                165                 170                 175

tcg cgg gtg cta gct gca ttg atc gtc gcc tct gtg gtg ggt ctg gcc       576
Ser Arg Val Leu Ala Ala Leu Ile Val Ala Ser Val Val Gly Leu Ala
            180                 185                 190

gag ctg tat gtc atg gtg cgg gca atg gaa ggc gag ctg gga gaa ctg       624
Glu Leu Tyr Val Met Val Arg Ala Met Glu Gly Glu Leu Gly Glu Leu
        195                 200                 205

taa                                                                   627
 *
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<210> 260
<211> 208
<212> PRT
<213> Homo sapiens

<400> 260
Met Ala Ser Ser Leu Leu Ala Gly Glu Arg Leu Val Arg Ala Leu Gly
1 5 10 15
Pro Gly Gly Glu Leu Glu Pro Glu Arg Leu Pro Arg Lys Leu Arg Ala
20 25 30
Glu Leu Glu Ala Ala Leu Gly Lys Lys His Lys Gly Gly Asp Ser Ser
35 40 45
Ser Gly Pro Gln Arg Leu Val Ser Phe Arg Leu Ile Arg Asp Leu His
50 55 60
Gln His Leu Arg Glu Arg Asp Ser Lys Leu Tyr Leu His Glu Leu Leu
65 70 75 80
Glu Gly Ser Glu Ile Tyr Leu Pro Glu Val Val Lys Pro Pro Arg Asn
85 90 95
Pro Glu Leu Val Ala Arg Leu Glu Lys Ile Lys Ile Gln Leu Ala Asn
100 105 110
Glu Glu Tyr Lys Arg Ile Thr Arg Asn Val Thr Cys Gln Asp Thr Arg
115 120 125
His Gly Gly Thr Leu Ser Asp Leu Gly Lys Gln Val Arg Ser Leu Lys
130 135 140
Ala Leu Val Ile Thr Ile Phe Asn Phe Ile Val Thr Val Val Ala Ala
145 150 155 160
Phe Val Cys Thr Tyr Leu Gly Ser Gln Tyr Ile Phe Thr Glu Met Ala
165 170 175
Ser Arg Val Leu Ala Ala Leu Ile Val Ala Ser Val Val Gly Leu Ala
180 185 190
Glu Leu Tyr Val Met Val Arg Ala Met Glu Gly Glu Leu Gly Glu Leu
195 200 205

<210> 261
<211> 1092
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1092)

<400> 261
atg gcc gca gcg gcg atg gcg gca gcg gca ggt gga ggg gct ggc gcg 48
Met Ala Ala Ala Ala Met Ala Ala Ala Ala Gly Gly Gly Ala Gly Ala
1 5 10 15

gcc cgc tcc ctc tcg cgc ttc cga ggc tgc ctg gct ggc gcg ctg ctc 96

Ala Arg Ser Leu Ser Arg Phe Arg Gly Cys Leu Ala Gly Ala Leu Leu
20 25 30

ggg gac tgc gtg ggc tcc ttc tac gag gcc cac gac acc gtc gac ctg 144
Gly Asp Cys Val Gly Ser Phe Tyr Glu Ala His Asp Thr Val Asp Leu
35 40 45

acg tca gtc ctg cgt cat gtc cag agt ctg gag ccg gac ccc ggc acg 192
Thr Ser Val Leu Arg His Val Gln Ser Leu Glu Pro Asp Pro Gly Thr
50 55 60

ccc ggg agt gag cgg aca gaa gcc ttg tac tac aca gat gac aca gcc 240
Pro Gly Ser Glu Arg Thr Glu Ala Leu Tyr Tyr Thr Asp Asp Thr Ala
65 70 75 80

atg gcc agg gcc ctg gtg cag tcc ctg cta gcc aag gag gcc ttt gac 288
Met Ala Arg Ala Leu Val Gln Ser Leu Leu Ala Lys Glu Ala Phe Asp
85 90 95

gag gtg gac atg gct cac aga ttt gct cag gag tac aag aaa gac cct 336
Glu Val Asp Met Ala His Arg Phe Ala Gln Glu Tyr Lys Lys Asp Pro
100 105 110

gac agg ggc tat ggt gct gga gta gtc act gtc ttc aag aag ctc ctg 384
Asp Arg Gly Tyr Gly Ala Gly Val Val Thr Val Phe Lys Lys Leu Leu
115 120 125

aac ccc aaa tgt cgc gat gtc ttt gag cct gcc cgg gcc cag ttt aac 432
Asn Pro Lys Cys Arg Asp Val Phe Glu Pro Ala Arg Ala Gln Phe Asn
130 135 140

ggg aaa ggc tcc tat ggc aat gga ggt gcc atg cgg gtg gct ggc atc 480
Gly Lys Gly Ser Tyr Gly Asn Gly Gly Ala Met Arg Val Ala Gly Ile
145 150 155 160

tcc ctg gcc tat agc agt gtc cag gat gtg cag aag ttt gcc cgg ctc 528
Ser Leu Ala Tyr Ser Ser Val Gln Asp Val Gln Lys Phe Ala Arg Leu
165 170 175

tcg gcc cag ctg aca cac gcc tcc tcc ctg ggt tac aat ggc gcc atc 576
Ser Ala Gln Leu Thr His Ala Ser Ser Leu Gly Tyr Asn Gly Ala Ile
180 185 190

ctg cag gcc ctg gct gtg cac ctg gcc ttg cag ggc gag tct tcc agc 624

```
Leu Gln Ala Leu Ala Val His Leu Ala Leu Gln Gly Glu Ser Ser Ser
        195                 200                 205

gag cac ttt ctc aag caa ctc ctg ggc cac atg gag gat ctg gag ggt      672
Glu His Phe Leu Lys Gln Leu Leu Gly His Met Glu Asp Leu Glu Gly
    210                 215                 220

gat gcc cag tcc gtc ttg gat gcc agg gag ttg ggc atg gag gag cgt      720
Asp Ala Gln Ser Val Leu Asp Ala Arg Glu Leu Gly Met Glu Glu Arg
225                 230                 235                 240

cca tac tcc agc cgc ctg aag aag att gga gag ctt cta gac cag gca      768
Pro Tyr Ser Ser Arg Leu Lys Lys Ile Gly Glu Leu Leu Asp Gln Ala
                245                 250                 255

tcg gtg acc agg gag gaa gtg gtg tct gag cta ggg aat ggc att gct      816
Ser Val Thr Arg Glu Glu Val Val Ser Glu Leu Gly Asn Gly Ile Ala
            260                 265                 270

gcc ttt gag tcg gta ccc acc gcc atc tac tgc ttc cta cgc tgc atg      864
Ala Phe Glu Ser Val Pro Thr Ala Ile Tyr Cys Phe Leu Arg Cys Met
        275                 280                 285

gag cca gac cct gag atc cct tct gcc ttc aat agc ctc caa agg act      912
Glu Pro Asp Pro Glu Ile Pro Ser Ala Phe Asn Ser Leu Gln Arg Thr
    290                 295                 300

ctc att tat tcc atc tca ctt ggt ggg gac aca gac acc att gcc acc      960
Leu Ile Tyr Ser Ile Ser Leu Gly Gly Asp Thr Asp Thr Ile Ala Thr
305                 310                 315                 320

atg gct ggg gcc att gct ggt gcc tac tat ggg atg gat cag gtg cca     1008
Met Ala Gly Ala Ile Ala Gly Ala Tyr Tyr Gly Met Asp Gln Val Pro
                325                 330                 335

gag agc tgg cag caa agc tgt gaa ggc tac gag gag aca gac atc ctg     1056
Glu Ser Trp Gln Gln Ser Cys Glu Gly Tyr Glu Glu Thr Asp Ile Leu
            340                 345                 350

gcc caa agc ctg cac cgt gtc ttc cag aag agt tga                     1092
Ala Gln Ser Leu His Arg Val Phe Gln Lys Ser  *
        355                 360
```

<210> 262
<211> 363
<212> PRT
<213> Homo sapiens

<400> 262
Met Ala Ala Ala Ala Met Ala Ala Ala Ala Gly Gly Gly Ala Gly Ala
1 5 10 15
Ala Arg Ser Leu Ser Arg Phe Arg Gly Cys Leu Ala Gly Ala Leu Leu
20 25 30
Gly Asp Cys Val Gly Ser Phe Tyr Glu Ala His Asp Thr Val Asp Leu
35 40 45
Thr Ser Val Leu Arg His Val Gln Ser Leu Glu Pro Asp Pro Gly Thr
50 55 60
Pro Gly Ser Glu Arg Thr Glu Ala Leu Tyr Tyr Thr Asp Asp Thr Ala
65 70 75 80
Met Ala Arg Ala Leu Val Gln Ser Leu Leu Ala Lys Glu Ala Phe Asp
85 90 95
Glu Val Asp Met Ala His Arg Phe Ala Gln Glu Tyr Lys Lys Asp Pro
100 105 110
Asp Arg Gly Tyr Gly Ala Gly Val Val Thr Val Phe Lys Lys Leu Leu
115 120 125
Asn Pro Lys Cys Arg Asp Val Phe Glu Pro Ala Arg Ala Gln Phe Asn
130 135 140
Gly Lys Gly Ser Tyr Gly Asn Gly Gly Ala Met Arg Val Ala Gly Ile
145 150 155 160
Ser Leu Ala Tyr Ser Ser Val Gln Asp Val Gln Lys Phe Ala Arg Leu
165 170 175
Ser Ala Gln Leu Thr His Ala Ser Ser Leu Gly Tyr Asn Gly Ala Ile
180 185 190
Leu Gln Ala Leu Ala Val His Leu Ala Leu Gln Gly Glu Ser Ser Ser
195 200 205
Glu His Phe Leu Lys Gln Leu Leu Gly His Met Glu Asp Leu Glu Gly
210 215 220
Asp Ala Gln Ser Val Leu Asp Ala Arg Glu Leu Gly Met Glu Glu Arg
225 230 235 240
Pro Tyr Ser Ser Arg Leu Lys Lys Ile Gly Glu Leu Leu Asp Gln Ala
245 250 255
Ser Val Thr Arg Glu Glu Val Val Ser Glu Leu Gly Asn Gly Ile Ala
260 265 270
Ala Phe Glu Ser Val Pro Thr Ala Ile Tyr Cys Phe Leu Arg Cys Met
275 280 285
Glu Pro Asp Pro Glu Ile Pro Ser Ala Phe Asn Ser Leu Gln Arg Thr
290 295 300

Leu Ile Tyr Ser Ile Ser Leu Gly Gly Asp Thr Asp Thr Ile Ala Thr
305 310 315 320
Met Ala Gly Ala Ile Ala Gly Ala Tyr Tyr Gly Met Asp Gln Val Pro
325 330 335
Glu Ser Trp Gln Gln Ser Cys Glu Gly Tyr Glu Glu Thr Asp Ile Leu
340 345 350
Ala Gln Ser Leu His Arg Val Phe Gln Lys Ser
355 360

<210> 263
<211> 1239
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1239)

<400> 263
atg gcc ttg gcc ctg ctg agc cgg ctg ctg ccc gga agt gag tac ctc 48
Met Ala Leu Ala Leu Leu Ser Arg Leu Leu Pro Gly Ser Glu Tyr Leu
1 5 10 15

acc cat gag ctg ctg ctg agc tgt gta ttc cgg ctg gag ttc ctc ccg 96
Thr His Glu Leu Leu Leu Ser Cys Val Phe Arg Leu Glu Phe Leu Pro
20 25 30

gaa aga aca tca ggg ggt cca gag gca gcc gac ttc tct gac cag ctg 144
Glu Arg Thr Ser Gly Gly Pro Glu Ala Ala Asp Phe Ser Asp Gln Leu
35 40 45

tcg tta gga agc agc agg gtc cct cgg tgt ggg caa ggg act ctg ctg 192
Ser Leu Gly Ser Ser Arg Val Pro Arg Cys Gly Gln Gly Thr Leu Leu
50 55 60

gct cag gcc tgc cag gac ctc ccc agc atc cgc aac tgc tac ctg act 240
Ala Gln Ala Cys Gln Asp Leu Pro Ser Ile Arg Asn Cys Tyr Leu Thr
65 70 75 80

cat tgc tcg cca gcc cga gcc agt ctg ctg gcc tcc cag gct ctg cac 288
His Cys Ser Pro Ala Arg Ala Ser Leu Leu Ala Ser Gln Ala Leu His
85 90 95

cga ggg gag cta cag cga gtc cca acc ctg cta ctg ccc atg cct acg 336

```
Arg Gly Glu Leu Gln Arg Val Pro Thr Leu Leu Leu Pro Met Pro Thr
            100                 105                 110

gag ccg ctg ctg ccc acc gac tgg ccc ttc ctg cca ctg att cgc ctc      384
Glu Pro Leu Leu Pro Thr Asp Trp Pro Phe Leu Pro Leu Ile Arg Leu
        115                 120                 125

tac cac cgg gct tca gac acc ccc tcg gga ctc tct ccc aca gac acc      432
Tyr His Arg Ala Ser Asp Thr Pro Ser Gly Leu Ser Pro Thr Asp Thr
    130                 135                 140

atg ggc aca gcc atg cgg gtc ctg cag tgg gtg cta gtt ttg gag agc      480
Met Gly Thr Ala Met Arg Val Leu Gln Trp Val Leu Val Leu Glu Ser
145                 150                 155                 160

tgg cgc ccc cag gct ctc tgg gct gtg ccc cct gct gcc cgc ctg gca      528
Trp Arg Pro Gln Ala Leu Trp Ala Val Pro Pro Ala Ala Arg Leu Ala
                165                 170                 175

cgg ctc atg tgt gtg ttc ctg gtg gac agt gag ctg ttc cgg gag tcc      576
Arg Leu Met Cys Val Phe Leu Val Asp Ser Glu Leu Phe Arg Glu Ser
            180                 185                 190

cca gta cag cat ctg gtg gca gcc ctc ctc gcc cag ctc tgt cag cct      624
Pro Val Gln His Leu Val Ala Ala Leu Leu Ala Gln Leu Cys Gln Pro
        195                 200                 205

caa gtc ttg cca aac ctc aac ctg gac tgc cga ctc cct ggc ctg acg      672
Gln Val Leu Pro Asn Leu Asn Leu Asp Cys Arg Leu Pro Gly Leu Thr
    210                 215                 220

tct ttc cct gac ctc tat gcc aac ttc ctg gat cat ttt gag gct gtc      720
Ser Phe Pro Asp Leu Tyr Ala Asn Phe Leu Asp His Phe Glu Ala Val
225                 230                 235                 240

tct ttt ggg gac cac ctc ttt ggg gcc ctg gtc ctc ctg ccc ctg cag      768
Ser Phe Gly Asp His Leu Phe Gly Ala Leu Val Leu Leu Pro Leu Gln
                245                 250                 255

cgt cgg ttc agt gtc acc ttg cgc ctt gcc ctc ttt ggg gaa cac gtg      816
Arg Arg Phe Ser Val Thr Leu Arg Leu Ala Leu Phe Gly Glu His Val
            260                 265                 270

gga gcc ttg cga gct ctg agc ctg cct ctg acc cag ttg cct gtg tcc      864
```

Gly Ala Leu Arg Ala Leu Ser Leu Pro Leu Thr Gln Leu Pro Val Ser
275 280 285

ctg gag tgt tac aca gtg cct cct gaa gac aac ctg gcc ctc ctt cag 912
Leu Glu Cys Tyr Thr Val Pro Pro Glu Asp Asn Leu Ala Leu Leu Gln
290 295 300

ctc tac ttc cgg acc ctg gtt act ggt gcg ctc cgc cca cgt tgg tgc 960
Leu Tyr Phe Arg Thr Leu Val Thr Gly Ala Leu Arg Pro Arg Trp Cys
305 310 315 320

ccc gtg ctc tat gct gtg gct gtg gct cat gtc aat agc ttc atc ttc 1008
Pro Val Leu Tyr Ala Val Ala Val Ala His Val Asn Ser Phe Ile Phe
325 330 335

tct cag gac cca cag agc tca gat gag gtc aaa gct gcc cgc agg agt 1056
Ser Gln Asp Pro Gln Ser Ser Asp Glu Val Lys Ala Ala Arg Arg Ser
340 345 350

atg ctg cag aaa aca tgg ctg ctg gca gat gag ggt ctc cgg cag cac 1104
Met Leu Gln Lys Thr Trp Leu Leu Ala Asp Glu Gly Leu Arg Gln His
355 360 365

ctc ctg cac tat aag ctt ccc aat tcc acg ctc cca gag ggc ttt gag 1152
Leu Leu His Tyr Lys Leu Pro Asn Ser Thr Leu Pro Glu Gly Phe Glu
370 375 380

ctc tat tct cag ttg ccc cct ctg cgt cag cac tac ctc cag aga ctg 1200
Leu Tyr Ser Gln Leu Pro Pro Leu Arg Gln His Tyr Leu Gln Arg Leu
385 390 395 400

act tca aca gtg ctc caa aat ggg gta tca gag acc tag 1239
Thr Ser Thr Val Leu Gln Asn Gly Val Ser Glu Thr *
405 410

<210> 264
<211> 412
<212> PRT
<213> Homo sapiens

<400> 264
Met Ala Leu Ala Leu Leu Ser Arg Leu Leu Pro Gly Ser Glu Tyr Leu
1 5 10 15

Thr His Glu Leu Leu Leu Ser Cys Val Phe Arg Leu Glu Phe Leu Pro
20 25 30

Glu Arg Thr Ser Gly Gly Pro Glu Ala Ala Asp Phe Ser Asp Gln Leu
35 40 45

Ser Leu Gly Ser Ser Arg Val Pro Arg Cys Gly Gln Gly Thr Leu Leu
50 55 60

Ala Gln Ala Cys Gln Asp Leu Pro Ser Ile Arg Asn Cys Tyr Leu Thr
65 70 75 80

His Cys Ser Pro Ala Arg Ala Ser Leu Leu Ala Ser Gln Ala Leu His
85 90 95

Arg Gly Glu Leu Gln Arg Val Pro Thr Leu Leu Leu Pro Met Pro Thr
100 105 110

Glu Pro Leu Leu Pro Thr Asp Trp Pro Phe Leu Pro Leu Ile Arg Leu
115 120 125

Tyr His Arg Ala Ser Asp Thr Pro Ser Gly Leu Ser Pro Thr Asp Thr
130 135 140

Met Gly Thr Ala Met Arg Val Leu Gln Trp Val Leu Val Leu Glu Ser
145 150 155 160

Trp Arg Pro Gln Ala Leu Trp Ala Val Pro Pro Ala Ala Arg Leu Ala
165 170 175

Arg Leu Met Cys Val Phe Leu Val Asp Ser Glu Leu Phe Arg Glu Ser
180 185 190

Pro Val Gln His Leu Val Ala Ala Leu Leu Ala Gln Leu Cys Gln Pro
195 200 205

Gln Val Leu Pro Asn Leu Asn Leu Asp Cys Arg Leu Pro Gly Leu Thr
210 215 220

Ser Phe Pro Asp Leu Tyr Ala Asn Phe Leu Asp His Phe Glu Ala Val
225 230 235 240

Ser Phe Gly Asp His Leu Phe Gly Ala Leu Val Leu Leu Pro Leu Gln
245 250 255

Arg Arg Phe Ser Val Thr Leu Arg Leu Ala Leu Phe Gly Glu His Val
260 265 270

Gly Ala Leu Arg Ala Leu Ser Leu Pro Leu Thr Gln Leu Pro Val Ser
275 280 285

Leu Glu Cys Tyr Thr Val Pro Pro Glu Asp Asn Leu Ala Leu Leu Gln
290 295 300

Leu Tyr Phe Arg Thr Leu Val Thr Gly Ala Leu Arg Pro Arg Trp Cys
305 310 315 320

Pro Val Leu Tyr Ala Val Ala Val Ala His Val Asn Ser Phe Ile Phe
325 330 335

Ser Gln Asp Pro Gln Ser Ser Asp Glu Val Lys Ala Ala Arg Arg Ser
340 345 350

Met Leu Gln Lys Thr Trp Leu Leu Ala Asp Glu Gly Leu Arg Gln His
355 360 365

Leu Leu His Tyr Lys Leu Pro Asn Ser Thr Leu Pro Glu Gly Phe Glu
370 375 380
Leu Tyr Ser Gln Leu Pro Pro Leu Arg Gln His Tyr Leu Gln Arg Leu
385 390 395 400
Thr Ser Thr Val Leu Gln Asn Gly Val Ser Glu Thr
405 410

<210> 265
<211> 576
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(576)

<400> 265
atg gcg ggc gct gca gaa gat gcg cga gct ctt ttc cgg gct ggg gtc 48
Met Ala Gly Ala Ala Glu Asp Ala Arg Ala Leu Phe Arg Ala Gly Val
1 5 10 15

tgc gcg gcc ctg gag gcc tgg ccg gcc ttg cag atc gct gtg gag aat 96
Cys Ala Ala Leu Glu Ala Trp Pro Ala Leu Gln Ile Ala Val Glu Asn
20 25 30

ggc ttc ggg ggt gtg cac agc cag gag aag gcc aag tgg ctg ggg ggt 144
Gly Phe Gly Gly Val His Ser Gln Glu Lys Ala Lys Trp Leu Gly Gly
35 40 45

gca gtg gag gat tac ttc atg cgc aat gct gac ttg gag cta gat gag 192
Ala Val Glu Asp Tyr Phe Met Arg Asn Ala Asp Leu Glu Leu Asp Glu
50 55 60

gtg gaa gac ttc ctt gga gag ctg ttg acc aac gag ttt gat aca gtt 240
Val Glu Asp Phe Leu Gly Glu Leu Leu Thr Asn Glu Phe Asp Thr Val
65 70 75 80

gtg gaa gac ggg agt ctg ccc cag gtg agc cag caa ctg cag acc atg 288
Val Glu Asp Gly Ser Leu Pro Gln Val Ser Gln Gln Leu Gln Thr Met
85 90 95

ttc cac cac ttc cag agg ggt gat ggg gct gct ctg agg gag atg gcc 336
Phe His His Phe Gln Arg Gly Asp Gly Ala Ala Leu Arg Glu Met Ala
100 105 110

tcc tgc atc act cag aga aaa tgc aag gtc aca gcc act gca ctt aag 384
Ser Cys Ile Thr Gln Arg Lys Cys Lys Val Thr Ala Thr Ala Leu Lys
115 120 125

aca gct aga gag act gat gag gat gaa gat gat gtg gac agt gtg gaa 432
Thr Ala Arg Glu Thr Asp Glu Asp Glu Asp Asp Val Asp Ser Val Glu
130 135 140

gag atg gag gtc aca gct acg aat gat ggg gct gct aca gat ggg gtc 480
Glu Met Glu Val Thr Ala Thr Asn Asp Gly Ala Ala Thr Asp Gly Val
145 150 155 160

tgc ccc cag cct gaa ccc tct gat cca gac gct cag act att aag gaa 528
Cys Pro Gln Pro Glu Pro Ser Asp Pro Asp Ala Gln Thr Ile Lys Glu
165 170 175

gag gat ata gtg gaa gat ggc tgg acc att gtc cgg aga aaa aaa tga 576
Glu Asp Ile Val Glu Asp Gly Trp Thr Ile Val Arg Arg Lys Lys *
180 185 190

<210> 266
<211> 191
<212> PRT
<213> Homo sapiens

<400> 266
Met Ala Gly Ala Ala Glu Asp Ala Arg Ala Leu Phe Arg Ala Gly Val
1 5 10 15
Cys Ala Ala Leu Glu Ala Trp Pro Ala Leu Gln Ile Ala Val Glu Asn
20 25 30
Gly Phe Gly Gly Val His Ser Gln Glu Lys Ala Lys Trp Leu Gly Gly
35 40 45
Ala Val Glu Asp Tyr Phe Met Arg Asn Ala Asp Leu Glu Leu Asp Glu
50 55 60
Val Glu Asp Phe Leu Gly Glu Leu Leu Thr Asn Glu Phe Asp Thr Val
65 70 75 80
Val Glu Asp Gly Ser Leu Pro Gln Val Ser Gln Gln Leu Gln Thr Met
85 90 95
Phe His His Phe Gln Arg Gly Asp Gly Ala Ala Leu Arg Glu Met Ala
100 105 110
Ser Cys Ile Thr Gln Arg Lys Cys Lys Val Thr Ala Thr Ala Leu Lys
115 120 125

Thr Ala Arg Glu Thr Asp Glu Asp Glu Asp Asp Val Asp Ser Val Glu
130 135 140
Glu Met Glu Val Thr Ala Thr Asn Asp Gly Ala Ala Thr Asp Gly Val
145 150 155 160
Cys Pro Gln Pro Glu Pro Ser Asp Pro Asp Ala Gln Thr Ile Lys Glu
165 170 175
Glu Asp Ile Val Glu Asp Gly Trp Thr Ile Val Arg Arg Lys Lys
180 185 190

<210> 267
<211> 567
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(567)

<400> 267
atg gtc ccc ggc gcc gcg ggc tgg tgt tgt ctc gtg ctc tgg ctc ccc 48
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro
1 5 10 15

gcg tgc gtc gcg gcc cac ggc ttc cgt atc cat gat tat ttg tac ttt 96
Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe
20 25 30

caa gtg ctg agt cct ggg gac att cga tac atc ttc aca gcc aca cct 144
Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro
35 40 45

gcc aag gac ttt ggt ggt atc ttt cac aca agg tat gag cag att cac 192
Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His
50 55 60

ctt gtc ccc gct gaa cct cca gag gcc tgc ggg gaa ctc agc aac ggt 240
Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly
65 70 75 80

ttc ttc atc cag gac cag att gct ctg gtg gag agg ggg ggc tgc tcc 288
Phe Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Gly Cys Ser
85 90 95

ttc ctc tcc aag act cgg gtg gtc cag gag cac ggc ggg cgg gcg gtg 336

```
Phe Leu Ser Lys Thr Arg Val Val Gln Glu His Gly Gly Arg Ala Val
            100                 105                 110

atc atc tct gac aac gca gtt gac aat gac agc ttc tac gtg gag atg       384
Ile Ile Ser Asp Asn Ala Val Asp Asn Asp Ser Phe Tyr Val Glu Met
        115                 120                 125

atc cag gac agt acc cag cgc aca gct gac atc ccc gcc ctc ttc ctg       432
Ile Gln Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu
    130                 135                 140

ctc ggc cga gac ggc tac atg atc cgc cgc tct ctg gaa cag cat ggg       480
Leu Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly
145                 150                 155                 160

ctg cca tgg gcc atc att tcc atc cca gtc aat gtc acc agc atc ccc       528
Leu Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro
                165                 170                 175

acc ttt gag ctg ctg caa ccg ccc tgg acc ttc tgg tag                   567
Thr Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp  *
            180                 185


      <210> 268
      <211> 188
      <212> PRT
      <213> Homo sapiens

      <400> 268
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro
 1               5                  10                  15
Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe
            20                  25                  30
Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro
        35                  40                  45
Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His
    50                  55                  60
Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly
65                  70                  75                  80
Phe Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Gly Cys Ser
                85                  90                  95
Phe Leu Ser Lys Thr Arg Val Val Gln Glu His Gly Gly Arg Ala Val
            100                 105                 110
```

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Ile Ile Ser Asp Asn Ala Val Asp Asn Asp Ser Phe Tyr Val Glu Met
        115                 120                 125
Ile Gln Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu
    130                 135                 140
Leu Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly
145                 150                 155                 160
Leu Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro
                165                 170                 175
Thr Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp
            180                 185

      <210> 269
      <211> 1419
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(1419)

      <400> 269
atg gtg ctg gcc tcg gcg ctg ctg tgt gtg att gtg tct gtt ctg acc      48
Met Val Leu Ala Ser Ala Leu Leu Cys Val Ile Val Ser Val Leu Thr
 1               5                  10                  15

aac gtg ctc gtg ggt gga aac acc cca agg aag aac ccc atg cat ccc      96
Asn Val Leu Val Gly Gly Asn Thr Pro Arg Lys Asn Pro Met His Pro
            20                  25                  30

agc tca agg tgg tca gag cta gac ctt ctt att ctg ttg ggg acg gcg     144
Ser Ser Arg Trp Ser Glu Leu Asp Leu Leu Ile Leu Leu Gly Thr Ala
        35                  40                  45

ggc cac gtc ttg agc ctg ggc gcc agc agc ttc gtg gag gag gag cac     192
Gly His Val Leu Ser Leu Gly Ala Ser Ser Phe Val Glu Glu Glu His
    50                  55                  60

cag acc tgg tac ttc ctt gtg aac acc ctg tgt cta gct ctg agc caa     240
Gln Thr Trp Tyr Phe Leu Val Asn Thr Leu Cys Leu Ala Leu Ser Gln
65                  70                  75                  80

gaa acc tac aga aac tac ttt ctg gga gat gac ggt gag cct ccg tgt     288
Glu Thr Tyr Arg Asn Tyr Phe Leu Gly Asp Asp Gly Glu Pro Pro Cys
                85                  90                  95
```

ggc ctc tgt gtg gaa caa ggg cat gac ggg gcc aca gca gcg tgg cag 336
Gly Leu Cys Val Glu Gln Gly His Asp Gly Ala Thr Ala Ala Trp Gln
100 105 110

gac ggg cct ggc tgt gat gtc ctg gag cga gac aaa ggc cac gga agc 384
Asp Gly Pro Gly Cys Asp Val Leu Glu Arg Asp Lys Gly His Gly Ser
115 120 125

ccc tct acc tcc gaa gtg ctc aga ggc cgc gag aag tgg atg gtg ctg 432
Pro Ser Thr Ser Glu Val Leu Arg Gly Arg Glu Lys Trp Met Val Leu
130 135 140

gcc agt ccg tgg cta ata ctg gcc tgc tgc cgg ctg ctg cgc tcc cta 480
Ala Ser Pro Trp Leu Ile Leu Ala Cys Cys Arg Leu Leu Arg Ser Leu
145 150 155 160

aac cag aca ggt gtg cag tgg gct cac cgg cct gac ctc ggc cac tgg 528
Asn Gln Thr Gly Val Gln Trp Ala His Arg Pro Asp Leu Gly His Trp
165 170 175

ctc acc agc tct gac cac aaa gcc gag ctc tct gtc ctg gct gcc ctc 576
Leu Thr Ser Ser Asp His Lys Ala Glu Leu Ser Val Leu Ala Ala Leu
180 185 190

tcc ctc ctc gta gtt ttt gtg ctg gtg cag agg ggg tgc tcc cct gtg 624
Ser Leu Leu Val Val Phe Val Leu Val Gln Arg Gly Cys Ser Pro Val
195 200 205

tcc aag gct gcc ctg gcg ctg ggg ctg ctg ggc gtc tac tgc tac cgg 672
Ser Lys Ala Ala Leu Ala Leu Gly Leu Leu Gly Val Tyr Cys Tyr Arg
210 215 220

gcg gcc atc ggg agt gtc cgg ttc ccg tgg cgg ccg gac agc aag gac 720
Ala Ala Ile Gly Ser Val Arg Phe Pro Trp Arg Pro Asp Ser Lys Asp
225 230 235 240

att tcc aag ggt att att gaa gct cgt ttt gtt tat gtc ttt gtc ctt 768
Ile Ser Lys Gly Ile Ile Glu Ala Arg Phe Val Tyr Val Phe Val Leu
245 250 255

ggc att ctg ttc acg ggc acc aaa gac tta ctt aaa tct caa gtc att 816
Gly Ile Leu Phe Thr Gly Thr Lys Asp Leu Leu Lys Ser Gln Val Ile
260 265 270

gct gca gac ttc aaa ctc aag act gta ggt tta tgg gag ata tat agt 864
Ala Ala Asp Phe Lys Leu Lys Thr Val Gly Leu Trp Glu Ile Tyr Ser
275 280 285

gga tta gtt ctt ctg gca gcc ttg ctc ttt aga cca cat aat ctt ccg 912
Gly Leu Val Leu Leu Ala Ala Leu Leu Phe Arg Pro His Asn Leu Pro
290 295 300

gtc tta gca ttt agc ctc ttg att cag act cta atg act aaa ttc atc 960
Val Leu Ala Phe Ser Leu Leu Ile Gln Thr Leu Met Thr Lys Phe Ile
305 310 315 320

tgg aag ccc ctg aga cac gat gca gct gag att act gtg atg cat tat 1008
Trp Lys Pro Leu Arg His Asp Ala Ala Glu Ile Thr Val Met His Tyr
325 330 335

tgg ttt ggt caa gca ttc ttc tat ttt cag ggc aac tcc aac aac att 1056
Trp Phe Gly Gln Ala Phe Phe Tyr Phe Gln Gly Asn Ser Asn Asn Ile
340 345 350

gcc acc gtg gac atc tcc gca ggc ttc gtg ggc tta gac acc tac gtg 1104
Ala Thr Val Asp Ile Ser Ala Gly Phe Val Gly Leu Asp Thr Tyr Val
355 360 365

gaa atc cca gcc gtg ctc ctg aca gcg ttt ggg acg tac gca ggg cct 1152
Glu Ile Pro Ala Val Leu Leu Thr Ala Phe Gly Thr Tyr Ala Gly Pro
370 375 380

gtg ctg tgg gcc agc cac tta gtg cac ttc ctg agc tca gaa aca cgc 1200
Val Leu Trp Ala Ser His Leu Val His Phe Leu Ser Ser Glu Thr Arg
385 390 395 400

agt ggt tca gca ctg agt cat gct tgc ttc tgc tac gca ctg att tgt 1248
Ser Gly Ser Ala Leu Ser His Ala Cys Phe Cys Tyr Ala Leu Ile Cys
405 410 415

tct att cca gtt ttc acg tac atc gtt ttg gtg aca tct ctg cgt tat 1296
Ser Ile Pro Val Phe Thr Tyr Ile Val Leu Val Thr Ser Leu Arg Tyr
420 425 430

cat tta ttt ata tgg agt gta ttt tct cca aaa ctt ctc tac gag gga 1344
His Leu Phe Ile Trp Ser Val Phe Ser Pro Lys Leu Leu Tyr Glu Gly
435 440 445

atg cac ctg ctc att aca gct gct gtc tgt gta ttc ttc acg gca atg 1392
Met His Leu Leu Ile Thr Ala Ala Val Cys Val Phe Phe Thr Ala Met
450 455 460

gat caa acc aga ctc aca cag tct tag 1419
Asp Gln Thr Arg Leu Thr Gln Ser *
465 470

<210> 270
<211> 472
<212> PRT
<213> Homo sapiens

<400> 270
Met Val Leu Ala Ser Ala Leu Leu Cys Val Ile Val Ser Val Leu Thr
1 5 10 15
Asn Val Leu Val Gly Gly Asn Thr Pro Arg Lys Asn Pro Met His Pro
20 25 30
Ser Ser Arg Trp Ser Glu Leu Asp Leu Leu Ile Leu Leu Gly Thr Ala
35 40 45
Gly His Val Leu Ser Leu Gly Ala Ser Ser Phe Val Glu Glu Glu His
50 55 60
Gln Thr Trp Tyr Phe Leu Val Asn Thr Leu Cys Leu Ala Leu Ser Gln
65 70 75 80
Glu Thr Tyr Arg Asn Tyr Phe Leu Gly Asp Asp Gly Glu Pro Pro Cys
85 90 95
Gly Leu Cys Val Glu Gln Gly His Asp Gly Ala Thr Ala Ala Trp Gln
100 105 110
Asp Gly Pro Gly Cys Asp Val Leu Glu Arg Asp Lys Gly His Gly Ser
115 120 125
Pro Ser Thr Ser Glu Val Leu Arg Gly Arg Glu Lys Trp Met Val Leu
130 135 140
Ala Ser Pro Trp Leu Ile Leu Ala Cys Cys Arg Leu Leu Arg Ser Leu
145 150 155 160
Asn Gln Thr Gly Val Gln Trp Ala His Arg Pro Asp Leu Gly His Trp
165 170 175
Leu Thr Ser Ser Asp His Lys Ala Glu Leu Ser Val Leu Ala Ala Leu
180 185 190
Ser Leu Leu Val Val Phe Val Leu Val Gln Arg Gly Cys Ser Pro Val
195 200 205
Ser Lys Ala Ala Leu Ala Leu Gly Leu Leu Gly Val Tyr Cys Tyr Arg
210 215 220

Ala Ala Ile Gly Ser Val Arg Phe Pro Trp Arg Pro Asp Ser Lys Asp
225 230 235 240
Ile Ser Lys Gly Ile Ile Glu Ala Arg Phe Val Tyr Val Phe Val Leu
245 250 255
Gly Ile Leu Phe Thr Gly Thr Lys Asp Leu Leu Lys Ser Gln Val Ile
260 265 270
Ala Ala Asp Phe Lys Leu Lys Thr Val Gly Leu Trp Glu Ile Tyr Ser
275 280 285
Gly Leu Val Leu Leu Ala Ala Leu Leu Phe Arg Pro His Asn Leu Pro
290 295 300
Val Leu Ala Phe Ser Leu Leu Ile Gln Thr Leu Met Thr Lys Phe Ile
305 310 315 320
Trp Lys Pro Leu Arg His Asp Ala Ala Glu Ile Thr Val Met His Tyr
325 330 335
Trp Phe Gly Gln Ala Phe Phe Tyr Phe Gln Gly Asn Ser Asn Asn Ile
340 345 350
Ala Thr Val Asp Ile Ser Ala Gly Phe Val Gly Leu Asp Thr Tyr Val
355 360 365
Glu Ile Pro Ala Val Leu Leu Thr Ala Phe Gly Thr Tyr Ala Gly Pro
370 375 380
Val Leu Trp Ala Ser His Leu Val His Phe Leu Ser Ser Glu Thr Arg
385 390 395 400
Ser Gly Ser Ala Leu Ser His Ala Cys Phe Cys Tyr Ala Leu Ile Cys
405 410 415
Ser Ile Pro Val Phe Thr Tyr Ile Val Leu Val Thr Ser Leu Arg Tyr
420 425 430
His Leu Phe Ile Trp Ser Val Phe Ser Pro Lys Leu Leu Tyr Glu Gly
435 440 445
Met His Leu Leu Ile Thr Ala Ala Val Cys Val Phe Phe Thr Ala Met
450 455 460
Asp Gln Thr Arg Leu Thr Gln Ser
465 470

<210> 271
<211> 1089
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1089)

<221> misc_feature
<222> (1)...(1089)

<223> n = A,T,C or G

<400> 271

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atg gac agc ccc gag gtg acc ttc act ctc gcc tat ctg gtg ttc gcc      48
Met Asp Ser Pro Glu Val Thr Phe Thr Leu Ala Tyr Leu Val Phe Ala
 1               5                  10                  15

gtg tgc ttc gtg ttc acg ccc aac gag ttc cac gcg gcg ggg ctc acg      96
Val Cys Phe Val Phe Thr Pro Asn Glu Phe His Ala Ala Gly Leu Thr
            20                  25                  30

gtg cag aac ctg ctg tcg ggc tgg ctg ggc agc gag gac gcc gcc ttc     144
Val Gln Asn Leu Leu Ser Gly Trp Leu Gly Ser Glu Asp Ala Ala Phe
        35                  40                  45

gtg ccc ttc cac ttg cgc cgc acg gcc gcc acg ctg ttg tgc cac tcg     192
Val Pro Phe His Leu Arg Arg Thr Ala Ala Thr Leu Leu Cys His Ser
    50                  55                  60

ctg ctg ccg ctc ggc tac tat gtg ggc atg tgc ctt gcg gct tca gaa     240
Leu Leu Pro Leu Gly Tyr Tyr Val Gly Met Cys Leu Ala Ala Ser Glu
65                  70                  75                  80

aag cgg ctc cac gcc ctc agc cag gcc cct gag gcc tgg cgg ctc ttc     288
Lys Arg Leu His Ala Leu Ser Gln Ala Pro Glu Ala Trp Arg Leu Phe
                85                  90                  95

ctg ctg ctg gcc gtg acc ctc ccc tcc atc gcc tgc atc ctg atc tac     336
Leu Leu Leu Ala Val Thr Leu Pro Ser Ile Ala Cys Ile Leu Ile Tyr
            100                 105                 110

tac tgg tcc cgt gac cgg tgg gcc tgc cac cca ctg gcg cgc acc ctg     384
Tyr Trp Ser Arg Asp Arg Trp Ala Cys His Pro Leu Ala Arg Thr Leu
        115                 120                 125

gcc ctc tac gcc ctc cca cag tct ggc tgg cag gct gtt gcc tcc tct     432
Ala Leu Tyr Ala Leu Pro Gln Ser Gly Trp Gln Ala Val Ala Ser Ser
    130                 135                 140

gtc aac act gag ttc cgg cgg att gac aag ttt gcc acc ggt gca cca     480
Val Asn Thr Glu Phe Arg Arg Ile Asp Lys Phe Ala Thr Gly Ala Pro
145                 150                 155                 160

ggt gcc cgt gtg att gtg aca gac acg tgg gtg atg aag gta acc acc     528
```

Gly Ala Arg Val Ile Val Thr Asp Thr Trp Val Met Lys Val Thr Thr
165 170 175

tac cga gtg cac gtg gcc cag cag cag gac gtg cac ctg act gtg acg 576
Tyr Arg Val His Val Ala Gln Gln Gln Asp Val His Leu Thr Val Thr
180 185 190

gag tct cgg cag cat gag ctc tcg cca gac tcg aac ttg ccc gtg cag 624
Glu Ser Arg Gln His Glu Leu Ser Pro Asp Ser Asn Leu Pro Val Gln
195 200 205

ctc ctc acc atc cgt gtg gcc agc acc aac cct gct gtg cag gcc ttt 672
Leu Leu Thr Ile Arg Val Ala Ser Thr Asn Pro Ala Val Gln Ala Phe
210 215 220

gac atc tgg ctg aac tcc act gag tac ggg gag ctc tgc gag aag ctc 720
Asp Ile Trp Leu Asn Ser Thr Glu Tyr Gly Glu Leu Cys Glu Lys Leu
225 230 235 240

cgg gca ccc atc cgc agg gca gcc cat gtg gtc atc cac cag agc ctg 768
Arg Ala Pro Ile Arg Arg Ala Ala His Val Val Ile His Gln Ser Leu
245 250 255

ggc gac ctg ttc ctg gag acn ttt gcc tcc ctg gta gag gtc aac ccg 816
Gly Asp Leu Phe Leu Glu Xaa Phe Ala Ser Leu Val Glu Val Asn Pro
260 265 270

gcc tac tca gtg ccc agc agc cag gag ctg gag gcc tgc ata ggc tgc 864
Ala Tyr Ser Val Pro Ser Ser Gln Glu Leu Glu Ala Cys Ile Gly Cys
275 280 285

atg cag aca cgt gcc agc gtg aag ctg gtg aag acc tgc cag gag gca 912
Met Gln Thr Arg Ala Ser Val Lys Leu Val Lys Thr Cys Gln Glu Ala
290 295 300

gcc aca ggc gag tgc cag cag tgt tac tgc cgc ccc atg tgg tgc ctc 960
Ala Thr Gly Glu Cys Gln Gln Cys Tyr Cys Arg Pro Met Trp Cys Leu
305 310 315 320

acc tgc atg ggc aag tgg ttc gcc agc cgc cag gac ccc ctg cgc cct 1008
Thr Cys Met Gly Lys Trp Phe Ala Ser Arg Gln Asp Pro Leu Arg Pro
325 330 335

gac acc tgg ctg gcc agc cgc gtg ccc tgc ccc acc tgc cgc gca cgc 1056

Asp Thr Trp Leu Ala Ser Arg Val Pro Cys Pro Thr Cys Arg Ala Arg
340 345 350

ttc tgc atc ctg gat gtg tgc acc gtg cgc tga 1089
Phe Cys Ile Leu Asp Val Cys Thr Val Arg *
355 360

<210> 272
<211> 362
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(362)
<223> Xaa = Any Amino Acid

<400> 272
Met Asp Ser Pro Glu Val Thr Phe Thr Leu Ala Tyr Leu Val Phe Ala
1 5 10 15
Val Cys Phe Val Phe Thr Pro Asn Glu Phe His Ala Ala Gly Leu Thr
20 25 30
Val Gln Asn Leu Leu Ser Gly Trp Leu Gly Ser Glu Asp Ala Ala Phe
35 40 45
Val Pro Phe His Leu Arg Arg Thr Ala Ala Thr Leu Leu Cys His Ser
50 55 60
Leu Leu Pro Leu Gly Tyr Tyr Val Gly Met Cys Leu Ala Ala Ser Glu
65 70 75 80
Lys Arg Leu His Ala Leu Ser Gln Ala Pro Glu Ala Trp Arg Leu Phe
85 90 95
Leu Leu Leu Ala Val Thr Leu Pro Ser Ile Ala Cys Ile Leu Ile Tyr
100 105 110
Tyr Trp Ser Arg Asp Arg Trp Ala Cys His Pro Leu Ala Arg Thr Leu
115 120 125
Ala Leu Tyr Ala Leu Pro Gln Ser Gly Trp Gln Ala Val Ala Ser Ser
130 135 140
Val Asn Thr Glu Phe Arg Arg Ile Asp Lys Phe Ala Thr Gly Ala Pro
145 150 155 160
Gly Ala Arg Val Ile Val Thr Asp Thr Trp Val Met Lys Val Thr Thr
165 170 175
Tyr Arg Val His Val Ala Gln Gln Gln Asp Val His Leu Thr Val Thr
180 185 190
Glu Ser Arg Gln His Glu Leu Ser Pro Asp Ser Asn Leu Pro Val Gln

195 200 205
Leu Leu Thr Ile Arg Val Ala Ser Thr Asn Pro Ala Val Gln Ala Phe
210 215 220
Asp Ile Trp Leu Asn Ser Thr Glu Tyr Gly Glu Leu Cys Glu Lys Leu
225 230 235 240
Arg Ala Pro Ile Arg Arg Ala Ala His Val Val Ile His Gln Ser Leu
245 250 255
Gly Asp Leu Phe Leu Glu Xaa Phe Ala Ser Leu Val Glu Val Asn Pro
260 265 270
Ala Tyr Ser Val Pro Ser Ser Gln Glu Leu Glu Ala Cys Ile Gly Cys
275 280 285
Met Gln Thr Arg Ala Ser Val Lys Leu Val Lys Thr Cys Gln Glu Ala
290 295 300
Ala Thr Gly Glu Cys Gln Gln Cys Tyr Cys Arg Pro Met Trp Cys Leu
305 310 315 320
Thr Cys Met Gly Lys Trp Phe Ala Ser Arg Gln Asp Pro Leu Arg Pro
325 330 335
Asp Thr Trp Leu Ala Ser Arg Val Pro Cys Pro Thr Cys Arg Ala Arg
340 345 350
Phe Cys Ile Leu Asp Val Cys Thr Val Arg
355 360

<210> 273
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(723)

<400> 273
atg tcc cct ttg ctc ttt ggg gct ggg ctg gtc gtt ctg aat cta gtg 48
Met Ser Pro Leu Leu Phe Gly Ala Gly Leu Val Val Leu Asn Leu Val
1 5 10 15

acg tct gcc agg agc cag aag aca gaa cct cta agt ggc tct ggg gac 96
Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu Ser Gly Ser Gly Asp
20 25 30

cag cca ctc ttc cgt gga gct gat cga tat gac ttt gcc atc atg ata 144
Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp Phe Ala Ile Met Ile
35 40 45

```
cct cca gga ggc acg gaa tgc ttt tgg caa ttt gcc cac cag act gga      192
Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe Ala His Gln Thr Gly
     50                  55                  60

tac ttc tat ttc agt tac gag gtt cag cgg aca gtg ggg atg tca cat      240
Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr Val Gly Met Ser His
 65                  70                  75                  80

gac cgg cat gtt gct gcc acg gca cat aac cca cag gga ttt ctc ata      288
Asp Arg His Val Ala Ala Thr Ala His Asn Pro Gln Gly Phe Leu Ile
                 85                  90                  95

gac acc tcc cag ggt gtt cgg ggc cag att aac ttc tct acc caa gag      336
Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn Phe Ser Thr Gln Glu
            100                 105                 110

aca ggt ttt tat cag ctt tgt cta agt aat cag cat aat cac ttc ggt      384
Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln His Asn His Phe Gly
        115                 120                 125

tct gtg caa gtg tac ctc aac ttt ggg gtc ttc tat gag ggg cct gag      432
Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe Tyr Glu Gly Pro Glu
    130                 135                 140

act gat cac aaa cag aag gaa aga aaa caa ctg aat gat act ctg gat      480
Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu Asn Asp Thr Leu Asp
145                 150                 155                 160

gca att gag gac ggc aca caa aag gtg cag aac aat atc ttt cac atg      528
Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn Asn Ile Phe His Met
                165                 170                 175

tgg cga tac tac aac ttt gcc cgg atg agg aaa atg gct gac ttt ttc      576
Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys Met Ala Asp Phe Phe
            180                 185                 190

ctt atc caa tca aac tat aac tac gtg aac tgg tgg tcg aca gcc cag      624
Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp Trp Ser Thr Ala Gln
        195                 200                 205

agc ctt gtt att att ctt tct ggg atc ctg caa ctg tat ttc ttg aag      672
Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln Leu Tyr Phe Leu Lys
    210                 215                 220
```

```
cgt ctc ttc aat gtt cca aca act aca gat aca aag aag cca aga tgc      720
Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr Lys Lys Pro Arg Cys
225                 230                 235                 240

taa                                                                  723
 *
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<210> 274
<211> 240
<212> PRT
<213> Homo sapiens

<400> 274

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Met Ser Pro Leu Leu Phe Gly Ala Gly Leu Val Val Leu Asn Leu Val
 1               5                  10                  15
Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu Ser Gly Ser Gly Asp
            20                  25                  30
Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp Phe Ala Ile Met Ile
        35                  40                  45
Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe Ala His Gln Thr Gly
    50                  55                  60
Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr Val Gly Met Ser His
65                  70                  75                  80
Asp Arg His Val Ala Ala Thr Ala His Asn Pro Gln Gly Phe Leu Ile
                85                  90                  95
Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn Phe Ser Thr Gln Glu
            100                 105                 110
Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln His Asn His Phe Gly
        115                 120                 125
Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe Tyr Glu Gly Pro Glu
    130                 135                 140
Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu Asn Asp Thr Leu Asp
145                 150                 155                 160
Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn Asn Ile Phe His Met
                165                 170                 175
Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys Met Ala Asp Phe Phe
            180                 185                 190
Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp Trp Ser Thr Ala Gln
        195                 200                 205
Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln Leu Tyr Phe Leu Lys
    210                 215                 220
Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr Lys Lys Pro Arg Cys
```

225 230 235 240

<210> 275
<211> 993
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(993)

<221> misc_feature
<222> (1)...(993)
<223> n = A,T,C or G

<400> 275
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atg gct gag cac gca ggg ccc cga ctc ccc ctg gtg ctg aag acg ctg      48
Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1               5                  10                  15

gca tgc aca cac agc agt gcg tat gag aac cag agg gtg acc acc acc      96
Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr
            20                  25                  30

gcc ttc ctg gcc gag ctg ctg aac agc aac gtg gcc aac gac ctc atg     144
Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
        35                  40                  45

ctc ttg gac tcg ctg ctg gag agc ctg gcg gct cgc cag aag gac aca     192
Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
    50                  55                  60

tgc gcc anc gtg cgg agg ctg gtg ctc cgc ggc ctg gcc aac ctg gcc     240
Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
65                  70                  75                  80

tcc ggc tgc cct gac aag gtg cga acc cac ggc ccc cag ctc ctc aca     288
Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
                85                  90                  95

gcc atg att ggc ggg ctg gac gac ggg gac aac cct cac agc cca gtg     336
Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
            100                 105                 110
```

gcc ctg gag gcc atg ctg ggc ctt gcg agg ctg gtg cac ctg gtg gag 384
Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
115 120 125

tcc tgg gac ctg cgc tca ggg ctg ctg cac gtg gcc atc cgc atc cgg 432
Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
130 135 140

cct ttc ttc gac agt gag aag atg gag ttc cgg acg gca tct atc cgc 480
Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
145 150 155 160

ctc ttt ggg cac ctt aac aag gtc tgc cac gga gac tgt gag gac gtc 528
Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val
165 170 175

ttc ctg gac cag gtg gtg ggc ggg ctg gcg ccc ctg ctg ctg cac ctg 576
Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu
180 185 190

cag gac cct cag gcc acc gtg gcc agc gcc tgc agg ttt gcc ctg cgc 624
Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg
195 200 205

atg tgt ggc ccc aat ctg gca tgt gag gag ctc tca gct gct ttc cag 672
Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln
210 215 220

aaa cac ctg cag gag ggc cga gcc ctg cac ttc ggg gag ttc ctc aac 720
Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn
225 230 235 240

acc acc tgc aag cac ctg atg cac cat ttc cca gac ctg ctg ggc cgt 768
Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg
245 250 255

ctc ctg acc acc tgc ctg ttc tac ttc aag agc agc tgg gag aac gtc 816
Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val
260 265 270

cga gct gct gca ccc ctg ttc acc ggg ttc ctg gtg ctg cac tcg gag 864
Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu
275 280 285

```
ccc agg cag cag ccg cag gtg gac ctg gac cag ctc att gcg gcg ctc      912
Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Ala Leu
    290                 295                 300

cag atc ctg ctg aag gac ccg gcc ccc gag gtg cgg acg agg gct gct      960
Gln Ile Leu Leu Lys Asp Pro Ala Pro Glu Val Arg Thr Arg Ala Ala
305                 310                 315                 320

gag gcc ctg ggc cgc ctg gtg aag ctc gcc taa                          993
Glu Ala Leu Gly Arg Leu Val Lys Leu Ala  *
                325                 330
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<210> 276
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(330)
<223> Xaa = Any Amino Acid

<400> 276

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Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1               5                  10                  15
Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr
            20                  25                  30
Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
        35                  40                  45
Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
    50                  55                  60
Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
65                  70                  75                  80
Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
                85                  90                  95
Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
            100                 105                 110
Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
        115                 120                 125
Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
    130                 135                 140
Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
145                 150                 155                 160
```

Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val
165 170 175
Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu
180 185 190
Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg
195 200 205
Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln
210 215 220
Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn
225 230 235 240
Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg
245 250 255
Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val
260 265 270
Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu
275 280 285
Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Ala Leu
290 295 300
Gln Ile Leu Leu Lys Asp Pro Ala Pro Glu Val Arg Thr Arg Ala Ala
305 310 315 320
Glu Ala Leu Gly Arg Leu Val Lys Leu Ala
325 330

<210> 277
<211> 642
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(642)

<400> 277
atg gat caa caa ctg cgt ggg aag ccg gaa tta ttg gtc ttc ttc agc 48
Met Asp Gln Gln Leu Arg Gly Lys Pro Glu Leu Leu Val Phe Phe Ser
1 5 10 15

act gtg gcc tcg gcc aca gct ggc atg ctc tgc ctg atc gcc atc ctg 96
Thr Val Ala Ser Ala Thr Ala Gly Met Leu Cys Leu Ile Ala Ile Leu
20 25 30

ctg tat gtc ctc gtc cag tac ctc gtg aac ccc ggg gtg ctc cgc acg 144
Leu Tyr Val Leu Val Gln Tyr Leu Val Asn Pro Gly Val Leu Arg Thr
35 40 45

```
gac ccc aga gat gtc aag aat atg aac acg tgg ctg ctg ttc ctc ccc      192
Asp Pro Arg Asp Val Lys Asn Met Asn Thr Trp Leu Leu Phe Leu Pro
     50                  55                  60

ctg ttc ccg gtg cag gtg cag acc ctg ata gtc gtg atc atc ggg atg      240
Leu Phe Pro Val Gln Val Gln Thr Leu Ile Val Val Ile Ile Gly Met
 65                  70                  75                  80

ctc gtg ctc ctg ctg gac ttt ctt ggc ttg gtg cac ctg ggc cag ctg      288
Leu Val Leu Leu Leu Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu
                 85                  90                  95

ctc atc ttc cac atc tac ctg aag gcc aag aag atg acc acc ttt gag      336
Leu Ile Phe His Ile Tyr Leu Lys Ala Lys Lys Met Thr Thr Phe Glu
            100                 105                 110

tat ctc att aat aac cgc aaa gaa gag agt tca aaa cat caa gca gtg      384
Tyr Leu Ile Asn Asn Arg Lys Glu Glu Ser Ser Lys His Gln Ala Val
        115                 120                 125

agg aaa gat cca tac gtg caa atg gac aaa gga gtt ctc cag caa gga      432
Arg Lys Asp Pro Tyr Val Gln Met Asp Lys Gly Val Leu Gln Gln Gly
    130                 135                 140

gct ggc gcc ctg ggc tca tct gca cag gga gtc aaa gcc aag agc tcc      480
Ala Gly Ala Leu Gly Ser Ser Ala Gln Gly Val Lys Ala Lys Ser Ser
145                 150                 155                 160

ctg ctg att cac aag cac tta tgt cac ttc tgc act tca gta aac cag      528
Leu Leu Ile His Lys His Leu Cys His Phe Cys Thr Ser Val Asn Gln
                165                 170                 175

gac ggg gat tcg aag gca cag gaa gca gat gat gcc ccg agt aca tct      576
Asp Gly Asp Ser Lys Ala Gln Glu Ala Asp Asp Ala Pro Ser Thr Ser
            180                 185                 190

aca ctt ggg ctg caa caa gaa aca aca gag ccc atg aaa act gac agt      624
Thr Leu Gly Leu Gln Gln Glu Thr Thr Glu Pro Met Lys Thr Asp Ser
        195                 200                 205

gct gaa agt gaa gac tga                                              642
Ala Glu Ser Glu Asp  *
    210
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<210> 278
<211> 213
<212> PRT
<213> Homo sapiens

<400> 278
Met Asp Gln Gln Leu Arg Gly Lys Pro Glu Leu Leu Val Phe Phe Ser
1   5   10   15
Thr Val Ala Ser Ala Thr Ala Gly Met Leu Cys Leu Ile Ala Ile Leu
            20   25   30
Leu Tyr Val Leu Val Gln Tyr Leu Val Asn Pro Gly Val Leu Arg Thr
        35   40   45
Asp Pro Arg Asp Val Lys Asn Met Asn Thr Trp Leu Leu Phe Leu Pro
    50   55   60
Leu Phe Pro Val Gln Val Gln Thr Leu Ile Val Val Ile Ile Gly Met
65   70   75   80
Leu Val Leu Leu Leu Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu
                85   90   95
Leu Ile Phe His Ile Tyr Leu Lys Ala Lys Lys Met Thr Thr Phe Glu
            100   105   110
Tyr Leu Ile Asn Asn Arg Lys Glu Glu Ser Ser Lys His Gln Ala Val
        115   120   125
Arg Lys Asp Pro Tyr Val Gln Met Asp Lys Gly Val Leu Gln Gln Gly
    130   135   140
Ala Gly Ala Leu Gly Ser Ser Ala Gln Gly Val Lys Ala Lys Ser Ser
145   150   155   160
Leu Leu Ile His Lys His Leu Cys His Phe Cys Thr Ser Val Asn Gln
                165   170   175
Asp Gly Asp Ser Lys Ala Gln Glu Ala Asp Asp Ala Pro Ser Thr Ser
            180   185   190
Thr Leu Gly Leu Gln Gln Glu Thr Thr Glu Pro Met Lys Thr Asp Ser
        195   200   205
Ala Glu Ser Glu Asp
    210

<210> 279
<211> 1194
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1)...(1194)

<400> 279

atg agc tgg ctt ttt ccc ctg acc aag agc gcc tcc tcc tcc gcg gct 48
Met Ser Trp Leu Phe Pro Leu Thr Lys Ser Ala Ser Ser Ser Ala Ala
1 5 10 15

ggg tcc ccc ggt ggc ctc acc agc ctc cag cag cag aag cag cgc ctg 96
Gly Ser Pro Gly Gly Leu Thr Ser Leu Gln Gln Gln Lys Gln Arg Leu
20 25 30

atc gag tcc ctc cgg aac tca cac tcc agt ata gcc gaa ata cag aaa 144
Ile Glu Ser Leu Arg Asn Ser His Ser Ser Ile Ala Glu Ile Gln Lys
35 40 45

gat gtg gaa tac aga ttg cca ttc acc ata aac aac ctg aca att aac 192
Asp Val Glu Tyr Arg Leu Pro Phe Thr Ile Asn Asn Leu Thr Ile Asn
50 55 60

att aat ata ttg ctt cct cca cag ttt cct cag gaa aaa cca gtg atc 240
Ile Asn Ile Leu Leu Pro Pro Gln Phe Pro Gln Glu Lys Pro Val Ile
65 70 75 80

agt gtt tat cca cca ata cga cat cac tta atg gat aaa caa gga gtg 288
Ser Val Tyr Pro Pro Ile Arg His His Leu Met Asp Lys Gln Gly Val
85 90 95

tat gtt acc tct cca tta gta aac aat ttt aca atg cac tca gat ctt 336
Tyr Val Thr Ser Pro Leu Val Asn Asn Phe Thr Met His Ser Asp Leu
100 105 110

gga aaa att att cag agt ctg ttg gat gag ttt tgg aag aat cct cca 384
Gly Lys Ile Ile Gln Ser Leu Leu Asp Glu Phe Trp Lys Asn Pro Pro
115 120 125

gtt tta gct cct act tca aca gca ttt cct tat cta tac agt aac cca 432
Val Leu Ala Pro Thr Ser Thr Ala Phe Pro Tyr Leu Tyr Ser Asn Pro
130 135 140

agt ggg atg tct cct tat gct tct cag ggt ttt cca ttt ctt cct cca 480
Ser Gly Met Ser Pro Tyr Ala Ser Gln Gly Phe Pro Phe Leu Pro Pro
145 150 155 160

tat cct cca caa gaa gca aac agg agt atc act tct tta tct gtt gct 528

Tyr Pro Pro Gln Glu Ala Asn Arg Ser Ile Thr Ser Leu Ser Val Ala
165 170 175

gac act gtt tct tct tca aca aca agt cat acc aca gcc aag cct gcc 576
Asp Thr Val Ser Ser Ser Thr Thr Ser His Thr Thr Ala Lys Pro Ala
180 185 190

gct cct tca ttt ggt gtc ctt tca aat ctg cca tta ccc att ccc aca 624
Ala Pro Ser Phe Gly Val Leu Ser Asn Leu Pro Leu Pro Ile Pro Thr
195 200 205

gtg gat gct tca ata ccg aca agc caa aat ggt ttt ggg tac aag atg 672
Val Asp Ala Ser Ile Pro Thr Ser Gln Asn Gly Phe Gly Tyr Lys Met
210 215 220

cca gat gtc cct gat gca ttt cca gaa ctc tca gaa cta agt gtg tca 720
Pro Asp Val Pro Asp Ala Phe Pro Glu Leu Ser Glu Leu Ser Val Ser
225 230 235 240

caa ctc aca gat atg aat gaa caa gag gag gta tta cta gaa cag ttt 768
Gln Leu Thr Asp Met Asn Glu Gln Glu Glu Val Leu Leu Glu Gln Phe
245 250 255

ctg act ttg cct caa cta aaa caa att att acc gac aaa gat gac tta 816
Leu Thr Leu Pro Gln Leu Lys Gln Ile Ile Thr Asp Lys Asp Asp Leu
260 265 270

gta aaa agt att gag gaa cta gca aga aaa aat ctc ctt ttg gag ccc 864
Val Lys Ser Ile Glu Glu Leu Ala Arg Lys Asn Leu Leu Leu Glu Pro
275 280 285

agc ttg gaa gcc aaa aga caa act gtt tta gat aag tat gaa tta ctt 912
Ser Leu Glu Ala Lys Arg Gln Thr Val Leu Asp Lys Tyr Glu Leu Leu
290 295 300

aca cag atg aag tcc act ttc gaa aag aag atg caa agg cag cat gaa 960
Thr Gln Met Lys Ser Thr Phe Glu Lys Lys Met Gln Arg Gln His Glu
305 310 315 320

ctt agt gag agc tgt agt gca agt gcc ctt cag gca aga ttg aaa gta 1008
Leu Ser Glu Ser Cys Ser Ala Ser Ala Leu Gln Ala Arg Leu Lys Val
325 330 335

gct gca cat gaa gct gag gaa gaa tct gat aat att gca gaa gac ttc 1056

Ala Ala His Glu Ala Glu Glu Glu Ser Asp Asn Ile Ala Glu Asp Phe
340 345 350

ttg gag gga aag atg gaa ata gat gat ttt ctc agt agc ttc atg gaa 1104
Leu Glu Gly Lys Met Glu Ile Asp Asp Phe Leu Ser Ser Phe Met Glu
355 360 365

aag aga aca att tgc cac tgt aga aga gcc aag gaa gag aaa ctt cag 1152
Lys Arg Thr Ile Cys His Cys Arg Arg Ala Lys Glu Glu Lys Leu Gln
370 375 380

cag gcg ata gca atg cac agc caa ttt cat gct cca cta tag 1194
Gln Ala Ile Ala Met His Ser Gln Phe His Ala Pro Leu *
385 390 395

<210> 280
<211> 397
<212> PRT
<213> Homo sapiens

<400> 280
Met Ser Trp Leu Phe Pro Leu Thr Lys Ser Ala Ser Ser Ser Ala Ala
1 5 10 15
Gly Ser Pro Gly Gly Leu Thr Ser Leu Gln Gln Gln Lys Gln Arg Leu
20 25 30
Ile Glu Ser Leu Arg Asn Ser His Ser Ser Ile Ala Glu Ile Gln Lys
35 40 45
Asp Val Glu Tyr Arg Leu Pro Phe Thr Ile Asn Asn Leu Thr Ile Asn
50 55 60
Ile Asn Ile Leu Leu Pro Pro Gln Phe Pro Gln Glu Lys Pro Val Ile
65 70 75 80
Ser Val Tyr Pro Pro Ile Arg His His Leu Met Asp Lys Gln Gly Val
85 90 95
Tyr Val Thr Ser Pro Leu Val Asn Asn Phe Thr Met His Ser Asp Leu
100 105 110
Gly Lys Ile Ile Gln Ser Leu Leu Asp Glu Phe Trp Lys Asn Pro Pro
115 120 125
Val Leu Ala Pro Thr Ser Thr Ala Phe Pro Tyr Leu Tyr Ser Asn Pro
130 135 140
Ser Gly Met Ser Pro Tyr Ala Ser Gln Gly Phe Pro Phe Leu Pro Pro
145 150 155 160
Tyr Pro Pro Gln Glu Ala Asn Arg Ser Ile Thr Ser Leu Ser Val Ala
165 170 175

Asp Thr Val Ser Ser Ser Thr Thr Ser His Thr Thr Ala Lys Pro Ala
180 185 190
Ala Pro Ser Phe Gly Val Leu Ser Asn Leu Pro Leu Pro Ile Pro Thr
195 200 205
Val Asp Ala Ser Ile Pro Thr Ser Gln Asn Gly Phe Gly Tyr Lys Met
210 215 220
Pro Asp Val Pro Asp Ala Phe Pro Glu Leu Ser Glu Leu Ser Val Ser
225 230 235 240
Gln Leu Thr Asp Met Asn Glu Gln Glu Glu Val Leu Leu Glu Gln Phe
245 250 255
Leu Thr Leu Pro Gln Leu Lys Gln Ile Ile Thr Asp Lys Asp Asp Leu
260 265 270
Val Lys Ser Ile Glu Glu Leu Ala Arg Lys Asn Leu Leu Leu Glu Pro
275 280 285
Ser Leu Glu Ala Lys Arg Gln Thr Val Leu Asp Lys Tyr Glu Leu Leu
290 295 300
Thr Gln Met Lys Ser Thr Phe Glu Lys Lys Met Gln Arg Gln His Glu
305 310 315 320
Leu Ser Glu Ser Cys Ser Ala Ser Ala Leu Gln Ala Arg Leu Lys Val
325 330 335
Ala Ala His Glu Ala Glu Glu Glu Ser Asp Asn Ile Ala Glu Asp Phe
340 345 350
Leu Glu Gly Lys Met Glu Ile Asp Asp Phe Leu Ser Ser Phe Met Glu
355 360 365
Lys Arg Thr Ile Cys His Cys Arg Arg Ala Lys Glu Glu Lys Leu Gln
370 375 380
Gln Ala Ile Ala Met His Ser Gln Phe His Ala Pro Leu
385 390 395

<210> 281
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(579)

<400> 281
atg gcg gcg caa att cca att gtg gcc acc act tcc act ccc gga ata 48
Met Ala Ala Gln Ile Pro Ile Val Ala Thr Thr Ser Thr Pro Gly Ile
1 5 10 15

gtc cgg aac agc aag aag agg ccg gcc agc cct tcc cac aat ggc agc 96

```
Val Arg Asn Ser Lys Lys Arg Pro Ala Ser Pro Ser His Asn Gly Ser
            20                  25                  30

agc ggc ggg ggc tat ggc gcc agt aag aag aaa aaa gcg tcc gct tcc      144
Ser Gly Gly Gly Tyr Gly Ala Ser Lys Lys Lys Lys Ala Ser Ala Ser
        35                  40                  45

agc ttt gcg cag ggt atc agc atg gaa gcc atg agt gag aat aaa atg      192
Ser Phe Ala Gln Gly Ile Ser Met Glu Ala Met Ser Glu Asn Lys Met
    50                  55                  60

gtg ccc tct gag ttt agc aca gga cct gtg gaa aaa gct gcc aaa cct      240
Val Pro Ser Glu Phe Ser Thr Gly Pro Val Glu Lys Ala Ala Lys Pro
65                  70                  75                  80

ttg cca ttt aag gat ccc aac ttt gtg cac tct ggc cac ggt ggc gca      288
Leu Pro Phe Lys Asp Pro Asn Phe Val His Ser Gly His Gly Gly Ala
                85                  90                  95

gta gct ggc aag aag aac aga acc tgg aag aac ctg aaa caa atc ctc      336
Val Ala Gly Lys Lys Asn Arg Thr Trp Lys Asn Leu Lys Gln Ile Leu
            100                 105                 110

gct tct gaa agg gca ttg ccg tgg caa ctg aac gat cct aac tac ttc      384
Ala Ser Glu Arg Ala Leu Pro Trp Gln Leu Asn Asp Pro Asn Tyr Phe
        115                 120                 125

agt att gat gct cct cca tcc ttt aag cca gct aag aag tat tct gat      432
Ser Ile Asp Ala Pro Pro Ser Phe Lys Pro Ala Lys Lys Tyr Ser Asp
    130                 135                 140

gtt tca ggt ctg ctt gcc aac tac aca gac ccc cag agc aaa ctg cgg      480
Val Ser Gly Leu Leu Ala Asn Tyr Thr Asp Pro Gln Ser Lys Leu Arg
145                 150                 155                 160

ttc agc acc att gaa gag ttt tcc tac att cgg agg ctg ccc tct gac      528
Phe Ser Thr Ile Glu Glu Phe Ser Tyr Ile Arg Arg Leu Pro Ser Asp
                165                 170                 175

gtc gtc acc ggc tac ctg gcc ctg agg aag gcc acg agc atc gtt ccc      576
Val Val Thr Gly Tyr Leu Ala Leu Arg Lys Ala Thr Ser Ile Val Pro
            180                 185                 190

tga                                                                  579
```

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<210> 282
<211> 192
<212> PRT
<213> Homo sapiens

<400> 282
Met Ala Ala Gln Ile Pro Ile Val Ala Thr Thr Ser Thr Pro Gly Ile
1 5 10 15
Val Arg Asn Ser Lys Lys Arg Pro Ala Ser Pro Ser His Asn Gly Ser
20 25 30
Ser Gly Gly Gly Tyr Gly Ala Ser Lys Lys Lys Lys Ala Ser Ala Ser
35 40 45
Ser Phe Ala Gln Gly Ile Ser Met Glu Ala Met Ser Glu Asn Lys Met
50 55 60
Val Pro Ser Glu Phe Ser Thr Gly Pro Val Glu Lys Ala Ala Lys Pro
65 70 75 80
Leu Pro Phe Lys Asp Pro Asn Phe Val His Ser Gly His Gly Gly Ala
85 90 95
Val Ala Gly Lys Lys Asn Arg Thr Trp Lys Asn Leu Lys Gln Ile Leu
100 105 110
Ala Ser Glu Arg Ala Leu Pro Trp Gln Leu Asn Asp Pro Asn Tyr Phe
115 120 125
Ser Ile Asp Ala Pro Pro Ser Phe Lys Pro Ala Lys Lys Tyr Ser Asp
130 135 140
Val Ser Gly Leu Leu Ala Asn Tyr Thr Asp Pro Gln Ser Lys Leu Arg
145 150 155 160
Phe Ser Thr Ile Glu Glu Phe Ser Tyr Ile Arg Arg Leu Pro Ser Asp
165 170 175
Val Val Thr Gly Tyr Leu Ala Leu Arg Lys Ala Thr Ser Ile Val Pro
180 185 190

<210> 283
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(948)

<400> 283

atg gcc tca gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt 48
Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
1 5 10 15

gcc ctg tta caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga 96
Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
20 25 30

aaa ggt aaa ggt cga aat act gga aag tct caa act tta gga agc aag 144
Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
35 40 45

tca act aca aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa 192
Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
50 55 60

cag caa cag agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa 240
Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
65 70 75 80

att ccc cag aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt 288
Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
85 90 95

cca ttg tca aac cca gta cag aag gat tca cga gaa gaa aat tgg caa 336
Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
100 105 110

gag tgg aga caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca 384
Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
115 120 125

gat ctt gag aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac 432
Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
130 135 140

aaa aag gag tat gaa gat gct gaa aat act tca act cag tcc aaa gtt 480
Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
145 150 155 160

atg aat aaa aaa gat aaa aga aag aat cat cag gga aaa gac aga cct 528
Met Asn Lys Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
165 170 175

```
ctc aca gta tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa      576
Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
            180                 185                 190

aag act gag gaa gtg gtt ctg aaa gat gga aga att gaa aga cta aag      624
Lys Thr Glu Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys
        195                 200                 205

tta gag ctt gaa agg aaa gat gct gaa atc cag aag ctg aaa aat gta      672
Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val
    210                 215                 220

atc act caa tgg gag gca aag tat aag gaa gta aag gca aga aat gca      720
Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala
225                 230                 235                 240

caa tta ttg aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa      768
Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu
                245                 250                 255

ata ctt ctg caa gtt gat gaa tca caa agt atc aag aat gag ctc act      816
Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr
            260                 265                 270

att cag gtg act tca ctt cat gct gca tta gaa caa gaa aga tct aaa      864
Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys
        275                 280                 285

gtg aaa gta tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa      912
Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys
    290                 295                 300

ggg aaa aga aac tct gaa tcc gac cag tgt agg tga                      948
Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg  *
305                 310                 315
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<210> 284
<211> 315
<212> PRT
<213> Homo sapiens

<400> 284

Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
1 5 10 15
Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
20 25 30
Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
35 40 45
Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
50 55 60
Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
65 70 75 80
Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
85 90 95
Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
100 105 110
Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
115 120 125
Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
130 135 140
Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
145 150 155 160
Met Asn Lys Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
165 170 175
Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
180 185 190
Lys Thr Glu Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys
195 200 205
Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val
210 215 220
Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala
225 230 235 240
Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu
245 250 255
Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr
260 265 270
Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys
275 280 285
Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys
290 295 300
Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg
305 310 315

<210> 285
<211> 1308
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1308)

<400> 285
atg ggc acc tct gtc acc ggc ttg tat cca gag ctg ttc act ctc ctc 48
Met Gly Thr Ser Val Thr Gly Leu Tyr Pro Glu Leu Phe Thr Leu Leu
1 5 10 15

ctg aag ctg gtt agc tgc aca ctg ggc cag aag atg ccc act tgt ccc 96
Leu Lys Leu Val Ser Cys Thr Leu Gly Gln Lys Met Pro Thr Cys Pro
20 25 30

tgg agc cat agg cgg cat gtg atg cag cag gga gaa cag cag cag atc 144
Trp Ser His Arg Arg His Val Met Gln Gln Gly Glu Gln Gln Gln Ile
35 40 45

cca gac ccc tgc agg ctt tca act gct act tta aaa tgt ttg caa gcc 192
Pro Asp Pro Cys Arg Leu Ser Thr Ala Thr Leu Lys Cys Leu Gln Ala
50 55 60

caa gcc atg aga gaa ggc ctt gca aag gaa tct gat gag ggg gac aac 240
Gln Ala Met Arg Glu Gly Leu Ala Lys Glu Ser Asp Glu Gly Asp Asn
65 70 75 80

tta tgg act cta ctc agc agt cct agt acc cac cac ata ggc gta tgt 288
Leu Trp Thr Leu Leu Ser Ser Pro Ser Thr His His Ile Gly Val Cys
85 90 95

tca ctg gcc agg agc atg gca gtg tgg caa cac gga gtc ata ctg gac 336
Ser Leu Ala Arg Ser Met Ala Val Trp Gln His Gly Val Ile Leu Asp
100 105 110

atc atg gaa cag ctg ctc tca tct ctt acc tcc tcc tcg gag aac tac 384
Ile Met Glu Gln Leu Leu Ser Ser Leu Thr Ser Ser Ser Glu Asn Tyr
115 120 125

cgg ata acc ggc gca gct ttc ttc tct gag ctc atg aag gaa cca atc 432
Arg Ile Thr Gly Ala Ala Phe Phe Ser Glu Leu Met Lys Glu Pro Ile
130 135 140

ctt tgg aag cat ggg aat ctg cga aat gtg ctg atc ttg atg gat caa 480

```
Leu Trp Lys His Gly Asn Leu Arg Asn Val Leu Ile Leu Met Asp Gln
145                 150                 155                 160

agt gcc tgg gac tcc aac gcc act ctg agg cag atg gcc atc cga ggg      528
Ser Ala Trp Asp Ser Asn Ala Thr Leu Arg Gln Met Ala Ile Arg Gly
                165                 170                 175

ctc ggc aac aca gca tcc ggg gct cct cac aag gtg aag aaa cat aag      576
Leu Gly Asn Thr Ala Ser Gly Ala Pro His Lys Val Lys Lys His Lys
            180                 185                 190

cag tta atg cta gaa tct atc atc aga ggc ctg tat cac cta gct cgc      624
Gln Leu Met Leu Glu Ser Ile Ile Arg Gly Leu Tyr His Leu Ala Arg
        195                 200                 205

act gaa gtc gtc tgt gaa agc ttg aag gct cta aaa aaa atc ctg gag      672
Thr Glu Val Val Cys Glu Ser Leu Lys Ala Leu Lys Lys Ile Leu Glu
    210                 215                 220

ctg ctg aca gac cga gac gtg agc ttc tac ttc aag gaa ata gtg ctg      720
Leu Leu Thr Asp Arg Asp Val Ser Phe Tyr Phe Lys Glu Ile Val Leu
225                 230                 235                 240

caa aca agg acc ttc ttt gaa gat gag cag gat gat gtg aga ttg act      768
Gln Thr Arg Thr Phe Phe Glu Asp Glu Gln Asp Asp Val Arg Leu Thr
                245                 250                 255

gcc atc ttc tta ttt gag gac ctg gca ccc cta aca gga aga agg tgg      816
Ala Ile Phe Leu Phe Glu Asp Leu Ala Pro Leu Thr Gly Arg Arg Trp
            260                 265                 270

aag att ttt ttt gct gaa gaa ata aaa aag agc ctg att tca ttc ctt      864
Lys Ile Phe Phe Ala Glu Glu Ile Lys Lys Ser Leu Ile Ser Phe Leu
        275                 280                 285

ctg cac ctt tgg gat ccc aac ccc aag att gga gtt gct tgc cgt gat      912
Leu His Leu Trp Asp Pro Asn Pro Lys Ile Gly Val Ala Cys Arg Asp
    290                 295                 300

gtc ttg atg gtc tgc att ccc ttt ttg ggc ctc cag gag ctc tat ggg      960
Val Leu Met Val Cys Ile Pro Phe Leu Gly Leu Gln Glu Leu Tyr Gly
305                 310                 315                 320

gta tta gac cgt ctc ctt gat cag gat cta cca agg gcc agg gat ttc     1008
```

Val Leu Asp Arg Leu Leu Asp Gln Asp Leu Pro Arg Ala Arg Asp Phe
325 330 335

tac agg caa ttc tgt gtg aaa ctg gcc aag aaa aac cag gaa att ctg 1056
Tyr Arg Gln Phe Cys Val Lys Leu Ala Lys Lys Asn Gln Glu Ile Leu
340 345 350

tgg atc ctc cac aca cac tcc ttc acc ttc ttc acc agc acc tgg gag 1104
Trp Ile Leu His Thr His Ser Phe Thr Phe Phe Thr Ser Thr Trp Glu
355 360 365

gtg atc agg agt gca gct gtc aaa ctc aca gat gcc gtt gtt ctc aat 1152
Val Ile Arg Ser Ala Ala Val Lys Leu Thr Asp Ala Val Val Leu Asn
370 375 380

ttg acc agc caa tat gtg gag tta cta gac aga gaa caa ctg acc aca 1200
Leu Thr Ser Gln Tyr Val Glu Leu Leu Asp Arg Glu Gln Leu Thr Thr
385 390 395 400

cga ctc caa gca ctt cgt caa gat ccg tgt att agt gtc cag aga gca 1248
Arg Leu Gln Ala Leu Arg Gln Asp Pro Cys Ile Ser Val Gln Arg Ala
405 410 415

gct gag gct gct ttg caa acc ctc ctg aga agg tgt aaa gag aca agc 1296
Ala Glu Ala Ala Leu Gln Thr Leu Leu Arg Arg Cys Lys Glu Thr Ser
420 425 430

att cct ctg taa 1308
Ile Pro Leu *
435

<210> 286
<211> 435
<212> PRT
<213> Homo sapiens

<400> 286
Met Gly Thr Ser Val Thr Gly Leu Tyr Pro Glu Leu Phe Thr Leu Leu
1 5 10 15
Leu Lys Leu Val Ser Cys Thr Leu Gly Gln Lys Met Pro Thr Cys Pro
20 25 30
Trp Ser His Arg Arg His Val Met Gln Gln Gly Glu Gln Gln Ile
35 40 45

Pro Asp Pro Cys Arg Leu Ser Thr Ala Thr Leu Lys Cys Leu Gln Ala
50 55 60
Gln Ala Met Arg Glu Gly Leu Ala Lys Glu Ser Asp Glu Gly Asp Asn
65 70 75 80
Leu Trp Thr Leu Leu Ser Ser Pro Ser Thr His His Ile Gly Val Cys
85 90 95
Ser Leu Ala Arg Ser Met Ala Val Trp Gln His Gly Val Ile Leu Asp
100 105 110
Ile Met Glu Gln Leu Leu Ser Ser Leu Thr Ser Ser Ser Glu Asn Tyr
115 120 125
Arg Ile Thr Gly Ala Ala Phe Phe Ser Glu Leu Met Lys Glu Pro Ile
130 135 140
Leu Trp Lys His Gly Asn Leu Arg Asn Val Leu Ile Leu Met Asp Gln
145 150 155 160
Ser Ala Trp Asp Ser Asn Ala Thr Leu Arg Gln Met Ala Ile Arg Gly
165 170 175
Leu Gly Asn Thr Ala Ser Gly Ala Pro His Lys Val Lys Lys His Lys
180 185 190
Gln Leu Met Leu Glu Ser Ile Ile Arg Gly Leu Tyr His Leu Ala Arg
195 200 205
Thr Glu Val Val Cys Glu Ser Leu Lys Ala Leu Lys Lys Ile Leu Glu
210 215 220
Leu Leu Thr Asp Arg Asp Val Ser Phe Tyr Phe Lys Glu Ile Val Leu
225 230 235 240
Gln Thr Arg Thr Phe Phe Glu Asp Glu Gln Asp Asp Val Arg Leu Thr
245 250 255
Ala Ile Phe Leu Phe Glu Asp Leu Ala Pro Leu Thr Gly Arg Arg Trp
260 265 270
Lys Ile Phe Phe Ala Glu Glu Ile Lys Lys Ser Leu Ile Ser Phe Leu
275 280 285
Leu His Leu Trp Asp Pro Asn Pro Lys Ile Gly Val Ala Cys Arg Asp
290 295 300
Val Leu Met Val Cys Ile Pro Phe Leu Gly Leu Gln Glu Leu Tyr Gly
305 310 315 320
Val Leu Asp Arg Leu Leu Asp Gln Asp Leu Pro Arg Ala Arg Asp Phe
325 330 335
Tyr Arg Gln Phe Cys Val Lys Leu Ala Lys Lys Asn Gln Glu Ile Leu
340 345 350
Trp Ile Leu His Thr His Ser Phe Thr Phe Phe Thr Ser Thr Trp Glu
355 360 365
Val Ile Arg Ser Ala Ala Val Lys Leu Thr Asp Ala Val Val Leu Asn
370 375 380
Leu Thr Ser Gln Tyr Val Glu Leu Leu Asp Arg Glu Gln Leu Thr Thr
385 390 395 400

Arg Leu Gln Ala Leu Arg Gln Asp Pro Cys Ile Ser Val Gln Arg Ala
405 410 415
Ala Glu Ala Ala Leu Gln Thr Leu Leu Arg Arg Cys Lys Glu Thr Ser
420 425 430
Ile Pro Leu
435

<210> 287
<211> 822
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(822)

<400> 287
atg gat ccc gta ccc ggg aca gac tcg gcg ccg ctg gct ggc ctg gcc 48
Met Asp Pro Val Pro Gly Thr Asp Ser Ala Pro Leu Ala Gly Leu Ala
1 5 10 15

tgg tcg tcg gcc tct gca ccc ccg ccg cgg ggg ttc agc gcg atc tcc 96
Trp Ser Ser Ala Ser Ala Pro Pro Pro Arg Gly Phe Ser Ala Ile Ser
20 25 30

tgc acc gtc gag ggg gca ccc gcc agc ttt ggc aag agc ttc gcg cag 144
Cys Thr Val Glu Gly Ala Pro Ala Ser Phe Gly Lys Ser Phe Ala Gln
35 40 45

aaa tct ggc tac ttc ctg tgc ctt agt tct ctg ggc agc cta gag aac 192
Lys Ser Gly Tyr Phe Leu Cys Leu Ser Ser Leu Gly Ser Leu Glu Asn
50 55 60

ccg cag gag aac gtg gtg gcc gat atc cag atc gtg gtg gac aag agc 240
Pro Gln Glu Asn Val Val Ala Asp Ile Gln Ile Val Val Asp Lys Ser
65 70 75 80

ccc ctg ccg ctg ggc ttc tcc ccc gtc tgc gac ccc atg gat tcc aag 288
Pro Leu Pro Leu Gly Phe Ser Pro Val Cys Asp Pro Met Asp Ser Lys
85 90 95

gcc tct gtg tcc aag aag aaa cgc atg tgt gtg aag ctg ttg ccc ctg 336
Ala Ser Val Ser Lys Lys Lys Arg Met Cys Val Lys Leu Leu Pro Leu
100 105 110

```
gga gcc acg gac acg gct gtg ttt gat gtc cgg ctg agt ggg aag acc      384
Gly Ala Thr Asp Thr Ala Val Phe Asp Val Arg Leu Ser Gly Lys Thr
        115                 120                 125

aag aca gtg cct gga tac ctt cga ata ggg gac atg ggc ggc ttt gcc      432
Lys Thr Val Pro Gly Tyr Leu Arg Ile Gly Asp Met Gly Gly Phe Ala
    130                 135                 140

atc tgg tgc aag aag gcc aag gcc ccg agg cca gtg ccc aag ccc cga      480
Ile Trp Cys Lys Lys Ala Lys Ala Pro Arg Pro Val Pro Lys Pro Arg
145                 150                 155                 160

ggt ctc agc cgg gac atg cag ggc ctc tct ctg gat gca gcc agc cag      528
Gly Leu Ser Arg Asp Met Gln Gly Leu Ser Leu Asp Ala Ala Ser Gln
                165                 170                 175

cca agt aag ggc ggc ctc ctg gag cgg aca gcg tca agg ctg ggc tct      576
Pro Ser Lys Gly Gly Leu Leu Glu Arg Thr Ala Ser Arg Leu Gly Ser
            180                 185                 190

cgg gca tcc act ctg cgg agg aat gac tcc atc tac gag gcc tcc agc      624
Arg Ala Ser Thr Leu Arg Arg Asn Asp Ser Ile Tyr Glu Ala Ser Ser
        195                 200                 205

ctc tat ggc atc tca gcc atg gat ggg gtt ccc ttc aca ctc cac cca      672
Leu Tyr Gly Ile Ser Ala Met Asp Gly Val Pro Phe Thr Leu His Pro
    210                 215                 220

cga ttt gag ggc aag agc tgc agc ccc ctg gcc ttc tct gct ttt ggg      720
Arg Phe Glu Gly Lys Ser Cys Ser Pro Leu Ala Phe Ser Ala Phe Gly
225                 230                 235                 240

gac ctg acc atc aag tct ctg gcg gac att gag gag gag tat aac tac      768
Asp Leu Thr Ile Lys Ser Leu Ala Asp Ile Glu Glu Glu Tyr Asn Tyr
                245                 250                 255

ggc ttc gtg gtg gag aag acc gcg gct gcc cgc ctg ccc ccc agc gtc      816
Gly Phe Val Val Glu Lys Thr Ala Ala Ala Arg Leu Pro Pro Ser Val
            260                 265                 270

tca tag                                                              822
Ser  *
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<210> 288
<211> 273
<212> PRT
<213> Homo sapiens

<400> 288
Met Asp Pro Val Pro Gly Thr Asp Ser Ala Pro Leu Ala Gly Leu Ala
1 5 10 15
Trp Ser Ser Ala Ser Ala Pro Pro Pro Arg Gly Phe Ser Ala Ile Ser
20 25 30
Cys Thr Val Glu Gly Ala Pro Ala Ser Phe Gly Lys Ser Phe Ala Gln
35 40 45
Lys Ser Gly Tyr Phe Leu Cys Leu Ser Ser Leu Gly Ser Leu Glu Asn
50 55 60
Pro Gln Glu Asn Val Val Ala Asp Ile Gln Ile Val Val Asp Lys Ser
65 70 75 80
Pro Leu Pro Leu Gly Phe Ser Pro Val Cys Asp Pro Met Asp Ser Lys
85 90 95
Ala Ser Val Ser Lys Lys Lys Arg Met Cys Val Lys Leu Leu Pro Leu
100 105 110
Gly Ala Thr Asp Thr Ala Val Phe Asp Val Arg Leu Ser Gly Lys Thr
115 120 125
Lys Thr Val Pro Gly Tyr Leu Arg Ile Gly Asp Met Gly Gly Phe Ala
130 135 140
Ile Trp Cys Lys Lys Ala Lys Ala Pro Arg Pro Val Pro Lys Pro Arg
145 150 155 160
Gly Leu Ser Arg Asp Met Gln Gly Leu Ser Leu Asp Ala Ala Ser Gln
165 170 175
Pro Ser Lys Gly Gly Leu Leu Glu Arg Thr Ala Ser Arg Leu Gly Ser
180 185 190
Arg Ala Ser Thr Leu Arg Arg Asn Asp Ser Ile Tyr Glu Ala Ser Ser
195 200 205
Leu Tyr Gly Ile Ser Ala Met Asp Gly Val Pro Phe Thr Leu His Pro
210 215 220
Arg Phe Glu Gly Lys Ser Cys Ser Pro Leu Ala Phe Ser Ala Phe Gly
225 230 235 240
Asp Leu Thr Ile Lys Ser Leu Ala Asp Ile Glu Glu Glu Tyr Asn Tyr
245 250 255
Gly Phe Val Val Glu Lys Thr Ala Ala Ala Arg Leu Pro Pro Ser Val
260 265 270
Ser

<210> 289
<211> 744
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(744)

<400> 289

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atg cca gga cgt tcc agt tca aat tca ggt tca act ggt ttc atc tcc       48
Met Pro Gly Arg Ser Ser Ser Asn Ser Gly Ser Thr Gly Phe Ile Ser
 1               5                  10                  15

ttc agt ggt gta gag tct gct ctc tcc tcc ttg aaa aac ttc caa gcc       96
Phe Ser Gly Val Glu Ser Ala Leu Ser Ser Leu Lys Asn Phe Gln Ala
            20                  25                  30

tgt atc aac tct ggt atg gac aca gct tct agt gtt gct ttg gat ctt      144
Cys Ile Asn Ser Gly Met Asp Thr Ala Ser Ser Val Ala Leu Asp Leu
        35                  40                  45

gtg gaa agt cag act gaa gtg agt agt gaa tat agt atg gac aag gca      192
Val Glu Ser Gln Thr Glu Val Ser Ser Glu Tyr Ser Met Asp Lys Ala
    50                  55                  60

atg gtt gaa ttt gct aca ttg gat cgg caa cta aac cat tat gta aag      240
Met Val Glu Phe Ala Thr Leu Asp Arg Gln Leu Asn His Tyr Val Lys
65                  70                  75                  80

gct gtt caa tct aca ata aat cat gtg aaa gaa gaa cgt cca gaa aaa      288
Ala Val Gln Ser Thr Ile Asn His Val Lys Glu Glu Arg Pro Glu Lys
                85                  90                  95

ata cca gat tta aaa tta ttg gta gag aag aaa ttt ttg gct tta cag      336
Ile Pro Asp Leu Lys Leu Leu Val Glu Lys Lys Phe Leu Ala Leu Gln
            100                 105                 110

agc aag aat tct gat gca gac ttt caa aat aat gaa aaa ttt gta cag      384
Ser Lys Asn Ser Asp Ala Asp Phe Gln Asn Asn Glu Lys Phe Val Gln
        115                 120                 125

ttt aaa caa cag ctg aaa gaa cta aag aag caa tgt ggt ctt caa gct      432
```

Phe Lys Gln Gln Leu Lys Glu Leu Lys Lys Gln Cys Gly Leu Gln Ala
130 135 140

gac aga gaa gct gac gga aca gaa gga gtg gat gaa gat ata att gtg 480
Asp Arg Glu Ala Asp Gly Thr Glu Gly Val Asp Glu Asp Ile Ile Val
145 150 155 160

acc caa agt cag acc aac ttc acc tgc ccc att aca aag gag gaa atg 528
Thr Gln Ser Gln Thr Asn Phe Thr Cys Pro Ile Thr Lys Glu Glu Met
165 170 175

aag aag cca gtg aaa aat aaa gtg tgt ggc cac acc tat gaa gag gac 576
Lys Lys Pro Val Lys Asn Lys Val Cys Gly His Thr Tyr Glu Glu Asp
180 185 190

gcc att gtt cgc atg att gag tcc agg caa aag cgg aag aaa aag gcc 624
Ala Ile Val Arg Met Ile Glu Ser Arg Gln Lys Arg Lys Lys Lys Ala
195 200 205

tat tgc cct caa att ggc tgt agc cac acg gat ata aga aag tca gat 672
Tyr Cys Pro Gln Ile Gly Cys Ser His Thr Asp Ile Arg Lys Ser Asp
210 215 220

ctt atc cag gat gaa gca ctt aga agg gca att gag aac cat aac aag 720
Leu Ile Gln Asp Glu Ala Leu Arg Arg Ala Ile Glu Asn His Asn Lys
225 230 235 240

aaa aga cat cgt cat tcc gag tag 744
Lys Arg His Arg His Ser Glu *
245

<210> 290
<211> 247
<212> PRT
<213> Homo sapiens

<400> 290
Met Pro Gly Arg Ser Ser Ser Asn Ser Gly Ser Thr Gly Phe Ile Ser
1 5 10 15
Phe Ser Gly Val Glu Ser Ala Leu Ser Ser Leu Lys Asn Phe Gln Ala
20 25 30
Cys Ile Asn Ser Gly Met Asp Thr Ala Ser Ser Val Ala Leu Asp Leu
35 40 45

```
Val Glu Ser Gln Thr Glu Val Ser Ser Glu Tyr Ser Met Asp Lys Ala
    50                  55                  60
Met Val Glu Phe Ala Thr Leu Asp Arg Gln Leu Asn His Tyr Val Lys
65                  70                  75                  80
Ala Val Gln Ser Thr Ile Asn His Val Lys Glu Glu Arg Pro Glu Lys
                85                  90                  95
Ile Pro Asp Leu Lys Leu Leu Val Glu Lys Lys Phe Leu Ala Leu Gln
            100                 105                 110
Ser Lys Asn Ser Asp Ala Asp Phe Gln Asn Asn Glu Lys Phe Val Gln
        115                 120                 125
Phe Lys Gln Gln Leu Lys Glu Leu Lys Lys Gln Cys Gly Leu Gln Ala
    130                 135                 140
Asp Arg Glu Ala Asp Gly Thr Glu Gly Val Asp Glu Asp Ile Ile Val
145                 150                 155                 160
Thr Gln Ser Gln Thr Asn Phe Thr Cys Pro Ile Thr Lys Glu Glu Met
                165                 170                 175
Lys Lys Pro Val Lys Asn Lys Val Cys Gly His Thr Tyr Glu Glu Asp
            180                 185                 190
Ala Ile Val Arg Met Ile Glu Ser Arg Gln Lys Arg Lys Lys Lys Ala
        195                 200                 205
Tyr Cys Pro Gln Ile Gly Cys Ser His Thr Asp Ile Arg Lys Ser Asp
    210                 215                 220
Leu Ile Gln Asp Glu Ala Leu Arg Arg Ala Ile Glu Asn His Asn Lys
225                 230                 235                 240
Lys Arg His Arg His Ser Glu
                245

      <210> 291
      <211> 957
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(957)

      <221> misc_feature
      <222> (1)...(957)
      <223> n = A,T,C or G

      <400> 291
atg gct gag cac gca ggg ccc cga ctc ccc ctg gtg ctg aag acg ctg      48
Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1               5                  10                  15
```

```
gca tgc aca cac agc agt gcg tat gag aac cag agg gtg acc acc acc      96
Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr
            20                  25                  30

gcc ttc ctg gcc gag ctg ctg aac agc aac gtg gcc aac gac ctc atg     144
Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
        35                  40                  45

ctc ttg gac tcg ctg ctg gag agc ctg gcg gct cgc cag aag gac aca     192
Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
    50                  55                  60

tgc gcc anc gtg cgg agg ctg gtg ctc cgc ggc ctg gcc aac ctg gcc     240
Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
65                  70                  75                  80

tcc ggc tgc cct gac aag gtg cga acc cac ggc ccc cag ctc ctc aca     288
Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
                85                  90                  95

gcc atg att ggc ggg ctg gac gac ggg gac aac cct cac agc cca gtg     336
Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
            100                 105                 110

gcc ctg gag gcc atg ctg ggc ctt gcg agg ctg gtg cac ctg gtg gag     384
Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
        115                 120                 125

tcc tgg gac ctg cgc tca ggg ctg ctg cac gtg gcc atc cgc atc cgg     432
Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
    130                 135                 140

cct ttc ttc gac agt gag aag atg gag ttc cgg acg gca tct atc cgc     480
Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
145                 150                 155                 160

ctc ttt ggg cac ctt aac aag gtc tgc cac gga gac tgt gag gac gtc     528
Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val
                165                 170                 175

ttc ctg gac cag gtg gtg ggc ggg ctg gcg ccc ctg ctg ctg cac ctg     576
Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu
            180                 185                 190
```

```
cag gac cct cag gcc acc gtg gcc agc gcc tgc agg ttt gcc ctg cgc       624
Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg
        195                 200                 205

atg tgt ggc ccc aat ctg gca tgt gag gag ctc tca gct gct ttc cag       672
Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln
    210                 215                 220

aaa cac ctg cag gag ggc cga gcc ctg cac ttc ggg gag ttc ctc aac       720
Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn
225                 230                 235                 240

acc acc tgc aag cac ctg atg cac cat ttc cca gac ctg ctg ggc cgt       768
Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg
                245                 250                 255

ctc ctg acc acc tgc ctg ttc tac ttc aag agc agc tgg gag aac gtc       816
Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val
            260                 265                 270

cga gct gct gca ccc ctg ttc acc ggg ttc ctg gtg ctg cac tcg gag       864
Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu
        275                 280                 285

ccc agg cag cag ccg cag gtg gac ctg gac cag ctc att gcg ggt gag       912
Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Gly Glu
    290                 295                 300

cac ccc tcc acg ggg ccc ctc cgc tgg gcc ctg ctg acc ctg tag           957
His Pro Ser Thr Gly Pro Leu Arg Trp Ala Leu Leu Thr Leu  *
305                 310                 315
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<210> 292
<211> 318
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(318)
<223> Xaa = Any Amino Acid

<400> 292

Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
1 5 10 15
Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr
20 25 30
Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
35 40 45
Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
50 55 60
Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
65 70 75 80
Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
85 90 95
Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
100 105 110
Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
115 120 125
Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
130 135 140
Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
145 150 155 160
Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val
165 170 175
Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu
180 185 190
Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg
195 200 205
Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln
210 215 220
Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn
225 230 235 240
Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg
245 250 255
Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val
260 265 270
Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu
275 280 285
Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Gly Glu
290 295 300
His Pro Ser Thr Gly Pro Leu Arg Trp Ala Leu Leu Thr Leu
305 310 315

<210> 293
<211> 1107

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1107)

<400> 293
atg cag cct gga tcc agc cgg tgt gaa gag gag acc cct tcc ctc ttg 48
Met Gln Pro Gly Ser Ser Arg Cys Glu Glu Glu Thr Pro Ser Leu Leu
1 5 10 15

tgg ggt ttg gat cct gtg ttt cta gcc ttt gca aaa ctc tac atc agg 96
Trp Gly Leu Asp Pro Val Phe Leu Ala Phe Ala Lys Leu Tyr Ile Arg
20 25 30

gat atc ctg gac atg aag gag tcc cgc cag gtg cca ggt gta ttt ttg 144
Asp Ile Leu Asp Met Lys Glu Ser Arg Gln Val Pro Gly Val Phe Leu
35 40 45

tac aat gga cat cca ata aaa cag gta gat gtc ttg gga act gtc att 192
Tyr Asn Gly His Pro Ile Lys Gln Val Asp Val Leu Gly Thr Val Ile
50 55 60

gga gtg aga gaa aga gat gct ttc tac agt tat gga gtg gat gac agc 240
Gly Val Arg Glu Arg Asp Ala Phe Tyr Ser Tyr Gly Val Asp Asp Ser
65 70 75 80

act gga gtt ata aac tgc atc tgc tgg aaa aag ttg aat act gag tct 288
Thr Gly Val Ile Asn Cys Ile Cys Trp Lys Lys Leu Asn Thr Glu Ser
85 90 95

gta tca gct gct cca agt gca gca aga gag ctc agc tta acc tca caa 336
Val Ser Ala Ala Pro Ser Ala Ala Arg Glu Leu Ser Leu Thr Ser Gln
100 105 110

ctt aag aag cta caa gag acc att gag cag aaa aca aag ata gag atc 384
Leu Lys Lys Leu Gln Glu Thr Ile Glu Gln Lys Thr Lys Ile Glu Ile
115 120 125

ggg gac acg atc cga gtc aga ggc agt atc cgc aca tac aga gaa gag 432
Gly Asp Thr Ile Arg Val Arg Gly Ser Ile Arg Thr Tyr Arg Glu Glu
130 135 140

cga gag att cat gcc acc gct tac tat aaa gtg gac gac cca gtg tgg 480
Arg Glu Ile His Ala Thr Ala Tyr Tyr Lys Val Asp Asp Pro Val Trp
145 150 155 160

aac att caa att gca agg atg ctt gag ctg ccc act atc tac agg aaa 528
Asn Ile Gln Ile Ala Arg Met Leu Glu Leu Pro Thr Ile Tyr Arg Lys
165 170 175

gtt tat gac cag cct ttt cac agc tca gcc cta gag aaa gaa gag gca 576
Val Tyr Asp Gln Pro Phe His Ser Ser Ala Leu Glu Lys Glu Glu Ala
180 185 190

cta agc aat cca ggc gcc ctg gac ctc ccc agt ctc acg agt ttg ctg 624
Leu Ser Asn Pro Gly Ala Leu Asp Leu Pro Ser Leu Thr Ser Leu Leu
195 200 205

agt gaa aaa gcc aaa gaa ttc ctc atg gag aac aga gtg cag agc ttt 672
Ser Glu Lys Ala Lys Glu Phe Leu Met Glu Asn Arg Val Gln Ser Phe
210 215 220

tac cag cag gag ctg gaa atg gtg gag tct ttg ctg tcc ctt gcc aat 720
Tyr Gln Gln Glu Leu Glu Met Val Glu Ser Leu Leu Ser Leu Ala Asn
225 230 235 240

cag cct gtg att cac agt gcc tgc tcc gac caa gtg aat ttt aag aag 768
Gln Pro Val Ile His Ser Ala Cys Ser Asp Gln Val Asn Phe Lys Lys
245 250 255

gac acc act tcc aag gca att cat agt ata ttt aag aat gct ata caa 816
Asp Thr Thr Ser Lys Ala Ile His Ser Ile Phe Lys Asn Ala Ile Gln
260 265 270

ctg ctg cag gaa aaa gga ctt gtt ttc cag aaa gat gat ggt ttt gat 864
Leu Leu Gln Glu Lys Gly Leu Val Phe Gln Lys Asp Asp Gly Phe Asp
275 280 285

aac cta tac tat gta acc aga gaa gac aaa gac ctg cac aga aag atc 912
Asn Leu Tyr Tyr Val Thr Arg Glu Asp Lys Asp Leu His Arg Lys Ile
290 295 300

cac cgg atc att cag cag gac tgc cag aaa cca aat cac atg gag aag 960
His Arg Ile Ile Gln Gln Asp Cys Gln Lys Pro Asn His Met Glu Lys
305 310 315 320

ggc tgt cac ttc ctg cac atc ttg gcc tgt gct cgc ctg agc atc cgc 1008
Gly Cys His Phe Leu His Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg
325 330 335

ccg ggc ctg agc gag gct gtg ctg cag caa gtt ctg gag ctc ctg gag 1056
Pro Gly Leu Ser Glu Ala Val Leu Gln Gln Val Leu Glu Leu Leu Glu
340 345 350

gac cag agt gac att gtc agc aca atg gag cac tac tac aca gcg ttc 1104
Asp Gln Ser Asp Ile Val Ser Thr Met Glu His Tyr Tyr Thr Ala Phe
355 360 365

tga 1107
*

<210> 294
<211> 368
<212> PRT
<213> Homo sapiens

<400> 294
Met Gln Pro Gly Ser Ser Arg Cys Glu Glu Glu Thr Pro Ser Leu Leu
1 5 10 15
Trp Gly Leu Asp Pro Val Phe Leu Ala Phe Ala Lys Leu Tyr Ile Arg
20 25 30
Asp Ile Leu Asp Met Lys Glu Ser Arg Gln Val Pro Gly Val Phe Leu
35 40 45
Tyr Asn Gly His Pro Ile Lys Gln Val Asp Val Leu Gly Thr Val Ile
50 55 60
Gly Val Arg Glu Arg Asp Ala Phe Tyr Ser Tyr Gly Val Asp Asp Ser
65 70 75 80
Thr Gly Val Ile Asn Cys Ile Cys Trp Lys Lys Leu Asn Thr Glu Ser
85 90 95
Val Ser Ala Ala Pro Ser Ala Ala Arg Glu Leu Ser Leu Thr Ser Gln
100 105 110
Leu Lys Lys Leu Gln Glu Thr Ile Glu Gln Lys Thr Lys Ile Glu Ile
115 120 125
Gly Asp Thr Ile Arg Val Arg Gly Ser Ile Arg Thr Tyr Arg Glu Glu
130 135 140
Arg Glu Ile His Ala Thr Ala Tyr Tyr Lys Val Asp Asp Pro Val Trp
145 150 155 160
Asn Ile Gln Ile Ala Arg Met Leu Glu Leu Pro Thr Ile Tyr Arg Lys

```
                165                 170                 175
Val Tyr Asp Gln Pro Phe His Ser Ser Ala Leu Glu Lys Glu Glu Ala
            180                 185                 190
Leu Ser Asn Pro Gly Ala Leu Asp Leu Pro Ser Leu Thr Ser Leu Leu
        195                 200                 205
Ser Glu Lys Ala Lys Glu Phe Leu Met Glu Asn Arg Val Gln Ser Phe
    210                 215                 220
Tyr Gln Gln Glu Leu Glu Met Val Glu Ser Leu Leu Ser Leu Ala Asn
225                 230                 235                 240
Gln Pro Val Ile His Ser Ala Cys Ser Asp Gln Val Asn Phe Lys Lys
                245                 250                 255
Asp Thr Thr Ser Lys Ala Ile His Ser Ile Phe Lys Asn Ala Ile Gln
            260                 265                 270
Leu Leu Gln Glu Lys Gly Leu Val Phe Gln Lys Asp Asp Gly Phe Asp
        275                 280                 285
Asn Leu Tyr Tyr Val Thr Arg Glu Asp Lys Asp Leu His Arg Lys Ile
    290                 295                 300
His Arg Ile Ile Gln Gln Asp Cys Gln Lys Pro Asn His Met Glu Lys
305                 310                 315                 320
Gly Cys His Phe Leu His Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg
                325                 330                 335
Pro Gly Leu Ser Glu Ala Val Leu Gln Gln Val Leu Glu Leu Leu Glu
            340                 345                 350
Asp Gln Ser Asp Ile Val Ser Thr Met Glu His Tyr Tyr Thr Ala Phe
        355                 360                 365

      <210> 295
      <211> 558
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(558)

      <400> 295
atg att aaa agc gcc cct gtg ggt cct gtg gct gga ggg atc atg gga      48
Met Ile Lys Ser Ala Pro Val Gly Pro Val Ala Gly Gly Ile Met Gly
 1               5                  10                  15

tgc atc atg gtc ttg gtc ctg gcg gtg tat gcc tac cgc cac cag att      96
Cys Ile Met Val Leu Val Leu Ala Val Tyr Ala Tyr Arg His Gln Ile
            20                  25                  30
```

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cat cgc cgg agc cat cag cat atg tct cct ctt gct gcc caa gaa atg      144
His Arg Arg Ser His Gln His Met Ser Pro Leu Ala Ala Gln Glu Met
         35                  40                  45

tca gtg cgt atg tcc aac ctg gag aat gac aga gat gaa agg gac gac      192
Ser Val Arg Met Ser Asn Leu Glu Asn Asp Arg Asp Glu Arg Asp Asp
     50                  55                  60

gac agc cac gaa gac aga ggc atc atc agc aac act cgg ttt ata gct      240
Asp Ser His Glu Asp Arg Gly Ile Ile Ser Asn Thr Arg Phe Ile Ala
 65                  70                  75                  80

gcg gtc atc gaa cga cat gca cac agt cca gaa aga agg cgc cgc tac      288
Ala Val Ile Glu Arg His Ala His Ser Pro Glu Arg Arg Arg Arg Tyr
                 85                  90                  95

tgg ggt cga tca gga aca gaa agt gat cat ggt tac agc acc atg agc      336
Trp Gly Arg Ser Gly Thr Glu Ser Asp His Gly Tyr Ser Thr Met Ser
            100                 105                 110

cca cag gag gac agt gaa aat cct cca tgc aac aat gac ccc ttg tca      384
Pro Gln Glu Asp Ser Glu Asn Pro Pro Cys Asn Asn Asp Pro Leu Ser
        115                 120                 125

gcc ggg gtc gat gtg gga aac cat gat gag gac tta gac ctg gat acc      432
Ala Gly Val Asp Val Gly Asn His Asp Glu Asp Leu Asp Leu Asp Thr
    130                 135                 140

ccc cct cag act gct gcc cta cta agt cac aag ttc cac cac tac cgg      480
Pro Pro Gln Thr Ala Ala Leu Leu Ser His Lys Phe His His Tyr Arg
145                 150                 155                 160

tca cac cac cct aca ctt cat cat agc cac cac tta cag gcg gcc gtc      528
Ser His His Pro Thr Leu His His Ser His His Leu Gln Ala Ala Val
                165                 170                 175

acg gta cac act gtc gat gca gaa tgc taa                              558
Thr Val His Thr Val Asp Ala Glu Cys  *
            180                 185
```

<210> 296
<211> 185
<212> PRT

<213> Homo sapiens

<400> 296
Met Ile Lys Ser Ala Pro Val Gly Pro Val Ala Gly Gly Ile Met Gly
1 5 10 15
Cys Ile Met Val Leu Val Leu Ala Val Tyr Ala Tyr Arg His Gln Ile
20 25 30
His Arg Arg Ser His Gln His Met Ser Pro Leu Ala Ala Gln Glu Met
35 40 45
Ser Val Arg Met Ser Asn Leu Glu Asn Asp Arg Asp Glu Arg Asp Asp
50 55 60
Asp Ser His Glu Asp Arg Gly Ile Ile Ser Asn Thr Arg Phe Ile Ala
65 70 75 80
Ala Val Ile Glu Arg His Ala His Ser Pro Glu Arg Arg Arg Arg Tyr
85 90 95
Trp Gly Arg Ser Gly Thr Glu Ser Asp His Gly Tyr Ser Thr Met Ser
100 105 110
Pro Gln Glu Asp Ser Glu Asn Pro Pro Cys Asn Asn Asp Pro Leu Ser
115 120 125
Ala Gly Val Asp Val Gly Asn His Asp Glu Asp Leu Asp Leu Asp Thr
130 135 140
Pro Pro Gln Thr Ala Ala Leu Leu Ser His Lys Phe His His Tyr Arg
145 150 155 160
Ser His His Pro Thr Leu His His Ser His His Leu Gln Ala Ala Val
165 170 175
Thr Val His Thr Val Asp Ala Glu Cys
180 185

<210> 297
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(501)

<400> 297
atg gat gat att gtg gtt gta gct cag ggc tcc cag gcc tca cgg aac 48
Met Asp Asp Ile Val Val Val Ala Gln Gly Ser Gln Ala Ser Arg Asn
1 5 10 15

gtc agc aac gat ccc gat gtc atc aag ttg caa gag att cca acc ttc 96
Val Ser Asn Asp Pro Asp Val Ile Lys Leu Gln Glu Ile Pro Thr Phe

```
                20                  25                  30

cag ccc ctt ttg aaa ggg cta ttg agt ggc cag act tcc cca aca aat      144
Gln Pro Leu Leu Lys Gly Leu Leu Ser Gly Gln Thr Ser Pro Thr Asn
            35                  40                  45

gcc aaa ttg gag aaa ctg gac tct cag cag gtg ttg cag ctc tgc ctc      192
Ala Lys Leu Glu Lys Leu Asp Ser Gln Gln Val Leu Gln Leu Cys Leu
        50                  55                  60

cga tat caa gat cac ctg cat cag tgt gca gag gcc gtt gct ttt gac      240
Arg Tyr Gln Asp His Leu His Gln Cys Ala Glu Ala Val Ala Phe Asp
 65                  70                  75                  80

cag aat gct ttg gtt aaa cga atc aaa gag atg gat ctg tct gta gaa      288
Gln Asn Ala Leu Val Lys Arg Ile Lys Glu Met Asp Leu Ser Val Glu
                 85                  90                  95

act ctg ttc agc ttc atg cag gag cgc cag aaa aga tac gcc aag tat      336
Thr Leu Phe Ser Phe Met Gln Glu Arg Gln Lys Arg Tyr Ala Lys Tyr
            100                 105                 110

gcc gag cag atc cag aaa gtg aac gag atg tcc gcc atc ctc cgc cgc      384
Ala Glu Gln Ile Gln Lys Val Asn Glu Met Ser Ala Ile Leu Arg Arg
        115                 120                 125

ata cag atg ggc atc gac cag act gtg ccc ctg ctg gac agg ctc aac      432
Ile Gln Met Gly Ile Asp Gln Thr Val Pro Leu Leu Asp Arg Leu Asn
    130                 135                 140

agc atg ctg ccc gag ggc gag cgg ctg gag ccc ttc agc atg aag ccc      480
Ser Met Leu Pro Glu Gly Glu Arg Leu Glu Pro Phe Ser Met Lys Pro
145                 150                 155                 160

gac cgc gag ctc agg ctg tag                                          501
Asp Arg Glu Leu Arg Leu  *
                165
```

<210> 298
<211> 166
<212> PRT
<213> Homo sapiens

<400> 298

Met Asp Asp Ile Val Val Val Ala Gln Gly Ser Gln Ala Ser Arg Asn
1 5 10 15
Val Ser Asn Asp Pro Asp Val Ile Lys Leu Gln Glu Ile Pro Thr Phe
20 25 30
Gln Pro Leu Leu Lys Gly Leu Leu Ser Gly Gln Thr Ser Pro Thr Asn
35 40 45
Ala Lys Leu Glu Lys Leu Asp Ser Gln Gln Val Leu Gln Leu Cys Leu
50 55 60
Arg Tyr Gln Asp His Leu His Gln Cys Ala Glu Ala Val Ala Phe Asp
65 70 75 80
Gln Asn Ala Leu Val Lys Arg Ile Lys Glu Met Asp Leu Ser Val Glu
85 90 95
Thr Leu Phe Ser Phe Met Gln Glu Arg Gln Lys Arg Tyr Ala Lys Tyr
100 105 110
Ala Glu Gln Ile Gln Lys Val Asn Glu Met Ser Ala Ile Leu Arg Arg
115 120 125
Ile Gln Met Gly Ile Asp Gln Thr Val Pro Leu Leu Asp Arg Leu Asn
130 135 140
Ser Met Leu Pro Glu Gly Glu Arg Leu Glu Pro Phe Ser Met Lys Pro
145 150 155 160
Asp Arg Glu Leu Arg Leu
165

<210> 299
<211> 828
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(828)

<221> misc_feature
<222> (1)...(828)
<223> n = A,T,C or G

<400> 299
atg agt gaa gag cct gac gct cta tcg gta gtt aac cag tta cgg gat 48
Met Ser Glu Glu Pro Asp Ala Leu Ser Val Val Asn Gln Leu Arg Asp
1 5 10 15

cta gca gca gat ccg tta aac aga aga gcc atc gtc cag gat cag gga 96
Leu Ala Ala Asp Pro Leu Asn Arg Arg Ala Ile Val Gln Asp Gln Gly

20 25 30

tgt ctg cct ggc ctt att tta ttt atg gac cat ccc aac cct cca gtc 144
Cys Leu Pro Gly Leu Ile Leu Phe Met Asp His Pro Asn Pro Pro Val
35 40 45

gtc cac tcc gct ttg ctt gct ctt cga tac ttg gca gaa tgc cgt gca 192
Val His Ser Ala Leu Leu Ala Leu Arg Tyr Leu Ala Glu Cys Arg Ala
50 55 60

aac aga gaa aag atg aaa gga gaa ctg ggt atg atg ttg agc tta caa 240
Asn Arg Glu Lys Met Lys Gly Glu Leu Gly Met Met Leu Ser Leu Gln
65 70 75 80

aat gtt ata cag aaa act aca act cca gga gaa aca aaa ctt ctg gcc 288
Asn Val Ile Gln Lys Thr Thr Thr Pro Gly Glu Thr Lys Leu Leu Ala
85 90 95

tct gaa atc tat gac att ctt cag tcc tcc aat atg gca gat ggt gat 336
Ser Glu Ile Tyr Asp Ile Leu Gln Ser Ser Asn Met Ala Asp Gly Asp
100 105 110

agt ttt aat gag atg aat tca cgt cga agg aaa gct can ttt ttt ctg 384
Ser Phe Asn Glu Met Asn Ser Arg Arg Arg Lys Ala Xaa Phe Phe Leu
115 120 125

gga act aca aac aaa cgt gcc aaa aca gtg gtt ttg cat ata gat ggc 432
Gly Thr Thr Asn Lys Arg Ala Lys Thr Val Val Leu His Ile Asp Gly
130 135 140

ctt gat gat acg tct cgg aga aat cta tgt gaa gag gct ttg tta aaa 480
Leu Asp Asp Thr Ser Arg Arg Asn Leu Cys Glu Glu Ala Leu Leu Lys
145 150 155 160

att aaa ggt gtt att agc ttt act ttt caa atg gct gtt caa agg tgt 528
Ile Lys Gly Val Ile Ser Phe Thr Phe Gln Met Ala Val Gln Arg Cys
165 170 175

gtg gtg cga atc cgt tca gat ttg aaa gct gag gct ttg gca tca gca 576
Val Val Arg Ile Arg Ser Asp Leu Lys Ala Glu Ala Leu Ala Ser Ala
180 185 190

ata gca tca acc aag gtt atg aaa gct cag caa gtt gtg aaa agt gaa 624
Ile Ala Ser Thr Lys Val Met Lys Ala Gln Gln Val Val Lys Ser Glu

195 200 205

agt gga gaa gag atg ttg gtc cca ttc caa gat act cct gtg gaa gtt 672
Ser Gly Glu Glu Met Leu Val Pro Phe Gln Asp Thr Pro Val Glu Val
210 215 220

gaa cag aac aca gag cta cct gac tac ctg cct gag gat gag agt ccc 720
Glu Gln Asn Thr Glu Leu Pro Asp Tyr Leu Pro Glu Asp Glu Ser Pro
225 230 235 240

aca aag gaa cag gac aaa gcg gtg tcc cgg gtc ggc tca cac cca gaa 768
Thr Lys Glu Gln Asp Lys Ala Val Ser Arg Val Gly Ser His Pro Glu
245 250 255

ggt gga gct agc tgg ctt agc aca gct gca aac ttt tta tcc aga tca 816
Gly Gly Ala Ser Trp Leu Ser Thr Ala Ala Asn Phe Leu Ser Arg Ser
260 265 270

ttt tat tgg tga 828
Phe Tyr Trp *
275

<210> 300
<211> 275
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(275)
<223> Xaa = Any Amino Acid

<400> 300
Met Ser Glu Glu Pro Asp Ala Leu Ser Val Val Asn Gln Leu Arg Asp
1 5 10 15
Leu Ala Ala Asp Pro Leu Asn Arg Arg Ala Ile Val Gln Asp Gln Gly
20 25 30
Cys Leu Pro Gly Leu Ile Leu Phe Met Asp His Pro Asn Pro Pro Val
35 40 45
Val His Ser Ala Leu Leu Ala Leu Arg Tyr Leu Ala Glu Cys Arg Ala
50 55 60
Asn Arg Glu Lys Met Lys Gly Glu Leu Gly Met Met Leu Ser Leu Gln
65 70 75 80

Asn Val Ile Gln Lys Thr Thr Thr Pro Gly Glu Thr Lys Leu Leu Ala
85 90 95
Ser Glu Ile Tyr Asp Ile Leu Gln Ser Ser Asn Met Ala Asp Gly Asp
100 105 110
Ser Phe Asn Glu Met Asn Ser Arg Arg Arg Lys Ala Xaa Phe Phe Leu
115 120 125
Gly Thr Thr Asn Lys Arg Ala Lys Thr Val Val Leu His Ile Asp Gly
130 135 140
Leu Asp Asp Thr Ser Arg Arg Asn Leu Cys Glu Glu Ala Leu Leu Lys
145 150 155 160
Ile Lys Gly Val Ile Ser Phe Thr Phe Gln Met Ala Val Gln Arg Cys
165 170 175
Val Val Arg Ile Arg Ser Asp Leu Lys Ala Glu Ala Leu Ala Ser Ala
180 185 190
Ile Ala Ser Thr Lys Val Met Lys Ala Gln Gln Val Val Lys Ser Glu
195 200 205
Ser Gly Glu Glu Met Leu Val Pro Phe Gln Asp Thr Pro Val Glu Val
210 215 220
Glu Gln Asn Thr Glu Leu Pro Asp Tyr Leu Pro Glu Asp Glu Ser Pro
225 230 235 240
Thr Lys Glu Gln Asp Lys Ala Val Ser Arg Val Gly Ser His Pro Glu
245 250 255
Gly Gly Ala Ser Trp Leu Ser Thr Ala Ala Asn Phe Leu Ser Arg Ser
260 265 270
Phe Tyr Trp
275

<210> 301
<211> 1101
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1101)

<221> misc_feature
<222> (1)...(1101)
<223> n = A,T,C or G

<400> 301
atg gcc tca gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt 48
Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
1 5 10 15

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gcc ctg tta caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga      96
Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
            20                  25                  30

aaa ggt aaa ggt cga aat act gga aag tct caa act tta gga agc aag     144
Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
        35                  40                  45

tca act aca aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa     192
Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
    50                  55                  60

cag caa cag agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa     240
Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
65                  70                  75                  80

att ccc cag aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt     288
Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
                85                  90                  95

cca ttg tca aac cca gta cag aag gat tca cga gaa gaa aat tgg caa     336
Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
            100                 105                 110

gag tgg aga caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca     384
Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
        115                 120                 125

gat ctt gag aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac     432
Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
    130                 135                 140

aaa aag gag tat gaa gat gct gaa aat act tca act cag tcc aaa gtt     480
Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
145                 150                 155                 160

atg aat ann aaa gat aaa aga aag aat cat cag gga aaa gac aga cct     528
Met Asn Xaa Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
                165                 170                 175

ctc aca gta tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa     576
Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
            180                 185                 190
```

```
aag act gag gaa ttg agt tct tct cag act tta tca cat gat gga gga      624
Lys Thr Glu Glu Leu Ser Ser Ser Gln Thr Leu Ser His Asp Gly Gly
        195                 200                 205

ttc ttc aat aga ctg gaa gat gat gtt cat aaa att ctt att aga gaa      672
Phe Phe Asn Arg Leu Glu Asp Asp Val His Lys Ile Leu Ile Arg Glu
    210                 215                 220

aaa cga aga gaa cag ctt aca gaa tat aat gga aca gat aat tgt aca      720
Lys Arg Arg Glu Gln Leu Thr Glu Tyr Asn Gly Thr Asp Asn Cys Thr
225                 230                 235                 240

gct cat gaa cac aac cag gaa gtg gtt ctg aaa gat gga aga att gaa      768
Ala His Glu His Asn Gln Glu Val Val Leu Lys Asp Gly Arg Ile Glu
                245                 250                 255

aga cta aag tta gag ctt gaa agg aaa gat gct gaa atc cag aag ctg      816
Arg Leu Lys Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu
            260                 265                 270

aaa aat gta atc act caa tgg gag gca aag tat aag gaa gta aag gca      864
Lys Asn Val Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala
        275                 280                 285

aga aat gca caa tta ttg aaa atg ctt cag gaa ggt gaa atg aaa gat      912
Arg Asn Ala Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp
    290                 295                 300

aag gca gaa ata ctt ctg caa gtt gat gaa tca caa agt atc aag aat      960
Lys Ala Glu Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn
305                 310                 315                 320

gag ctc act att cag gtg act tca ctt cat gct gca tta gaa caa gaa     1008
Glu Leu Thr Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu
                325                 330                 335

aga tct aaa gtg aaa gta tta caa gca gag tta gcc aaa tac cag ggt     1056
Arg Ser Lys Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly
            340                 345                 350

ggc aga aaa ggg aaa aga aac tct gaa tcc gac cag tgt agg tga         1101
Gly Arg Lys Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg  *
        355                 360                 365
```

<210> 302
<211> 366
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(366)
<223> Xaa = Any Amino Acid

<400> 302
Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
1   5   10   15
Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
            20   25   30
Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
        35   40   45
Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
    50   55   60
Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
65   70   75   80
Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
                85   90   95
Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
            100   105   110
Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
        115   120   125
Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
    130   135   140
Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
145   150   155   160
Met Asn Xaa Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
                165   170   175
Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
            180   185   190
Lys Thr Glu Glu Leu Ser Ser Ser Gln Thr Leu Ser His Asp Gly Gly
        195   200   205
Phe Phe Asn Arg Leu Glu Asp Asp Val His Lys Ile Leu Ile Arg Glu
    210   215   220
Lys Arg Arg Glu Gln Leu Thr Glu Tyr Asn Gly Thr Asp Asn Cys Thr
225   230   235   240
Ala His Glu His Asn Gln Glu Val Val Leu Lys Asp Gly Arg Ile Glu

245 250 255
Arg Leu Lys Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu
260 265 270
Lys Asn Val Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala
275 280 285
Arg Asn Ala Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp
290 295 300
Lys Ala Glu Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn
305 310 315 320
Glu Leu Thr Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu
325 330 335
Arg Ser Lys Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly
340 345 350
Gly Arg Lys Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg
355 360 365

<210> 303
<211> 807
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(807)

<400> 303
atg cta agg aag ctg tgg caa gaa aat aaa gca acc aac aca gac cat 48
Met Leu Arg Lys Leu Trp Gln Glu Asn Lys Ala Thr Asn Thr Asp His
1 5 10 15

tta acc acg gta ctc tac ctc cag ctt gct att tgt tca agt ttg cag 96
Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
20 25 30

aac ttg gag aaa aca att ttc tgc ctg cag aaa ctg att tct ttg cat 144
Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
35 40 45

cct ttt aat cct tgg aac tgg ggc aaa ttg gca gag gct tac ctg aat 192
Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
50 55 60

ctg ggg cca gct ctt tca gca gca ctt gcg tca tct cag aaa cag cac 240
Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His

```
65                  70                  75                  80

agt ttc acc tca agt gac aaa act atc aaa tcc ttc ttt cca cac tca      288
Ser Phe Thr Ser Ser Asp Lys Thr Ile Lys Ser Phe Phe Pro His Ser
                85                  90                  95

gga aaa gac tgt ctt ttg tgt ttt cct gaa acc ttg cct gag agc tct      336
Gly Lys Asp Cys Leu Leu Cys Phe Pro Glu Thr Leu Pro Glu Ser Ser
            100                 105                 110

tta ttt tct gtg gaa gcg aat agc agt aat agc cag aaa aat gag aaa      384
Leu Phe Ser Val Glu Ala Asn Ser Ser Asn Ser Gln Lys Asn Glu Lys
        115                 120                 125

gct ctg aca aat atc caa aac tgt atg gca gaa aag aga gaa aca gtg      432
Ala Leu Thr Asn Ile Gln Asn Cys Met Ala Glu Lys Arg Glu Thr Val
    130                 135                 140

ttg ata gag act cag ctg aaa gca tgt gcc tct ttt ata cga acc agg      480
Leu Ile Glu Thr Gln Leu Lys Ala Cys Ala Ser Phe Ile Arg Thr Arg
145                 150                 155                 160

ctt ctg ctt cag ttt acc caa cct cag caa aca tcg ttt gct ttg gag      528
Leu Leu Leu Gln Phe Thr Gln Pro Gln Gln Thr Ser Phe Ala Leu Glu
                165                 170                 175

agg aac tta agg act cag cag gaa att gaa gat aaa atg aaa ggg ttc      576
Arg Asn Leu Arg Thr Gln Gln Glu Ile Glu Asp Lys Met Lys Gly Phe
            180                 185                 190

agc ttc aaa gaa gac act ttg ctg ttg ata gct gag gtt atg gga gaa      624
Ser Phe Lys Glu Asp Thr Leu Leu Leu Ile Ala Glu Val Met Gly Glu
        195                 200                 205

gat atc cca gaa aaa ata aaa gat gaa gtt cac cca gag gtg aag tgt      672
Asp Ile Pro Glu Lys Ile Lys Asp Glu Val His Pro Glu Val Lys Cys
    210                 215                 220

gtt ggc tcc gta gcc ctg act gcc ttg gtg act gta tcc tca gaa gaa      720
Val Gly Ser Val Ala Leu Thr Ala Leu Val Thr Val Ser Ser Glu Glu
225                 230                 235                 240

ttt gaa gac aag tgg ttc aga aag atc aaa gac cat ttc tgt cca ttt      768
Phe Glu Asp Lys Trp Phe Arg Lys Ile Lys Asp His Phe Cys Pro Phe
```

245 250 255

gaa aat cag ttc cat aca gag ata caa atc ttg gct tag 807
Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala *
260 265

<210> 304
<211> 268
<212> PRT
<213> Homo sapiens

<400> 304
Met Leu Arg Lys Leu Trp Gln Glu Asn Lys Ala Thr Asn Thr Asp His
1 5 10 15
Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
20 25 30
Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
35 40 45
Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
50 55 60
Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His
65 70 75 80
Ser Phe Thr Ser Ser Asp Lys Thr Ile Lys Ser Phe Phe Pro His Ser
85 90 95
Gly Lys Asp Cys Leu Leu Cys Phe Pro Glu Thr Leu Pro Glu Ser Ser
100 105 110
Leu Phe Ser Val Glu Ala Asn Ser Ser Asn Ser Gln Lys Asn Glu Lys
115 120 125
Ala Leu Thr Asn Ile Gln Asn Cys Met Ala Glu Lys Arg Glu Thr Val
130 135 140
Leu Ile Glu Thr Gln Leu Lys Ala Cys Ala Ser Phe Ile Arg Thr Arg
145 150 155 160
Leu Leu Leu Gln Phe Thr Gln Pro Gln Gln Thr Ser Phe Ala Leu Glu
165 170 175
Arg Asn Leu Arg Thr Gln Gln Glu Ile Glu Asp Lys Met Lys Gly Phe
180 185 190
Ser Phe Lys Glu Asp Thr Leu Leu Leu Ile Ala Glu Val Met Gly Glu
195 200 205
Asp Ile Pro Glu Lys Ile Lys Asp Glu Val His Pro Glu Val Lys Cys
210 215 220
Val Gly Ser Val Ala Leu Thr Ala Leu Val Thr Val Ser Ser Glu Glu
225 230 235 240
Phe Glu Asp Lys Trp Phe Arg Lys Ile Lys Asp His Phe Cys Pro Phe

```
                245                 250                 255
Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala
            260                 265

      <210> 305
      <211> 810
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(810)

      <400> 305
atg gcc ata ttt ctg cag cat gcc gca gga ctc tta cat gca atg tgt       48
Met Ala Ile Phe Leu Gln His Ala Ala Gly Leu Leu His Ala Met Cys
 1               5                  10                  15

aca ctg tgc ttt gct gtc act gga agg tca tac agc ata ttt gac aat       96
Thr Leu Cys Phe Ala Val Thr Gly Arg Ser Tyr Ser Ile Phe Asp Asn
            20                  25                  30

aat cgc cag gat ccc aca ggg ctg aca gct gct ctt cag gca acc gac      144
Asn Arg Gln Asp Pro Thr Gly Leu Thr Ala Ala Leu Gln Ala Thr Asp
        35                  40                  45

ctg gct gga gtt ctt cat atg ctc tac tgt gtc ctc ttc cat ggc acc      192
Leu Ala Gly Val Leu His Met Leu Tyr Cys Val Leu Phe His Gly Thr
    50                  55                  60

atc ttg gac ccc agc act gcc agt ccc aag gag aat tac act caa aat      240
Ile Leu Asp Pro Ser Thr Ala Ser Pro Lys Glu Asn Tyr Thr Gln Asn
65                  70                  75                  80

acc atc caa gtg gcc att cag agt tta cgt ttc ttc aac agc ttt gca      288
Thr Ile Gln Val Ala Ile Gln Ser Leu Arg Phe Phe Asn Ser Phe Ala
                85                  90                  95

gct ctt cat ctg cct gct ttt cag tct att gta ggg gca gag ggc ttg      336
Ala Leu His Leu Pro Ala Phe Gln Ser Ile Val Gly Ala Glu Gly Leu
            100                 105                 110

tcc ctt gca ttc cgg cac atg gcc agc tcc ctg ctg ggc cac tgc agc      384
Ser Leu Ala Phe Arg His Met Ala Ser Ser Leu Leu Gly His Cys Ser
```

115 120 125

caa gtc tcc tgt gaa agc ctc ctt cat gag gtc atc gtc tgt gtg ggc 432
Gln Val Ser Cys Glu Ser Leu Leu His Glu Val Ile Val Cys Val Gly
130 135 140

tac ttc act gtc aac cac cca gat aac cag gtg atc gtg cag tcc ggc 480
Tyr Phe Thr Val Asn His Pro Asp Asn Gln Val Ile Val Gln Ser Gly
145 150 155 160

cgc cac ccc aca gtg ctg cag aag ctc tgc cag ttg ccc ttc cag tat 528
Arg His Pro Thr Val Leu Gln Lys Leu Cys Gln Leu Pro Phe Gln Tyr
165 170 175

ttc agt gac cca cgg ctg atc aaa gta ctg ttc cct tca ctt atc gct 576
Phe Ser Asp Pro Arg Leu Ile Lys Val Leu Phe Pro Ser Leu Ile Ala
180 185 190

gct tgt tac aac aac cat cag aac aag atc att ctg gag caa gag atg 624
Ala Cys Tyr Asn Asn His Gln Asn Lys Ile Ile Leu Glu Gln Glu Met
195 200 205

agc tgt gtt tta ctg gcc act ttc att cag gat ttg gca cag act cca 672
Ser Cys Val Leu Leu Ala Thr Phe Ile Gln Asp Leu Ala Gln Thr Pro
210 215 220

ggt caa gcg gaa aac cag cct tac caa ccc aaa ggg aaa tgc ctt ggt 720
Gly Gln Ala Glu Asn Gln Pro Tyr Gln Pro Lys Gly Lys Cys Leu Gly
225 230 235 240

tcc caa gac tat ctt gag ctg gct aac aga ttt cct cag cag gcc tgg 768
Ser Gln Asp Tyr Leu Glu Leu Ala Asn Arg Phe Pro Gln Gln Ala Trp
245 250 255

gaa gaa gct cga cag ttt ttc ttg aaa aaa gag aaa aaa taa 810
Glu Glu Ala Arg Gln Phe Phe Leu Lys Lys Glu Lys Lys *
260 265

<210> 306
<211> 269
<212> PRT
<213> Homo sapiens

<400> 306

```
Met Ala Ile Phe Leu Gln His Ala Ala Gly Leu Leu His Ala Met Cys
 1               5                  10                  15
Thr Leu Cys Phe Ala Val Thr Gly Arg Ser Tyr Ser Ile Phe Asp Asn
            20                  25                  30
Asn Arg Gln Asp Pro Thr Gly Leu Thr Ala Ala Leu Gln Ala Thr Asp
        35                  40                  45
Leu Ala Gly Val Leu His Met Leu Tyr Cys Val Leu Phe His Gly Thr
    50                  55                  60
Ile Leu Asp Pro Ser Thr Ala Ser Pro Lys Glu Asn Tyr Thr Gln Asn
65                  70                  75                  80
Thr Ile Gln Val Ala Ile Gln Ser Leu Arg Phe Phe Asn Ser Phe Ala
                85                  90                  95
Ala Leu His Leu Pro Ala Phe Gln Ser Ile Val Gly Ala Glu Gly Leu
            100                 105                 110
Ser Leu Ala Phe Arg His Met Ala Ser Ser Leu Leu Gly His Cys Ser
        115                 120                 125
Gln Val Ser Cys Glu Ser Leu Leu His Glu Val Ile Val Cys Val Gly
    130                 135                 140
Tyr Phe Thr Val Asn His Pro Asp Asn Gln Val Ile Val Gln Ser Gly
145                 150                 155                 160
Arg His Pro Thr Val Leu Gln Lys Leu Cys Gln Leu Pro Phe Gln Tyr
                165                 170                 175
Phe Ser Asp Pro Arg Leu Ile Lys Val Leu Phe Pro Ser Leu Ile Ala
            180                 185                 190
Ala Cys Tyr Asn Asn His Gln Asn Lys Ile Ile Leu Glu Gln Glu Met
        195                 200                 205
Ser Cys Val Leu Leu Ala Thr Phe Ile Gln Asp Leu Ala Gln Thr Pro
    210                 215                 220
Gly Gln Ala Glu Asn Gln Pro Tyr Gln Pro Lys Gly Lys Cys Leu Gly
225                 230                 235                 240
Ser Gln Asp Tyr Leu Glu Leu Ala Asn Arg Phe Pro Gln Gln Ala Trp
                245                 250                 255
Glu Glu Ala Arg Gln Phe Phe Leu Lys Lys Glu Lys Lys
            260                 265
```

<210> 307
<211> 831
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(831)

<400> 307

```
atg cag aac aag gtg act cag cta gtc ctg tct gcc ttg cag tcc ctg       48
Met Gln Asn Lys Val Thr Gln Leu Val Leu Ser Ala Leu Gln Ser Leu
1               5                   10                  15

act gac acc ttg ctt ttt ccc ttt tat tct ggg ccg agt ggt acc ctg       96
Thr Asp Thr Leu Leu Phe Pro Phe Tyr Ser Gly Pro Ser Gly Thr Leu
            20                  25                  30

aaa aca gcc ctg ctg gac tac atc aaa cgc tgc cgt cct gga gac agt      144
Lys Thr Ala Leu Leu Asp Tyr Ile Lys Arg Cys Arg Pro Gly Asp Ser
        35                  40                  45

gaa aag cac aat atg att gcc ctg tgc ttc agc atg tgc cgg gag att      192
Glu Lys His Asn Met Ile Ala Leu Cys Phe Ser Met Cys Arg Glu Ile
    50                  55                  60

ggc gag aac cac gag gca gct gcc cgc atc caa ctg aaa ttg att gag      240
Gly Glu Asn His Glu Ala Ala Ala Arg Ile Gln Leu Lys Leu Ile Glu
65                  70                  75                  80

tct cag ccc tgg gag gac agc ctc aag gat ggg cac cag ctg aaa caa      288
Ser Gln Pro Trp Glu Asp Ser Leu Lys Asp Gly His Gln Leu Lys Gln
                85                  90                  95

ctg ctg ctg aag gcc ctg act ctg atg ttg gat gca gca gag agt tat      336
Leu Leu Leu Lys Ala Leu Thr Leu Met Leu Asp Ala Ala Glu Ser Tyr
            100                 105                 110

gcc aag gac tcc tgt gtg cga cag gcc cag cac tgt cag cgg ctc acc      384
Ala Lys Asp Ser Cys Val Arg Gln Ala Gln His Cys Gln Arg Leu Thr
        115                 120                 125

aag ttg ata act ctg cag att cac ttt ctg aac act ggc cag aac aca      432
Lys Leu Ile Thr Leu Gln Ile His Phe Leu Asn Thr Gly Gln Asn Thr
    130                 135                 140

atg ctc atc aac ttg ggc cgc cac aag ctg atg gac tgt att ctg gcc      480
Met Leu Ile Asn Leu Gly Arg His Lys Leu Met Asp Cys Ile Leu Ala
145                 150                 155                 160

cta cct cgg ttc tac cag gct tct att gtg gct gag gcc tac gat ttt      528
Leu Pro Arg Phe Tyr Gln Ala Ser Ile Val Ala Glu Ala Tyr Asp Phe
```

165 170 175

gtt cca gat tgg gct gaa att tta tac cag caa gtg att ctt aaa gga 576
Val Pro Asp Trp Ala Glu Ile Leu Tyr Gln Gln Val Ile Leu Lys Gly
180 185 190

gac ttt aat tac ttg gaa gaa ttt aag cag caa agg tta tta aag tcc 624
Asp Phe Asn Tyr Leu Glu Glu Phe Lys Gln Gln Arg Leu Leu Lys Ser
195 200 205

agt ata ttt gaa gag att tcc aaa aaa tat aaa caa cat cag cct act 672
Ser Ile Phe Glu Glu Ile Ser Lys Lys Tyr Lys Gln His Gln Pro Thr
210 215 220

gac atg gtc atg gaa aac ctg aag aaa tta ctc aca tat tgt gaa gat 720
Asp Met Val Met Glu Asn Leu Lys Lys Leu Leu Thr Tyr Cys Glu Asp
225 230 235 240

gtt tac ctg tat tac aag ttg gca tac gaa cac aag ttt tat gaa att 768
Val Tyr Leu Tyr Tyr Lys Leu Ala Tyr Glu His Lys Phe Tyr Glu Ile
245 250 255

gta aat gtg ctt ctg aag gac cct cag aca ggt tgc tgt cta aag gac 816
Val Asn Val Leu Leu Lys Asp Pro Gln Thr Gly Cys Cys Leu Lys Asp
260 265 270

atg cta gca ggt tag 831
Met Leu Ala Gly *
275

<210> 308
<211> 276
<212> PRT
<213> Homo sapiens

<400> 308
Met Gln Asn Lys Val Thr Gln Leu Val Leu Ser Ala Leu Gln Ser Leu
1 5 10 15
Thr Asp Thr Leu Leu Phe Pro Phe Tyr Ser Gly Pro Ser Gly Thr Leu
20 25 30
Lys Thr Ala Leu Leu Asp Tyr Ile Lys Arg Cys Arg Pro Gly Asp Ser
35 40 45
Glu Lys His Asn Met Ile Ala Leu Cys Phe Ser Met Cys Arg Glu Ile

```
    50                  55                  60
Gly Glu Asn His Glu Ala Ala Ala Arg Ile Gln Leu Lys Leu Ile Glu
65                  70                  75                  80
Ser Gln Pro Trp Glu Asp Ser Leu Lys Asp Gly His Gln Leu Lys Gln
                85                  90                  95
Leu Leu Leu Lys Ala Leu Thr Leu Met Leu Asp Ala Ala Glu Ser Tyr
            100                 105                 110
Ala Lys Asp Ser Cys Val Arg Gln Ala Gln His Cys Gln Arg Leu Thr
        115                 120                 125
Lys Leu Ile Thr Leu Gln Ile His Phe Leu Asn Thr Gly Gln Asn Thr
    130                 135                 140
Met Leu Ile Asn Leu Gly Arg His Lys Leu Met Asp Cys Ile Leu Ala
145                 150                 155                 160
Leu Pro Arg Phe Tyr Gln Ala Ser Ile Val Ala Glu Ala Tyr Asp Phe
                165                 170                 175
Val Pro Asp Trp Ala Glu Ile Leu Tyr Gln Gln Val Ile Leu Lys Gly
            180                 185                 190
Asp Phe Asn Tyr Leu Glu Glu Phe Lys Gln Gln Arg Leu Leu Lys Ser
        195                 200                 205
Ser Ile Phe Glu Glu Ile Ser Lys Lys Tyr Lys Gln His Gln Pro Thr
    210                 215                 220
Asp Met Val Met Glu Asn Leu Lys Lys Leu Leu Thr Tyr Cys Glu Asp
225                 230                 235                 240
Val Tyr Leu Tyr Tyr Lys Leu Ala Tyr Glu His Lys Phe Tyr Glu Ile
                245                 250                 255
Val Asn Val Leu Leu Lys Asp Pro Gln Thr Gly Cys Cys Leu Lys Asp
            260                 265                 270
Met Leu Ala Gly
        275
```

<210> 309
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(369)

<400> 309

```
atg agg aca att gat gac aga ata gta cat gaa tta aac act acg gtt      48
Met Arg Thr Ile Asp Asp Arg Ile Val His Glu Leu Asn Thr Thr Val
 1               5                  10                  15
```

```
cca aca gct tcc ttt gca ggg aaa att gat gcc agc caa acc tgt aaa       96
Pro Thr Ala Ser Phe Ala Gly Lys Ile Asp Ala Ser Gln Thr Cys Lys
            20                  25                  30

caa ctt tat gag tct ttg atg gca gct cat gcc agt aga gac aga gtc      144
Gln Leu Tyr Glu Ser Leu Met Ala Ala His Ala Ser Arg Asp Arg Val
        35                  40                  45

ata aaa aac tgt ata gcc cag act tca gca gta gta aaa aac ctc cga      192
Ile Lys Asn Cys Ile Ala Gln Thr Ser Ala Val Val Lys Asn Leu Arg
    50                  55                  60

gaa gag aga gaa aag aat ttg gac gat tta acg tta tta aaa caa ctt      240
Glu Glu Arg Glu Lys Asn Leu Asp Asp Leu Thr Leu Leu Lys Gln Leu
65                  70                  75                  80

aga aaa gag cag aca aag ttg aaa tgg atg cag tca gaa ctg aat gtt      288
Arg Lys Glu Gln Thr Lys Leu Lys Trp Met Gln Ser Glu Leu Asn Val
                85                  90                  95

gaa gaa gtg gta aat gac agg agc tgg aag gtg ttt aat gaa cgc tgc      336
Glu Glu Val Val Asn Asp Arg Ser Trp Lys Val Phe Asn Glu Arg Cys
            100                 105                 110

cga att cac ttc aag cct cca aag aat gaa taa                          369
Arg Ile His Phe Lys Pro Pro Lys Asn Glu  *
        115                 120


      <210> 310
      <211> 122
      <212> PRT
      <213> Homo sapiens

      <400> 310
Met Arg Thr Ile Asp Asp Arg Ile Val His Glu Leu Asn Thr Thr Val
 1               5                  10                  15
Pro Thr Ala Ser Phe Ala Gly Lys Ile Asp Ala Ser Gln Thr Cys Lys
            20                  25                  30
Gln Leu Tyr Glu Ser Leu Met Ala Ala His Ala Ser Arg Asp Arg Val
        35                  40                  45
Ile Lys Asn Cys Ile Ala Gln Thr Ser Ala Val Val Lys Asn Leu Arg
    50                  55                  60
Glu Glu Arg Glu Lys Asn Leu Asp Asp Leu Thr Leu Leu Lys Gln Leu
```

```
65                  70                  75                  80
Arg Lys Glu Gln Thr Lys Leu Lys Trp Met Gln Ser Glu Leu Asn Val
                85                  90                  95
Glu Glu Val Val Asn Asp Arg Ser Trp Lys Val Phe Asn Glu Arg Cys
            100                 105                 110
Arg Ile His Phe Lys Pro Pro Lys Asn Glu
        115                 120
```

<210> 311
<211> 549
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(549)

<400> 311

```
atg gtc ccc gcc gcc ggc gcg ctg ctg tgg gtc ctg ctg ctg aat ctg      48
Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu
 1               5                  10                  15

ggt ccc cgg gcg gcg ggg gcc caa ggc ctg acc cag act ccg acc gaa      96
Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu
            20                  25                  30

atg cag cgg gtc agt tta cgc ttt ggg ggc ccc atg acc cgc agc tac     144
Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Ser Tyr
        35                  40                  45

cgg agc acc gcc cgg act ggt ctt ccc cgg aag aca agg ata atc cta     192
Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr Arg Ile Ile Leu
    50                  55                  60

gag gac gag aat gat gcc atg gcc gac gcc gac cgc ctg gct gga cca     240
Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp Arg Leu Ala Gly Pro
65                  70                  75                  80

gcg gct gcc gag ctc ttg gcc gcc acg gtg tcc acc ggc ttt agc cgg     288
Ala Ala Ala Glu Leu Leu Ala Ala Thr Val Ser Thr Gly Phe Ser Arg
                85                  90                  95

tcg tcc gcc att aac gag gag gat ggg tct tca gaa gag ggg gtt gtg     336
Ser Ser Ala Ile Asn Glu Glu Asp Gly Ser Ser Glu Glu Gly Val Val
```

```
            100                 105                 110

att aat gct gat gcc ctg ggg ccc gtg gca ctg cca ctg caa gtc ggg      384
Ile Asn Ala Asp Ala Leu Gly Pro Val Ala Leu Pro Leu Gln Val Gly
        115                 120                 125

cac cat gag ccg gag ccg gtc tgg gaa gct gca cgg cct ttc cgg gcg      432
His His Glu Pro Glu Pro Val Trp Glu Ala Ala Arg Pro Phe Arg Ala
    130                 135                 140

cct tcg agt tgg ggc gct gag cca gct ccg cac gga gca caa gcc ttg      480
Pro Ser Ser Trp Gly Ala Glu Pro Ala Pro His Gly Ala Gln Ala Leu
145                 150                 155                 160

cac cta tca aca atg tcc ctg caa ccg act tcg gga aga gtg ccc cct      528
His Leu Ser Thr Met Ser Leu Gln Pro Thr Ser Gly Arg Val Pro Pro
                165                 170                 175

gga cac aag tct ctg tac tga                                          549
Gly His Lys Ser Leu Tyr  *
            180


      <210> 312
      <211> 182
      <212> PRT
      <213> Homo sapiens

      <400> 312
Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu
 1               5                  10                  15
Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu
            20                  25                  30
Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Ser Tyr
        35                  40                  45
Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr Arg Ile Ile Leu
    50                  55                  60
Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp Arg Leu Ala Gly Pro
65                  70                  75                  80
Ala Ala Ala Glu Leu Leu Ala Ala Thr Val Ser Thr Gly Phe Ser Arg
                85                  90                  95
Ser Ser Ala Ile Asn Glu Glu Asp Gly Ser Ser Glu Glu Gly Val Val
            100                 105                 110
Ile Asn Ala Asp Ala Leu Gly Pro Val Ala Leu Pro Leu Gln Val Gly
```

```
        115                 120                 125
His His Glu Pro Glu Pro Val Trp Glu Ala Ala Arg Pro Phe Arg Ala
    130                 135                 140
Pro Ser Ser Trp Gly Ala Glu Pro Ala Pro His Gly Ala Gln Ala Leu
145                 150                 155                 160
His Leu Ser Thr Met Ser Leu Gln Pro Thr Ser Gly Arg Val Pro Pro
                165                 170                 175
Gly His Lys Ser Leu Tyr
            180

      <210> 313
      <211> 225
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(225)

      <221> misc_feature
      <222> (1)...(225)
      <223> n = A,T,C or G

      <400> 313
atg cac cca gct aag act ggc ttg acc gnn agc ctg gcc ttt ggt ggg      48
Met His Pro Ala Lys Thr Gly Leu Thr Xaa Ser Leu Ala Phe Gly Gly
 1               5                  10                  15

ggg ctt cct ggg gcc tgg gga aag ctg gcc acc ttc aac agc tgg tac      96
Gly Leu Pro Gly Ala Trp Gly Lys Leu Ala Thr Phe Asn Ser Trp Tyr
            20                  25                  30

ctc ttc aac agt gtg gcc ttt caa aat gca gat gcc acc agg aga aca     144
Leu Phe Asn Ser Val Ala Phe Gln Asn Ala Asp Ala Thr Arg Arg Thr
        35                  40                  45

tgc cca cag ctc acc acc tat gga tgc cat ggc tct ggg cag ctt tca     192
Cys Pro Gln Leu Thr Thr Tyr Gly Cys His Gly Ser Gly Gln Leu Ser
    50                  55                  60

aag cag gtt cct gtg gtc tcc tca gct gtt tga                         225
Lys Gln Val Pro Val Val Ser Ser Ala Val  *
 65                  70
```

<210> 314
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(74)
<223> Xaa = Any Amino Acid

<400> 314
Met His Pro Ala Lys Thr Gly Leu Thr Xaa Ser Leu Ala Phe Gly Gly
1 5 10 15
Gly Leu Pro Gly Ala Trp Gly Lys Leu Ala Thr Phe Asn Ser Trp Tyr
20 25 30
Leu Phe Asn Ser Val Ala Phe Gln Asn Ala Asp Ala Thr Arg Arg Thr
35 40 45
Cys Pro Gln Leu Thr Thr Tyr Gly Cys His Gly Ser Gly Gln Leu Ser
50 55 60
Lys Gln Val Pro Val Val Ser Ser Ala Val
65 70

<210> 315
<211> 1086
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1086)

<400> 315
atg gcc agc ctg ggg ctg ctg ctc ctg ctc tta ctg aca gca ctg cca 48
Met Ala Ser Leu Gly Leu Leu Leu Leu Leu Leu Leu Thr Ala Leu Pro
1 5 10 15

ccg ctg tgg tcc tcc tca ctg cct ggg ctg gac act gct gaa agt aaa 96
Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
20 25 30

gcc acc att gca gac ctg atc ctg tct gcg ctg gag aga gcc acc gtc 144
Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
35 40 45

```
ttc cta gaa cag agg ctg cct gaa atc aac ctg gat ggc atg gtg ggg      192
Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
     50                  55                  60

gtc cga gtg ctg gaa gag cag cta aaa agt gtc cgg gag aag tgg gcc      240
Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala
 65                  70                  75                  80

cag gag ccc ctg ctg cag ccg ctg agc ctg cgc gtg ggg atg ctg ggg      288
Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly
                 85                  90                  95

gag aag ctg gag gct gcc atc cag aga tcc ctc cac tac ctc aag ctg      336
Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu
            100                 105                 110

agt gat ccc aag tac cta aga gag ttc cag ctg acc ctc cag ccc ggg      384
Ser Asp Pro Lys Tyr Leu Arg Glu Phe Gln Leu Thr Leu Gln Pro Gly
        115                 120                 125

ttt tgg aag ctc cca cat gcc tgg atc cac act gat gcc tcc ttg gtg      432
Phe Trp Lys Leu Pro His Ala Trp Ile His Thr Asp Ala Ser Leu Val
    130                 135                 140

tac ccc acg ttc ggg ccc cag gac tca ttc tca gag gag aga agt gac      480
Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe Ser Glu Glu Arg Ser Asp
145                 150                 155                 160

gtg tgc ctg gtg cag ctg ctg gga acc ggg acg gac agc agc gag ccc      528
Val Cys Leu Val Gln Leu Leu Gly Thr Gly Thr Asp Ser Ser Glu Pro
                165                 170                 175

tgc ggc ctc tca gac ctc tgc agg agc ctc atg acc aag ccc ggc tgc      576
Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu Met Thr Lys Pro Gly Cys
            180                 185                 190

tca ggc tac tgc ctg tcc cac caa ctg ctc ttc ttc ctc tgg gcc aga      624
Ser Gly Tyr Cys Leu Ser His Gln Leu Leu Phe Phe Leu Trp Ala Arg
        195                 200                 205

atg agg gga tgc aca cag gga cca ctc caa cag agc cag gac tat atc      672
Met Arg Gly Cys Thr Gln Gly Pro Leu Gln Gln Ser Gln Asp Tyr Ile
    210                 215                 220
```

```
aac ctc ttc tgc gcc aac atg atg gac ttg aac cgc aga gct gag gcc      720
Asn Leu Phe Cys Ala Asn Met Met Asp Leu Asn Arg Arg Ala Glu Ala
225                 230                 235                 240

atc gga tac gcc tac cct acc cgg gac atc ttc atg gaa aac atc atg      768
Ile Gly Tyr Ala Tyr Pro Thr Arg Asp Ile Phe Met Glu Asn Ile Met
                245                 250                 255

ttc tgt gga atg ggc ggc ttc tcc gac ttc tac aag ctc cgg tgg ctg      816
Phe Cys Gly Met Gly Gly Phe Ser Asp Phe Tyr Lys Leu Arg Trp Leu
            260                 265                 270

gag gcc att ctc agc tgg cag aaa cag cag gaa gga tgc ttc ggg gag      864
Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu
        275                 280                 285

cct gat gct gaa gat gaa gaa tca tct aaa gct att caa tat cag cag      912
Pro Asp Ala Glu Asp Glu Glu Ser Ser Lys Ala Ile Gln Tyr Gln Gln
    290                 295                 300

cat ttt tcg agg aga gtg aag agg cga gaa aaa caa ttt cca gat ggc      960
His Phe Ser Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Gly
305                 310                 315                 320

tgc tcc tcc cac aac aca gcc aca gca gtg gca gcc ctg ggt ggc ttc     1008
Cys Ser Ser His Asn Thr Ala Thr Ala Val Ala Ala Leu Gly Gly Phe
                325                 330                 335

cta tac atc ctg gca gaa tac ccc cca gca aac aga gag cca cac cca     1056
Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala Asn Arg Glu Pro His Pro
            340                 345                 350

tcc aca ccg cca cca cca agc agc cgc tga                             1086
Ser Thr Pro Pro Pro Pro Ser Ser Arg  *
        355                 360
```

<210> 316
<211> 361
<212> PRT
<213> Homo sapiens

<400> 316

Met Ala Ser Leu Gly Leu Leu Leu Leu Leu Leu Leu Thr Ala Leu Pro
1 5 10 15
Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
20 25 30
Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
35 40 45
Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
50 55 60
Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala
65 70 75 80
Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly
85 90 95
Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu
100 105 110
Ser Asp Pro Lys Tyr Leu Arg Glu Phe Gln Leu Thr Leu Gln Pro Gly
115 120 125
Phe Trp Lys Leu Pro His Ala Trp Ile His Thr Asp Ala Ser Leu Val
130 135 140
Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe Ser Glu Glu Arg Ser Asp
145 150 155 160
Val Cys Leu Val Gln Leu Leu Gly Thr Gly Thr Asp Ser Ser Glu Pro
165 170 175
Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu Met Thr Lys Pro Gly Cys
180 185 190
Ser Gly Tyr Cys Leu Ser His Gln Leu Leu Phe Phe Leu Trp Ala Arg
195 200 205
Met Arg Gly Cys Thr Gln Gly Pro Leu Gln Gln Ser Gln Asp Tyr Ile
210 215 220
Asn Leu Phe Cys Ala Asn Met Met Asp Leu Asn Arg Arg Ala Glu Ala
225 230 235 240
Ile Gly Tyr Ala Tyr Pro Thr Arg Asp Ile Phe Met Glu Asn Ile Met
245 250 255
Phe Cys Gly Met Gly Gly Phe Ser Asp Phe Tyr Lys Leu Arg Trp Leu
260 265 270
Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu
275 280 285
Pro Asp Ala Glu Asp Glu Glu Ser Ser Lys Ala Ile Gln Tyr Gln Gln
290 295 300
His Phe Ser Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Gly
305 310 315 320
Cys Ser Ser His Asn Thr Ala Thr Ala Val Ala Ala Leu Gly Gly Phe
325 330 335
Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala Asn Arg Glu Pro His Pro
340 345 350

Ser Thr Pro Pro Pro Pro Ser Ser Arg
355 360

<210> 317
<211> 1440
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1440)

<221> misc_feature
<222> (1)...(1440)
<223> n = A,T,C or G

<400> 317
atg gcg gtc ctc gga gta cag ctg gtg gtg acc ctg ctc act gcc acc 48
Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala Thr
1 5 10 15

ctc atg cac agg ctg gcg cca cac tgc tcc ttc gcg cgc tgg ctg ctc 96
Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp Leu Leu
20 25 30

tgt aac ggc agt ttg ttc cga tac aag cac ccg tct gag gag gag ctt 144
Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu Glu Glu Leu
35 40 45

cgg gcc ctg gcg ggg aag ccg agg ccc aga ggc agg aaa gag cgg tgg 192
Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg Lys Glu Arg Trp
50 55 60

gcc aat ggc ctt agt gag gag aag cca ctg tct gtg ccc cga gat gcc 240
Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser Val Pro Arg Asp Ala
65 70 75 80

ccg ttc cag ctg gag acc tgc ccc ctc acg acc gtg gat gcc ctg gtc 288
Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr Thr Val Asp Ala Leu Val
85 90 95

ctg cgc ttc ttc ctg gag tac cag tgg ttt gtg gac ttt gct gtg tac 336
Leu Arg Phe Phe Leu Glu Tyr Gln Trp Phe Val Asp Phe Ala Val Tyr
100 105 110

```
tcg ggc ggc gtg tac ctc ttc aca gag gcc tac tac tac atg ctg gga      384
Ser Gly Gly Val Tyr Leu Phe Thr Glu Ala Tyr Tyr Tyr Met Leu Gly
        115                 120                 125

cca gcc aag gag act aac att gct gtg ttc tgg tgc ctg ctc acg gtg      432
Pro Ala Lys Glu Thr Asn Ile Ala Val Phe Trp Cys Leu Leu Thr Val
    130                 135                 140

acc ttc tcc atc aag atg ttc ctg aca gtg aca cgg ctg tac ttc agc      480
Thr Phe Ser Ile Lys Met Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser
145                 150                 155                 160

gcc gag gag ggg ggt gag cgc tct gtc tgc ctc acc ttt gcc ttc ctc      528
Ala Glu Glu Gly Gly Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu
                165                 170                 175

ttc ctg ctg ctg gcc atg ctg gtg caa gtg gtg cgg gag gag acc ctc      576
Phe Leu Leu Leu Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu
            180                 185                 190

gag ctg ggc ctg gag cct ggt ctg gcc agc atg acc cag aac tta gag      624
Glu Leu Gly Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu
        195                 200                 205

cca ctt ctg aag aag cag ggc tgg gac tgg gcg ctt cct gtg gcc aag      672
Pro Leu Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys
    210                 215                 220

ctg gct atc cgc gtg gga ctg gca gtg gtg ggc tct gtg ctg ggt gcc      720
Leu Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala
225                 230                 235                 240

ttc ctc acc ttc cca ggc ctg cgg ctg gcc cag acc cac cgg gac gca      768
Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp Ala
                245                 250                 255

ctg acc atg tcg gag gac aga ccc atg ctg cag ttc ctc ctg cac acc      816
Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu His Thr
            260                 265                 270

agc ttc ctg tct ccc ctg ttc atc ctg tgg ctc tgg aca aag ccc att      864
Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr Lys Pro Ile
        275                 280                 285
```

```
gca cgg gac ttc ctg cac cag ccg ccg ttt ggg gag acg cgt ttc tcc      912
Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu Thr Arg Phe Ser
    290                 295                 300

ctg ctg tcc gat tct gcc ttc gac tct ggg cgc ctc tgg ttg ctg gtg      960
Leu Leu Ser Asp Ser Ala Phe Asp Ser Gly Arg Leu Trp Leu Leu Val
305                 310                 315                 320

gtg ctg tgc ctg ctg cgg ctg gcg gtg acc cgg ccc cac ctg cag gcc      1008
Val Leu Cys Leu Leu Arg Leu Ala Val Thr Arg Pro His Leu Gln Ala
                325                 330                 335

tac ctg tgc ctg gcc aag gcc cgg gtg gag cag ctg cga agg gag gct      1056
Tyr Leu Cys Leu Ala Lys Ala Arg Val Glu Gln Leu Arg Arg Glu Ala
            340                 345                 350

ggc cgc atc gaa gcc cgt gaa atc cag cag agg gtg gtc cga gtc tac      1104
Gly Arg Ile Glu Ala Arg Glu Ile Gln Gln Arg Val Val Arg Val Tyr
        355                 360                 365

tgc tat gtg acc gtg gtg agc ttg cag tac ctg acg ccg ctc atc ctc      1152
Cys Tyr Val Thr Val Val Ser Leu Gln Tyr Leu Thr Pro Leu Ile Leu
    370                 375                 380

acc ctc aac tgc aca ctt ctg ctc aag acg ctg gga ggc tat tcc tgg      1200
Thr Leu Asn Cys Thr Leu Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp
385                 390                 395                 400

ggc ctg ggc cca gct cct cta cta tcc ccc gac cca tcc tca gcc agc      1248
Gly Leu Gly Pro Ala Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala Ser
                405                 410                 415

gct gcc ccc atc ggc tct ggg gag gac gaa gtc nag cag act gca gcg      1296
Ala Ala Pro Ile Gly Ser Gly Glu Asp Glu Val Xaa Gln Thr Ala Ala
            420                 425                 430

cgg att gcc ggg gcc ctg ggt ggc ctg ctt act ccc ctc ttc ctc cgt      1344
Arg Ile Ala Gly Ala Leu Gly Gly Leu Leu Thr Pro Leu Phe Leu Arg
        435                 440                 445

ggc gtc ctg gcc tac ctc atc tgg tgg acg gct gcc tgc cag ctg ctc      1392
Gly Val Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala Cys Gln Leu Leu
    450                 455                 460
```

gcc agc ctt ttc ggc ctc tac ttc cac cag cac ttg gca ggc tcc tag 1440
Ala Ser Leu Phe Gly Leu Tyr Phe His Gln His Leu Ala Gly Ser *
465 470 475

<210> 318
<211> 479
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(479)
<223> Xaa = Any Amino Acid

<400> 318
Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala Thr
1 5 10 15
Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp Leu Leu
20 25 30
Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu Glu Glu Leu
35 40 45
Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg Lys Glu Arg Trp
50 55 60
Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser Val Pro Arg Asp Ala
65 70 75 80
Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr Thr Val Asp Ala Leu Val
85 90 95
Leu Arg Phe Phe Leu Glu Tyr Gln Trp Phe Val Asp Phe Ala Val Tyr
100 105 110
Ser Gly Gly Val Tyr Leu Phe Thr Glu Ala Tyr Tyr Tyr Met Leu Gly
115 120 125
Pro Ala Lys Glu Thr Asn Ile Ala Val Phe Trp Cys Leu Leu Thr Val
130 135 140
Thr Phe Ser Ile Lys Met Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser
145 150 155 160
Ala Glu Glu Gly Gly Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu
165 170 175
Phe Leu Leu Leu Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu
180 185 190
Glu Leu Gly Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu
195 200 205
Pro Leu Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys

210 215 220
Leu Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala
225 230 235 240
Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp Ala
245 250 255
Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu His Thr
260 265 270
Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr Lys Pro Ile
275 280 285
Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu Thr Arg Phe Ser
290 295 300
Leu Leu Ser Asp Ser Ala Phe Asp Ser Gly Arg Leu Trp Leu Leu Val
305 310 315 320
Val Leu Cys Leu Leu Arg Leu Ala Val Thr Arg Pro His Leu Gln Ala
325 330 335
Tyr Leu Cys Leu Ala Lys Ala Arg Val Glu Gln Leu Arg Arg Glu Ala
340 345 350
Gly Arg Ile Glu Ala Arg Glu Ile Gln Gln Arg Val Val Arg Val Tyr
355 360 365
Cys Tyr Val Thr Val Val Ser Leu Gln Tyr Leu Thr Pro Leu Ile Leu
370 375 380
Thr Leu Asn Cys Thr Leu Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp
385 390 395 400
Gly Leu Gly Pro Ala Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala Ser
405 410 415
Ala Ala Pro Ile Gly Ser Gly Glu Asp Glu Val Xaa Gln Thr Ala Ala
420 425 430
Arg Ile Ala Gly Ala Leu Gly Gly Leu Leu Thr Pro Leu Phe Leu Arg
435 440 445
Gly Val Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala Cys Gln Leu Leu
450 455 460
Ala Ser Leu Phe Gly Leu Tyr Phe His Gln His Leu Ala Gly Ser
465 470 475

<210> 319
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(333)

<400> 319

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atg gct gct tca tca tca tcc tcc tca gct ggt ggg gtc agt gga agt       48
Met Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly Gly Val Ser Gly Ser
 1               5                  10                  15

tct gtc act gga tct ggt ttc agt gtc tca gac ctt gcc cca cca cgg       96
Ser Val Thr Gly Ser Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg
            20                  25                  30

aaa gcc ctt ttc acc tac ccc aaa gga gct gga gag atg tta gaa gat      144
Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp
        35                  40                  45

ggc tct gag aga ttc ctc tgc gaa tct gtt ttt agc tat caa gtg gca      192
Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala
    50                  55                  60

tcc acg ctt aaa cag gtg aaa cat gat cag caa gtt gct cgg atg gaa      240
Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu
 65                  70                  75                  80

aaa cta gct ggt ttg gta gaa gag ctg gag gct gac gag tgg cgg ttt      288
Lys Leu Ala Gly Leu Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe
                85                  90                  95

aag ccc atc gag cag ctg ctg gga ttc acc ccc tct tca ggt tga          333
Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly  *
            100                 105                 110


      <210> 320
      <211> 110
      <212> PRT
      <213> Homo sapiens

      <400> 320
Met Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly Gly Val Ser Gly Ser
 1               5                  10                  15
Ser Val Thr Gly Ser Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg
            20                  25                  30
Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp
        35                  40                  45
Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala
    50                  55                  60
Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu
```

65 70 75 80
Lys Leu Ala Gly Leu Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe
85 90 95
Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly
100 105 110

<210> 321
<211> 1383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1383)

<221> misc_feature
<222> (1)...(1383)
<223> n = A,T,C or G

<400> 321
atg ctt tgt ctg gca gct ctt cat ggc atg gng gcc ttg gta ggc tct 48
Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
1 5 10 15

gaa ggg gat gta atg cag ctg aaa tca gaa gcc atc cag acc tct cat 96
Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
20 25 30

ttt caa ggc aga ctt aat gaa gtc att aga acc tta act cag gtc att 144
Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
35 40 45

agt gtc tct ggg gtg att ggt ctc cag tca aat gca gtc tgg ctt ctt 192
Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
50 55 60

gga cat ctt cat cta tct act cta tcc tca agt caa agt aga gcc tct 240
Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
65 70 75 80

gtt cct act gac tat agc tac ttg cct gaa agc agt ttt att gga gca 288
Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
85 90 95

gct att ggc ttc ttc att aca gga gga aaa aaa ggt cct gaa tct gtg 336
Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val
100 105 110

cct cct tcc ctt ctt aaa gta gtg atg aaa ccc ata gca act gtt gga 384
Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly
115 120 125

gaa agc tac caa tat cct cct gtg aac tgg gct gca ctt ctc tct cca 432
Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro
130 135 140

ctt atg agg cta aat ttt ggt gaa gag atc cag caa ctg tgc ctt gaa 480
Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu
145 150 155 160

att atg gtg acc cag gca cag tca tcc cag aat gca gct gca cta ttg 528
Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu
165 170 175

ggc ttg tgg gtg aca cca cca ctg atc cac agt ctg agt ctg aat acc 576
Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr
180 185 190

aag aga tat ctc ctg ata tct gca cct ctg tgg ata aaa cac atc tct 624
Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser
195 200 205

gat gaa cag atc ctg ggt ttt gtt gaa aat tta atg gtg gca gtt ttt 672
Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe
210 215 220

aaa gca gct tcc cca ctt gga agt cct gag cta tgc cca agt gct tta 720
Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu
225 230 235 240

cac ggt ctg agc cag gcc atg aaa ctg ccc agc cct gcc cac cac ctc 768
His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu
245 250 255

tgg agt ctg ctc tct gaa gct act ggg aaa att ttt gac ctc ctg cca 816
Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro
260 265 270

aat aag att cgg aga aag gat cta gag ctg tat atc agc ata gca aaa 864
Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys
275 280 285

tgc ctc tta gaa atg aca gat gat gat gcc aat cgg atc gcc cag gtt 912
Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val
290 295 300

act aag agc aac ata gaa aaa gct gcc ttt gtc aaa ctg tac tta gtc 960
Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val
305 310 315 320

tct caa gga cga ttc ccc ttg gtg aac ctg acc gat atg ctg aga ttt 1008
Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Arg Phe
325 330 335

gca acc gca gtg gtt gca tgg gct gac cac act gcc cct ctc ctc ctc 1056
Ala Thr Ala Val Val Ala Trp Ala Asp His Thr Ala Pro Leu Leu Leu
340 345 350

ggc ctc agt gcc agt tgg ttg cca tgg cat cag gag aat ggc ccg gct 1104
Gly Leu Ser Ala Ser Trp Leu Pro Trp His Gln Glu Asn Gly Pro Ala
355 360 365

ggg cca gta cca agc ttc ctt ggc agg agt cca atg cac agg gtc act 1152
Gly Pro Val Pro Ser Phe Leu Gly Arg Ser Pro Met His Arg Val Thr
370 375 380

ctg cag gag gtt ctc act ctc ctt ccc aat agc atg gct ctg ctg ctg 1200
Leu Gln Glu Val Leu Thr Leu Leu Pro Asn Ser Met Ala Leu Leu Leu
385 390 395 400

cag aaa gag cca tgg aag gaa cag acc cag aag ttc att gac tgg cta 1248
Gln Lys Glu Pro Trp Lys Glu Gln Thr Gln Lys Phe Ile Asp Trp Leu
405 410 415

ttc agc atc atg gaa agc cct aaa gaa gcc ctc tca gca cag tcc agg 1296
Phe Ser Ile Met Glu Ser Pro Lys Glu Ala Leu Ser Ala Gln Ser Arg
420 425 430

gat ctt ttg aaa gcc acc ctg ctg tcc ttg aga gtt ctc cca gag ttt 1344
Asp Leu Leu Lys Ala Thr Leu Leu Ser Leu Arg Val Leu Pro Glu Phe
435 440 445

aag aag aaa gct gta tgg acc aga gca tat ggt tgg tga 1383
Lys Lys Lys Ala Val Trp Thr Arg Ala Tyr Gly Trp *
450 455 460

<210> 322
<211> 460
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(460)
<223> Xaa = Any Amino Acid

<400> 322
Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
1 5 10 15
Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
20 25 30
Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
35 40 45
Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
50 55 60
Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
65 70 75 80
Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
85 90 95
Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val
100 105 110
Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly
115 120 125
Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro
130 135 140
Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu
145 150 155 160
Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu
165 170 175
Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr
180 185 190
Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser
195 200 205
Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe
210 215 220

Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu
225 230 235 240
His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu
245 250 255
Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro
260 265 270
Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys
275 280 285
Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val
290 295 300
Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val
305 310 315 320
Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Arg Phe
325 330 335
Ala Thr Ala Val Val Ala Trp Ala Asp His Thr Ala Pro Leu Leu Leu
340 345 350
Gly Leu Ser Ala Ser Trp Leu Pro Trp His Gln Glu Asn Gly Pro Ala
355 360 365
Gly Pro Val Pro Ser Phe Leu Gly Arg Ser Pro Met His Arg Val Thr
370 375 380
Leu Gln Glu Val Leu Thr Leu Leu Pro Asn Ser Met Ala Leu Leu Leu
385 390 395 400
Gln Lys Glu Pro Trp Lys Glu Gln Thr Gln Lys Phe Ile Asp Trp Leu
405 410 415
Phe Ser Ile Met Glu Ser Pro Lys Glu Ala Leu Ser Ala Gln Ser Arg
420 425 430
Asp Leu Leu Lys Ala Thr Leu Leu Ser Leu Arg Val Leu Pro Glu Phe
435 440 445
Lys Lys Lys Ala Val Trp Thr Arg Ala Tyr Gly Trp
450 455 460

<210> 323
<211> 1596
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1596)

<221> misc_feature
<222> (1)...(1596)
<223> n = A,T,C or G

<400> 323

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atg ctt tgt ctg gca gct ctt cat ggc atg gng gcc ttg gta ggc tct       48
Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
 1               5                  10                  15

gaa ggg gat gta atg cag ctg aaa tca gaa gcc atc cag acc tct cat       96
Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
            20                  25                  30

ttt caa ggc aga ctt aat gaa gtc att aga acc tta act cag gtc att      144
Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
        35                  40                  45

agt gtc tct ggg gtg att ggt ctc cag tca aat gca gtc tgg ctt ctt      192
Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
    50                  55                  60

gga cat ctt cat cta tct act cta tcc tca agt caa agt aga gcc tct      240
Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
65                  70                  75                  80

gtt cct act gac tat agc tac ttg cct gaa agc agt ttt att gga gca      288
Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
                85                  90                  95

gct att ggc ttc ttc att aca gga gga aaa aaa ggt cct gaa tct gtg      336
Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val
            100                 105                 110

cct cct tcc ctt ctt aaa gta gtg atg aaa ccc ata gca act gtt gga      384
Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly
        115                 120                 125

gaa agc tac caa tat cct cct gtg aac tgg gct gca ctt ctc tct cca      432
Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro
    130                 135                 140

ctt atg agg cta aat ttt ggt gaa gag atc cag caa ctg tgc ctt gaa      480
Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu
145                 150                 155                 160

att atg gtg acc cag gca cag tca tcc cag aat gca gct gca cta ttg      528
Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu
                165                 170                 175
```

ggc ttg tgg gtg aca cca cca ctg atc cac agt ctg agt ctg aat acc 576
Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr
180 185 190

aag aga tat ctc ctg ata tct gca cct ctg tgg ata aaa cac atc tct 624
Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser
195 200 205

gat gaa cag atc ctg ggt ttt gtt gaa aat tta atg gtg gca gtt ttt 672
Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe
210 215 220

aaa gca gct tcc cca ctt gga agt cct gag cta tgc cca agt gct tta 720
Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu
225 230 235 240

cac ggt ctg agc cag gcc atg aaa ctg ccc agc cct gcc cac cac ctc 768
His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu
245 250 255

tgg agt ctg ctc tct gaa gct act ggg aaa att ttt gac ctc ctg cca 816
Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro
260 265 270

aat aag att cgg aga aag gat cta gag ctg tat atc agc ata gca aaa 864
Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys
275 280 285

tgc ctc tta gaa atg aca gat gat gat gcc aat cgg atc gcc cag gtt 912
Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val
290 295 300

act aag agc aac ata gaa aaa gct gcc ttt gtc aaa ctg tac tta gtc 960
Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val
305 310 315 320

tct caa gga cga ttc ccc ttg gtg aac ctg acc gat atg ctg agc gtt 1008
Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Ser Val
325 330 335

gct gtg cag cac cgt gag aaa gag gtg ttg gcc tgg atg att ctg cac 1056
Ala Val Gln His Arg Glu Lys Glu Val Leu Ala Trp Met Ile Leu His
340 345 350

agc tta tac cag gca cgg att gtg agc cat gcc aat acg ggc gtt ttg 1104
Ser Leu Tyr Gln Ala Arg Ile Val Ser His Ala Asn Thr Gly Val Leu
355 360 365

aag aga atg gag tgg ctc ttg gaa ctg atg ggt tat att aga aat gtt 1152
Lys Arg Met Glu Trp Leu Leu Glu Leu Met Gly Tyr Ile Arg Asn Val
370 375 380

gct tac cag tca aca tcc ttt cac aat acg gct ctt gac gag gct ttg 1200
Ala Tyr Gln Ser Thr Ser Phe His Asn Thr Ala Leu Asp Glu Ala Leu
385 390 395 400

gac ttc ttc ttg ctg ata ttt gca acc gca gtg gtt gca tgg gct gac 1248
Asp Phe Phe Leu Leu Ile Phe Ala Thr Ala Val Val Ala Trp Ala Asp
405 410 415

cac act gcc cct ctc ctc ctc ggc ctc agt gcc agt tgg ttg cca tgg 1296
His Thr Ala Pro Leu Leu Leu Gly Leu Ser Ala Ser Trp Leu Pro Trp
420 425 430

cat cag gag aat ggc ccg gct ggg cca gta cca agc ttc ctt ggc agg 1344
His Gln Glu Asn Gly Pro Ala Gly Pro Val Pro Ser Phe Leu Gly Arg
435 440 445

agt cca atg cac agg gtc act ctg cag gag gtt ctc act ctc ctt ccc 1392
Ser Pro Met His Arg Val Thr Leu Gln Glu Val Leu Thr Leu Leu Pro
450 455 460

aat agc atg gct ctg ctg ctg cag aaa gag cca tgg aag gaa cag acc 1440
Asn Ser Met Ala Leu Leu Leu Gln Lys Glu Pro Trp Lys Glu Gln Thr
465 470 475 480

cag aag ttc att gac tgg cta ttc agc atc atg gaa agc cct aaa gaa 1488
Gln Lys Phe Ile Asp Trp Leu Phe Ser Ile Met Glu Ser Pro Lys Glu
485 490 495

gcc ctc tca gca cag tcc agg gat ctt ttg aaa gcc acc ctg ctg tcc 1536
Ala Leu Ser Ala Gln Ser Arg Asp Leu Leu Lys Ala Thr Leu Leu Ser
500 505 510

ttg aga gtt ctc cca gag ttt aag aag aaa gct gta tgg acc aga gca 1584
Leu Arg Val Leu Pro Glu Phe Lys Lys Lys Ala Val Trp Thr Arg Ala
515 520 525

```
tat ggt tgg tga                                                    1596
Tyr Gly Trp  *
    530


      <210> 324
      <211> 531
      <212> PRT
      <213> Homo sapiens

      <220>
      <221> VARIANT
      <222> (1)...(531)
      <223> Xaa = Any Amino Acid

      <400> 324
Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
 1               5                  10                  15
Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
            20                  25                  30
Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
        35                  40                  45
Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
    50                  55                  60
Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
65                  70                  75                  80
Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
                85                  90                  95
Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val
            100                 105                 110
Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly
        115                 120                 125
Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro
    130                 135                 140
Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu
145                 150                 155                 160
Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu
                165                 170                 175
Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr
            180                 185                 190
Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser
        195                 200                 205
Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe
```

210 215 220
Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu
225 230 235 240
His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu
245 250 255
Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro
260 265 270
Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys
275 280 285
Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val
290 295 300
Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val
305 310 315 320
Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Ser Val
325 330 335
Ala Val Gln His Arg Glu Lys Glu Val Leu Ala Trp Met Ile Leu His
340 345 350
Ser Leu Tyr Gln Ala Arg Ile Val Ser His Ala Asn Thr Gly Val Leu
355 360 365
Lys Arg Met Glu Trp Leu Leu Glu Leu Met Gly Tyr Ile Arg Asn Val
370 375 380
Ala Tyr Gln Ser Thr Ser Phe His Asn Thr Ala Leu Asp Glu Ala Leu
385 390 395 400
Asp Phe Phe Leu Leu Ile Phe Ala Thr Ala Val Val Ala Trp Ala Asp
405 410 415
His Thr Ala Pro Leu Leu Leu Gly Leu Ser Ala Ser Trp Leu Pro Trp
420 425 430
His Gln Glu Asn Gly Pro Ala Gly Pro Val Pro Ser Phe Leu Gly Arg
435 440 445
Ser Pro Met His Arg Val Thr Leu Gln Glu Val Leu Thr Leu Leu Pro
450 455 460
Asn Ser Met Ala Leu Leu Leu Gln Lys Glu Pro Trp Lys Glu Gln Thr
465 470 475 480
Gln Lys Phe Ile Asp Trp Leu Phe Ser Ile Met Glu Ser Pro Lys Glu
485 490 495
Ala Leu Ser Ala Gln Ser Arg Asp Leu Leu Lys Ala Thr Leu Leu Ser
500 505 510
Leu Arg Val Leu Pro Glu Phe Lys Lys Lys Ala Val Trp Thr Arg Ala
515 520 525
Tyr Gly Trp
530

<210> 325
<211> 666

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(666)

<400> 325
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atg gcc ggg act ggg ctg ctg gcg ctg cgg acg ctg cca ggg ccc agc      48
Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser
 1               5                  10                  15

tgg gtg cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg      96
Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala
            20                  25                  30

gcc gtg gtg cgg cct ggc ttc ctg agc acg gca gag gag gag acg ctg     144
Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu
        35                  40                  45

agc cga gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat     192
Ser Arg Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp
    50                  55                  60

cac tgg gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc     240
His Trp Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg
 65                  70                  75                  80

tgg tca gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc     288
Trp Ser Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala
                85                  90                  95

ttt ggc ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg     336
Phe Gly Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu
            100                 105                 110

gaa gcc cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc     384
Glu Ala Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys
        115                 120                 125

ggg gcc acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg     432
Gly Ala Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg
    130                 135                 140
```

ctg gtg cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag 480
Leu Val His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu
145 150 155 160

ccg ggc tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc 528
Pro Gly Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser
165 170 175

cat gag atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cgg att 576
His Glu Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Arg Ile
180 185 190

ccc cgg ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc 624
Pro Arg Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly
195 200 205

atg ggg cca ggg gag tct gga cag ccg ccc cca gcc tgc tga 666
Met Gly Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys *
210 215 220

<210> 326
<211> 221
<212> PRT
<213> Homo sapiens

<400> 326
Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser
1 5 10 15
Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala
20 25 30
Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu
35 40 45
Ser Arg Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp
50 55 60
His Trp Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg
65 70 75 80
Trp Ser Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala
85 90 95
Phe Gly Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu
100 105 110
Glu Ala Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys
115 120 125
Gly Ala Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg

130 135 140
Leu Val His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu
145 150 155 160
Pro Gly Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser
165 170 175
His Glu Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Arg Ile
180 185 190
Pro Arg Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly
195 200 205
Met Gly Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys
210 215 220

<210> 327
<211> 294
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(294)

<400> 327
atg gct gaa aat agt gta tta aca tcc act act ggg agg act agc ttg 48
Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
1 5 10 15

gca gac tct tcc att ttt gat tct aaa gtt act gag att tcc aag gaa 96
Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
20 25 30

aac tta ctt att gga tct act tca tat gta gaa gaa gag atg cct cag 144
Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
35 40 45

att gaa aca aga gtg ata ttg gtt caa gaa gct gga aaa caa gaa gaa 192
Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
50 55 60

ctt ata aaa gcc tta aag gac att aaa gtg ggc ttt gta aag atg gag 240
Leu Ile Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65 70 75 80

tca gtg gaa gaa ttt gaa ggt ttg gat tct ccg gaa ttt gaa atg tat 288
Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Met Tyr

85 90 95

ttg tag 294
Leu *

<210> 328
<211> 97
<212> PRT
<213> Homo sapiens

<400> 328
Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
1 5 10 15
Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
20 25 30
Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
35 40 45
Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
50 55 60
Leu Ile Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65 70 75 80
Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Met Tyr
85 90 95
Leu

<210> 329
<211> 270
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(270)

<400> 329
atg gtg tca gct agc gtg ttt gtg ggc ctg gtg atc ttc tac atc gcc 48
Met Val Ser Ala Ser Val Phe Val Gly Leu Val Ile Phe Tyr Ile Ala
1 5 10 15

ttc tgc ctc ctg tgg ccc ctc gtg gtg aag ggc tgc acg atg atc cgg 96
Phe Cys Leu Leu Trp Pro Leu Val Val Lys Gly Cys Thr Met Ile Arg

20 25 30

tgg aag ata aac aac ctc att gcc tca gaa tcc tac tac acc tac gcc 144
Trp Lys Ile Asn Asn Leu Ile Ala Ser Glu Ser Tyr Tyr Thr Tyr Ala
35 40 45

tcc att tcc gga atc tcg agc atg cca tct ctg aga cat tcc agg atg 192
Ser Ile Ser Gly Ile Ser Ser Met Pro Ser Leu Arg His Ser Arg Met
50 55 60

ggc tcc atg ttc agc tcc agg atg aca gag gac agg gct gaa ccc aag 240
Gly Ser Met Phe Ser Ser Arg Met Thr Glu Asp Arg Ala Glu Pro Lys
65 70 75 80

gaa gcc gtg gag aga cag ttg atg acc tga 270
Glu Ala Val Glu Arg Gln Leu Met Thr *
85

<210> 330
<211> 89
<212> PRT
<213> Homo sapiens

<400> 330
Met Val Ser Ala Ser Val Phe Val Gly Leu Val Ile Phe Tyr Ile Ala
1 5 10 15
Phe Cys Leu Leu Trp Pro Leu Val Val Lys Gly Cys Thr Met Ile Arg
20 25 30
Trp Lys Ile Asn Asn Leu Ile Ala Ser Glu Ser Tyr Tyr Thr Tyr Ala
35 40 45
Ser Ile Ser Gly Ile Ser Ser Met Pro Ser Leu Arg His Ser Arg Met
50 55 60
Gly Ser Met Phe Ser Ser Arg Met Thr Glu Asp Arg Ala Glu Pro Lys
65 70 75 80
Glu Ala Val Glu Arg Gln Leu Met Thr
85

<210> 331
<211> 255
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)...(255)

<400> 331
atg tta ggc ctt ttg cag ttt gac tct ggc ttt att tgc ctt tgt gct 48
Met Leu Gly Leu Leu Gln Phe Asp Ser Gly Phe Ile Cys Leu Cys Ala
1 5 10 15

cgt gtt tat cct tcc tgc ctt gaa cct ggt cag agt ttt att act gag 96
Arg Val Tyr Pro Ser Cys Leu Glu Pro Gly Gln Ser Phe Ile Thr Glu
20 25 30

gaa gat gat gca cgg agt gag tct agt act gaa tgg gac tta gat gga 144
Glu Asp Asp Ala Arg Ser Glu Ser Ser Thr Glu Trp Asp Leu Asp Gly
35 40 45

ttc agt gag ctg gac tct gag tca gga agt tca agt tct ttt tca gat 192
Phe Ser Glu Leu Asp Ser Glu Ser Gly Ser Ser Ser Ser Phe Ser Asp
50 55 60

gat gaa gtc tgg gtg caa gta gca cct cag cga aat gca cag gat cag 240
Asp Glu Val Trp Val Gln Val Ala Pro Gln Arg Asn Ala Gln Asp Gln
65 70 75 80

cag ggt tct ttg taa 255
Gln Gly Ser Leu *

<210> 332
<211> 84
<212> PRT
<213> Homo sapiens

<400> 332
Met Leu Gly Leu Leu Gln Phe Asp Ser Gly Phe Ile Cys Leu Cys Ala
1 5 10 15
Arg Val Tyr Pro Ser Cys Leu Glu Pro Gly Gln Ser Phe Ile Thr Glu
20 25 30
Glu Asp Asp Ala Arg Ser Glu Ser Ser Thr Glu Trp Asp Leu Asp Gly
35 40 45
Phe Ser Glu Leu Asp Ser Glu Ser Gly Ser Ser Ser Ser Phe Ser Asp
50 55 60
Asp Glu Val Trp Val Gln Val Ala Pro Gln Arg Asn Ala Gln Asp Gln

```
65                  70                  75                  80
Gln Gly Ser Leu


      <210> 333
      <211> 243
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(243)

      <400> 333
atg gag att ctc tgg ctg atg gtc aag tcc tgg aat acc gga gta ctt         48
Met Glu Ile Leu Trp Leu Met Val Lys Ser Trp Asn Thr Gly Val Leu
 1               5                  10                  15

atg ttt agc agg agc aag tat gca tct gct gaa aag tgg tgt ggc ctg         96
Met Phe Ser Arg Ser Lys Tyr Ala Ser Ala Glu Lys Trp Cys Gly Leu
            20                  25                  30

gcc ttg cgt ttc ctt aac cac ctt acc tcc ttc aag gaa agc tat gaa        144
Ala Leu Arg Phe Leu Asn His Leu Thr Ser Phe Lys Glu Ser Tyr Glu
        35                  40                  45

act cag atg aat atg ctg tat agt cag ctt gtg gaa gca ttg agt aac        192
Thr Gln Met Asn Met Leu Tyr Ser Gln Leu Val Glu Ala Leu Ser Asn
    50                  55                  60

aac aag ggc cca gtt ttt cat gaa cat ggc tac tgg agc aag tca gat        240
Asn Lys Gly Pro Val Phe His Glu His Gly Tyr Trp Ser Lys Ser Asp
 65                  70                  75                  80

tag                                                                    243
 *


      <210> 334
      <211> 80
      <212> PRT
      <213> Homo sapiens
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```
      <400> 334
Met Glu Ile Leu Trp Leu Met Val Lys Ser Trp Asn Thr Gly Val Leu
 1               5                  10                  15
Met Phe Ser Arg Ser Lys Tyr Ala Ser Ala Glu Lys Trp Cys Gly Leu
            20                  25                  30
Ala Leu Arg Phe Leu Asn His Leu Thr Ser Phe Lys Glu Ser Tyr Glu
        35                  40                  45
Thr Gln Met Asn Met Leu Tyr Ser Gln Leu Val Glu Ala Leu Ser Asn
    50                  55                  60
Asn Lys Gly Pro Val Phe His Glu His Gly Tyr Trp Ser Lys Ser Asp
65                  70                  75                  80

      <210> 335
      <211> 237
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(237)

      <400> 335
atg cct gtg gtc ctg tcg caa gag gtg gag tcc gtt ctt gtg ggt gct        48
Met Pro Val Val Leu Ser Gln Glu Val Glu Ser Val Leu Val Gly Ala
 1               5                  10                  15

gct gtt ctg ggt gcc tgt gcc tca ggg gat ttc gct tct gta cag gaa        96
Ala Val Leu Gly Ala Cys Ala Ser Gly Asp Phe Ala Ser Val Gln Glu
            20                  25                  30

gca atg gca aaa atg agc aaa gtt ggg aaa gtt gtg ttc ccg aga cta       144
Ala Met Ala Lys Met Ser Lys Val Gly Lys Val Val Phe Pro Arg Leu
        35                  40                  45

cag gat aaa aaa tac tat gat aag aaa tac caa gta ttc ctg aag ctg       192
Gln Asp Lys Lys Tyr Tyr Asp Lys Lys Tyr Gln Val Phe Leu Lys Leu
    50                  55                  60

gtt gaa cac cag aag gag tat ttg gcg atc atg aat gat gac tga           237
Val Glu His Gln Lys Glu Tyr Leu Ala Ile Met Asn Asp Asp  *
 65                  70                  75


      <210> 336
```

<211> 78
<212> PRT
<213> Homo sapiens

<400> 336
Met Pro Val Val Leu Ser Gln Glu Val Glu Ser Val Leu Val Gly Ala
1 5 10 15
Ala Val Leu Gly Ala Cys Ala Ser Gly Asp Phe Ala Ser Val Gln Glu
20 25 30
Ala Met Ala Lys Met Ser Lys Val Gly Lys Val Val Phe Pro Arg Leu
35 40 45
Gln Asp Lys Lys Tyr Tyr Asp Lys Lys Tyr Gln Val Phe Leu Lys Leu
50 55 60
Val Glu His Gln Lys Glu Tyr Leu Ala Ile Met Asn Asp Asp
65 70 75

<210> 337
<211> 567
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(567)

<400> 337
atg cac tct att ctg gat att att gct gga ttc cta tat acc att tta 48
Met His Ser Ile Leu Asp Ile Ile Ala Gly Phe Leu Tyr Thr Ile Leu
1 5 10 15

atc tta gct gtc ttc tat cca ttt gtg gac ctg att gac aac ttc aac 96
Ile Leu Ala Val Phe Tyr Pro Phe Val Asp Leu Ile Asp Asn Phe Asn
20 25 30

caa act cac aaa tat gct cca ttc atc atc atc ggg ctt cat tta gct 144
Gln Thr His Lys Tyr Ala Pro Phe Ile Ile Ile Gly Leu His Leu Ala
35 40 45

ttg ggg atc ttt tct ttc act ctt gac acc tgg agc aca tcc cga gga 192
Leu Gly Ile Phe Ser Phe Thr Leu Asp Thr Trp Ser Thr Ser Arg Gly
50 55 60

gac aca gcc gag ata cta gga agt ggt gct gga att gca tgt gga tct 240
Asp Thr Ala Glu Ile Leu Gly Ser Gly Ala Gly Ile Ala Cys Gly Ser

```
 65                  70                  75                  80

cat gtt act tat aac atg ggt cta gta tta gat cct tct cta gat aca      288
His Val Thr Tyr Asn Met Gly Leu Val Leu Asp Pro Ser Leu Asp Thr
                 85                  90                  95

tta cct tta gct ggg ccc ccc att act gtg act ctg ttt gga aaa gcc      336
Leu Pro Leu Ala Gly Pro Pro Ile Thr Val Thr Leu Phe Gly Lys Ala
            100                 105                 110

ata ttg cgg atc ctc ata ggg atg gta ttt gta cta ata atc aga gat      384
Ile Leu Arg Ile Leu Ile Gly Met Val Phe Val Leu Ile Ile Arg Asp
        115                 120                 125

gta atg aaa aag atc acc att cct tta gcc tgc aaa atc ttc aat ata      432
Val Met Lys Lys Ile Thr Ile Pro Leu Ala Cys Lys Ile Phe Asn Ile
    130                 135                 140

ccg tgt gat gat att cga aaa gca aga cag cac atg gaa gtt gaa ctt      480
Pro Cys Asp Asp Ile Arg Lys Ala Arg Gln His Met Glu Val Glu Leu
145                 150                 155                 160

cct tat cgg tat att acc tat gga atg gtt ggt ttc tcc atc aca ttt      528
Pro Tyr Arg Tyr Ile Thr Tyr Gly Met Val Gly Phe Ser Ile Thr Phe
                165                 170                 175

ttt gtt cct tac ata ttt ttc ttt att ggt atc tct tga                  567
Phe Val Pro Tyr Ile Phe Phe Phe Ile Gly Ile Ser  *
            180                 185


      <210> 338
      <211> 188
      <212> PRT
      <213> Homo sapiens

      <400> 338
Met His Ser Ile Leu Asp Ile Ile Ala Gly Phe Leu Tyr Thr Ile Leu
 1               5                  10                  15
Ile Leu Ala Val Phe Tyr Pro Phe Val Asp Leu Ile Asp Asn Phe Asn
            20                  25                  30
Gln Thr His Lys Tyr Ala Pro Phe Ile Ile Ile Gly Leu His Leu Ala
        35                  40                  45
Leu Gly Ile Phe Ser Phe Thr Leu Asp Thr Trp Ser Thr Ser Arg Gly
```

```
    50                  55                  60
Asp Thr Ala Glu Ile Leu Gly Ser Gly Ala Gly Ile Ala Cys Gly Ser
65                  70                  75                  80
His Val Thr Tyr Asn Met Gly Leu Val Leu Asp Pro Ser Leu Asp Thr
                85                  90                  95
Leu Pro Leu Ala Gly Pro Pro Ile Thr Val Thr Leu Phe Gly Lys Ala
            100                 105                 110
Ile Leu Arg Ile Leu Ile Gly Met Val Phe Val Leu Ile Ile Arg Asp
        115                 120                 125
Val Met Lys Lys Ile Thr Ile Pro Leu Ala Cys Lys Ile Phe Asn Ile
    130                 135                 140
Pro Cys Asp Asp Ile Arg Lys Ala Arg Gln His Met Glu Val Glu Leu
145                 150                 155                 160
Pro Tyr Arg Tyr Ile Thr Tyr Gly Met Val Gly Phe Ser Ile Thr Phe
                165                 170                 175
Phe Val Pro Tyr Ile Phe Phe Phe Ile Gly Ile Ser
            180                 185
```

<210> 339
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(210)

<400> 339

```
atg gtt tcc cat ttc atg ggg tct ctc agt gtc ctg tgt ttc ctt ctg      48
Met Val Ser His Phe Met Gly Ser Leu Ser Val Leu Cys Phe Leu Leu
 1               5                  10                  15

ctg ctt gga ttc cag ttc gtc tgc cca cag ccc tcc act caa cac agg      96
Leu Leu Gly Phe Gln Phe Val Cys Pro Gln Pro Ser Thr Gln His Arg
            20                  25                  30

aag gtc ccg cag cgg atg gcg gcg gag ggc gcc ccc gag gac gac ggc     144
Lys Val Pro Gln Arg Met Ala Ala Glu Gly Ala Pro Glu Asp Asp Gly
        35                  40                  45

ggc ggc ggc gcc ccg gga gtg tgg ggc gct ggg gcc cct gct gaa ggt     192
Gly Gly Gly Ala Pro Gly Val Trp Gly Ala Gly Ala Pro Ala Glu Gly
    50                  55                  60
```

tac cta acc att ctt taa 210
Tyr Leu Thr Ile Leu *
65

<210> 340
<211> 69
<212> PRT
<213> Homo sapiens

<400> 340
Met Val Ser His Phe Met Gly Ser Leu Ser Val Leu Cys Phe Leu Leu
1 5 10 15
Leu Leu Gly Phe Gln Phe Val Cys Pro Gln Pro Ser Thr Gln His Arg
20 25 30
Lys Val Pro Gln Arg Met Ala Ala Glu Gly Ala Pro Glu Asp Asp Gly
35 40 45
Gly Gly Gly Ala Pro Gly Val Trp Gly Ala Gly Ala Pro Ala Glu Gly
50 55 60
Tyr Leu Thr Ile Leu
65

<210> 341
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(225)

<400> 341
atg ccg gct aag gac aca agt tca gtg ttt gcc ctg gct tgt agc cca 48
Met Pro Ala Lys Asp Thr Ser Ser Val Phe Ala Leu Ala Cys Ser Pro
1 5 10 15

gcg ggg gct ccg tca tcc cct ggg gaa tgc ctc ggc ctg caa gac cgc 96
Ala Gly Ala Pro Ser Ser Pro Gly Glu Cys Leu Gly Leu Gln Asp Arg
20 25 30

ata ccg cat tgg aac agg gaa acc acc tac ttc agc acc tcc ctc agc 144
Ile Pro His Trp Asn Arg Glu Thr Thr Tyr Phe Ser Thr Ser Leu Ser
35 40 45

aag gtg gca ggt ccc aac aag cct tgc acc acg agg aag tgg cag tgg 192
Lys Val Ala Gly Pro Asn Lys Pro Cys Thr Thr Arg Lys Trp Gln Trp
50 55 60

cat tcg gga tat ggc tcc ctg gcc agc ttg tga 225
His Ser Gly Tyr Gly Ser Leu Ala Ser Leu *
65 70

<210> 342
<211> 74
<212> PRT
<213> Homo sapiens

<400> 342
Met Pro Ala Lys Asp Thr Ser Ser Val Phe Ala Leu Ala Cys Ser Pro
1 5 10 15
Ala Gly Ala Pro Ser Ser Pro Gly Glu Cys Leu Gly Leu Gln Asp Arg
20 25 30
Ile Pro His Trp Asn Arg Glu Thr Thr Tyr Phe Ser Thr Ser Leu Ser
35 40 45
Lys Val Ala Gly Pro Asn Lys Pro Cys Thr Thr Arg Lys Trp Gln Trp
50 55 60
His Ser Gly Tyr Gly Ser Leu Ala Ser Leu
65 70

<210> 343
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(240)

<400> 343
atg tgc atc acg cac ctg gac cac aaa gac tac atc ttc ctg ctg ctc 48
Met Cys Ile Thr His Leu Asp His Lys Asp Tyr Ile Phe Leu Leu Leu
1 5 10 15

atc ggc ttc tgc atc ttc gcc gcg gga act gtg gct gcc tgg ctc aca 96
Ile Gly Phe Cys Ile Phe Ala Ala Gly Thr Val Ala Ala Trp Leu Thr
20 25 30

ggt gtg tgt gct gtg ctc tac cag aac acc cgc cac aag tcg agt gaa 144
Gly Val Cys Ala Val Leu Tyr Gln Asn Thr Arg His Lys Ser Ser Glu
35 40 45

gaa gat gag gac gag gcc ggg act agg gtg gaa gtc agc cgg cgg att 192
Glu Asp Glu Asp Glu Ala Gly Thr Arg Val Glu Val Ser Arg Arg Ile
50 55 60

ttt caa acc cag acg agc tcg gtc cag gag ttc cct cag ctt att tag 240
Phe Gln Thr Gln Thr Ser Ser Val Gln Glu Phe Pro Gln Leu Ile *
65 70 75

<210> 344
<211> 79
<212> PRT
<213> Homo sapiens

<400> 344
Met Cys Ile Thr His Leu Asp His Lys Asp Tyr Ile Phe Leu Leu Leu
1 5 10 15
Ile Gly Phe Cys Ile Phe Ala Ala Gly Thr Val Ala Ala Trp Leu Thr
20 25 30
Gly Val Cys Ala Val Leu Tyr Gln Asn Thr Arg His Lys Ser Ser Glu
35 40 45
Glu Asp Glu Asp Glu Ala Gly Thr Arg Val Glu Val Ser Arg Arg Ile
50 55 60
Phe Gln Thr Gln Thr Ser Ser Val Gln Glu Phe Pro Gln Leu Ile
65 70 75

<210> 345
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(285)

<400> 345
atg act gcc aag gac tgc tcc atc atg att gca ctg tct ccc tgt ctg 48
Met Thr Ala Lys Asp Cys Ser Ile Met Ile Ala Leu Ser Pro Cys Leu
1 5 10 15

```
cag gat gcc agc tct gat caa agg cct gtc gtc cct tca tcg agg tcc        96
Gln Asp Ala Ser Ser Asp Gln Arg Pro Val Val Pro Ser Ser Arg Ser
            20                  25                  30

agg ttt gcc ttt tcc gtg tct gtg ctg gac ctt gac ctc aag ccc tac       144
Arg Phe Ala Phe Ser Val Ser Val Leu Asp Leu Asp Leu Lys Pro Tyr
        35                  40                  45

gag agc att ccc cat cag tat aaa ctg gac ggc aag atc gtc aac tat       192
Glu Ser Ile Pro His Gln Tyr Lys Leu Asp Gly Lys Ile Val Asn Tyr
    50                  55                  60

tat tca aag act gta cgt gcc aaa gac aac gcc gtg atg tcg act cgg       240
Tyr Ser Lys Thr Val Arg Ala Lys Asp Asn Ala Val Met Ser Thr Arg
65                  70                  75                  80

ttc aag gaa agc gaa gat tgc aca tta gtt ctc cac aag gtc taa           285
Phe Lys Glu Ser Glu Asp Cys Thr Leu Val Leu His Lys Val  *
                85                  90
```

<210> 346
<211> 94
<212> PRT
<213> Homo sapiens

<400> 346

```
Met Thr Ala Lys Asp Cys Ser Ile Met Ile Ala Leu Ser Pro Cys Leu
1               5                   10                  15
Gln Asp Ala Ser Ser Asp Gln Arg Pro Val Val Pro Ser Ser Arg Ser
            20                  25                  30
Arg Phe Ala Phe Ser Val Ser Val Leu Asp Leu Asp Leu Lys Pro Tyr
        35                  40                  45
Glu Ser Ile Pro His Gln Tyr Lys Leu Asp Gly Lys Ile Val Asn Tyr
    50                  55                  60
Tyr Ser Lys Thr Val Arg Ala Lys Asp Asn Ala Val Met Ser Thr Arg
65                  70                  75                  80
Phe Lys Glu Ser Glu Asp Cys Thr Leu Val Leu His Lys Val
                85                  90
```

<210> 347
<211> 474
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(474)

<400> 347
atg gag gcc ctg agg agg gcc cac gag gtc gcg ctc cgc ctg ctg ctg 48
Met Glu Ala Leu Arg Arg Ala His Glu Val Ala Leu Arg Leu Leu Leu
1 5 10 15

tgt agg ccg tgg gcc tcg cgc gcc gcc gcc cgc ccc aag ccc agc gcc 96
Cys Arg Pro Trp Ala Ser Arg Ala Ala Ala Arg Pro Lys Pro Ser Ala
20 25 30

tcg gag gtg ctg acg cgg cat ctg ctg cag cgg cgc ctg ccg cac tgg 144
Ser Glu Val Leu Thr Arg His Leu Leu Gln Arg Arg Leu Pro His Trp
35 40 45

acc tcc ttc tgc gtg ccc tac agc gcc gtc cgc aac gac cag ttc ggc 192
Thr Ser Phe Cys Val Pro Tyr Ser Ala Val Arg Asn Asp Gln Phe Gly
50 55 60

ctc tcg cac ttc aac tgg ccg gtg cag ggc gcc aac tac cac gtc ctg 240
Leu Ser His Phe Asn Trp Pro Val Gln Gly Ala Asn Tyr His Val Leu
65 70 75 80

cgc acc ggc tgc ttc ccc ttc atc aag tac cac tgc tcc aag gct ccc 288
Arg Thr Gly Cys Phe Pro Phe Ile Lys Tyr His Cys Ser Lys Ala Pro
85 90 95

tgg cag gac ctg gcc cgg cag aac cgc ttc ttc acg gcg ctc aag gtc 336
Trp Gln Asp Leu Ala Arg Gln Asn Arg Phe Phe Thr Ala Leu Lys Val
100 105 110

gtc aac ctc ggt att cca act tta tta tat gga ctt ggc tcc tgg tta 384
Val Asn Leu Gly Ile Pro Thr Leu Leu Tyr Gly Leu Gly Ser Trp Leu
115 120 125

ttt gcc aga gtc aca gag act gtg cat acc agt tat gga ccc ata aca 432
Phe Ala Arg Val Thr Glu Thr Val His Thr Ser Tyr Gly Pro Ile Thr
130 135 140

gtt tat ttt ctc aat aaa gaa gat gaa ggt gcc atg tat tga 474
Val Tyr Phe Leu Asn Lys Glu Asp Glu Gly Ala Met Tyr *

145 150 155

<210> 348
<211> 157
<212> PRT
<213> Homo sapiens

<400> 348
Met Glu Ala Leu Arg Arg Ala His Glu Val Ala Leu Arg Leu Leu Leu
1 5 10 15
Cys Arg Pro Trp Ala Ser Arg Ala Ala Ala Arg Pro Lys Pro Ser Ala
20 25 30
Ser Glu Val Leu Thr Arg His Leu Leu Gln Arg Arg Leu Pro His Trp
35 40 45
Thr Ser Phe Cys Val Pro Tyr Ser Ala Val Arg Asn Asp Gln Phe Gly
50 55 60
Leu Ser His Phe Asn Trp Pro Val Gln Gly Ala Asn Tyr His Val Leu
65 70 75 80
Arg Thr Gly Cys Phe Pro Phe Ile Lys Tyr His Cys Ser Lys Ala Pro
85 90 95
Trp Gln Asp Leu Ala Arg Gln Asn Arg Phe Phe Thr Ala Leu Lys Val
100 105 110
Val Asn Leu Gly Ile Pro Thr Leu Leu Tyr Gly Leu Gly Ser Trp Leu
115 120 125
Phe Ala Arg Val Thr Glu Thr Val His Thr Ser Tyr Gly Pro Ile Thr
130 135 140
Val Tyr Phe Leu Asn Lys Glu Asp Glu Gly Ala Met Tyr
145 150 155

<210> 349
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(288)

<400> 349
atg gcg aaa gca ctg att gtc att ttt agc agt cac tta agg cct ata 48
Met Ala Lys Ala Leu Ile Val Ile Phe Ser Ser His Leu Arg Pro Ile
1 5 10 15

gaa ctt ttt tca agt cgg aag gtc ctg ttc tta cta tct caa aaa tgg 96
Glu Leu Phe Ser Ser Arg Lys Val Leu Phe Leu Leu Ser Gln Lys Trp
20 25 30

gca tcg aac aat caa tct agg agc gtg gca gtg ggt aaa atg gtg gac 144
Ala Ser Asn Asn Gln Ser Arg Ser Val Ala Val Gly Lys Met Val Asp
35 40 45

agg cac caa agc tat ttt ctc atc tgt cct gtg gat gag tgg aac tgt 192
Arg His Gln Ser Tyr Phe Leu Ile Cys Pro Val Asp Glu Trp Asn Cys
50 55 60

gga aca agt gat gtg gaa tta atg ggt gca aca gct gta cag aca atc 240
Gly Thr Ser Asp Val Glu Leu Met Gly Ala Thr Ala Val Gln Thr Ile
65 70 75 80

aat aac aca cac agt tct gga aag aac aca tca ctt gtg ctt gtt tga 288
Asn Asn Thr His Ser Ser Gly Lys Asn Thr Ser Leu Val Leu Val *
85 90 95

<210> 350
<211> 95
<212> PRT
<213> Homo sapiens

<400> 350
Met Ala Lys Ala Leu Ile Val Ile Phe Ser Ser His Leu Arg Pro Ile
1 5 10 15
Glu Leu Phe Ser Ser Arg Lys Val Leu Phe Leu Leu Ser Gln Lys Trp
20 25 30
Ala Ser Asn Asn Gln Ser Arg Ser Val Ala Val Gly Lys Met Val Asp
35 40 45
Arg His Gln Ser Tyr Phe Leu Ile Cys Pro Val Asp Glu Trp Asn Cys
50 55 60
Gly Thr Ser Asp Val Glu Leu Met Gly Ala Thr Ala Val Gln Thr Ile
65 70 75 80
Asn Asn Thr His Ser Ser Gly Lys Asn Thr Ser Leu Val Leu Val
85 90 95

<210> 351
<211> 165
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(165)

<400> 351
atg tgc tcc atc ccc cgg cat ctg ctg cca ttg gtc ctg cct gtt gcg 48
Met Cys Ser Ile Pro Arg His Leu Leu Pro Leu Val Leu Pro Val Ala
1 5 10 15

tta ctt ctc tgt gcc ctg gag ccc ctc aag cac aga ggc ctc gaa agg 96
Leu Leu Leu Cys Ala Leu Glu Pro Leu Lys His Arg Gly Leu Glu Arg
20 25 30

ttg atc aga cat cct cag cac ctg gag cgg ggc ctg gca cac aag acg 144
Leu Ile Arg His Pro Gln His Leu Glu Arg Gly Leu Ala His Lys Thr
35 40 45

gca atg aac ggc caa ccc tag 165
Ala Met Asn Gly Gln Pro *
50

<210> 352
<211> 54
<212> PRT
<213> Homo sapiens

<400> 352
Met Cys Ser Ile Pro Arg His Leu Leu Pro Leu Val Leu Pro Val Ala
1 5 10 15
Leu Leu Leu Cys Ala Leu Glu Pro Leu Lys His Arg Gly Leu Glu Arg
20 25 30
Leu Ile Arg His Pro Gln His Leu Glu Arg Gly Leu Ala His Lys Thr
35 40 45
Ala Met Asn Gly Gln Pro
50

<210> 353
<211> 159
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)...(159)

<400> 353

```
atg tgc ttg agg gtt ttc acc ctg gcc ctc agt tgc ctg ctg tgc ggg        48
Met Cys Leu Arg Val Phe Thr Leu Ala Leu Ser Cys Leu Leu Cys Gly
 1               5                  10                  15

tcc ctg ggg cag ctg cag ggg ctc acg gac cca tca ggg tct cca cag        96
Ser Leu Gly Gln Leu Gln Gly Leu Thr Asp Pro Ser Gly Ser Pro Gln
            20                  25                  30

ctc ccc tgc agt gtg tgc acc cca caa tgt ctg cgg ctc ttc ttc cgg       144
Leu Pro Cys Ser Val Cys Thr Pro Gln Cys Leu Arg Leu Phe Phe Arg
        35                  40                  45

cgt gtc ggg ctt tga                                                   159
Arg Val Gly Leu  *
     50
```

<210> 354
<211> 52
<212> PRT
<213> Homo sapiens

<400> 354

```
Met Cys Leu Arg Val Phe Thr Leu Ala Leu Ser Cys Leu Leu Cys Gly
 1               5                  10                  15
Ser Leu Gly Gln Leu Gln Gly Leu Thr Asp Pro Ser Gly Ser Pro Gln
            20                  25                  30
Leu Pro Cys Ser Val Cys Thr Pro Gln Cys Leu Arg Leu Phe Phe Arg
        35                  40                  45
Arg Val Gly Leu
     50
```

<210> 355
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(210)

<400> 355

```
atg ggt gcc atg aac cat gat acc aac tac agc ttt cag gtt caa tgt      48
Met Gly Ala Met Asn His Asp Thr Asn Tyr Ser Phe Gln Val Gln Cys
 1               5                  10                  15

ggc tta att gtg gtg gcc tac aaa gat gga tca cct gcc cac cca cat      96
Gly Leu Ile Val Val Ala Tyr Lys Asp Gly Ser Pro Ala His Pro His
            20                  25                  30

ttc atg gat gca gag ctc tgt tcc cag tac tgg acc aag tgg ctt ctt     144
Phe Met Asp Ala Glu Leu Cys Ser Gln Tyr Trp Thr Lys Trp Leu Leu
        35                  40                  45

cga cta gaa gaa tat acg gaa aag aaa aag aac cag aat att cag aaa     192
Arg Leu Glu Glu Tyr Thr Glu Lys Lys Lys Asn Gln Asn Ile Gln Lys
    50                  55                  60

cca gaa tat tca gaa tag                                             210
Pro Glu Tyr Ser Glu  *
 65
```

<210> 356
<211> 69
<212> PRT
<213> Homo sapiens

<400> 356

```
Met Gly Ala Met Asn His Asp Thr Asn Tyr Ser Phe Gln Val Gln Cys
 1               5                  10                  15
Gly Leu Ile Val Val Ala Tyr Lys Asp Gly Ser Pro Ala His Pro His
            20                  25                  30
Phe Met Asp Ala Glu Leu Cys Ser Gln Tyr Trp Thr Lys Trp Leu Leu
        35                  40                  45
Arg Leu Glu Glu Tyr Thr Glu Lys Lys Lys Asn Gln Asn Ile Gln Lys
    50                  55                  60
Pro Glu Tyr Ser Glu
65
```

<210> 357
<211> 243
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(243)

<221> misc_feature
<222> (1)...(243)
<223> n = A,T,C or G

<400> 357

```
atg gtc ctg ccg gtg gca gcc tat ggn ctg atc ctg atg gcc atg ctg       48
Met Val Leu Pro Val Ala Ala Tyr Xaa Leu Ile Leu Met Ala Met Leu
 1               5                  10                  15

tgg cgc ggc ctg gcc cag ggc ggg agt gcc ggc tgg ggc gcg ctg ctc       96
Trp Arg Gly Leu Ala Gln Gly Gly Ser Ala Gly Trp Gly Ala Leu Leu
            20                  25                  30

ttc acg ctc tct gat ggc gtg ctg gcc tgg gac acc ttc gcc cag ccc      144
Phe Thr Leu Ser Asp Gly Val Leu Ala Trp Asp Thr Phe Ala Gln Pro
        35                  40                  45

ctg ccc cat gcc cgc ctg gtg atc atg acc acc tac tat gct gcc cag      192
Leu Pro His Ala Arg Leu Val Ile Met Thr Thr Tyr Tyr Ala Ala Gln
    50                  55                  60

ctc ctc atc aca ctg tca gcc ctc agg agc ccg gtg ccc aag act gac      240
Leu Leu Ile Thr Leu Ser Ala Leu Arg Ser Pro Val Pro Lys Thr Asp
 65                  70                  75                  80

tga                                                                  243
 *
```

<210> 358
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(80)
<223> Xaa = Any Amino Acid

<400> 358
Met Val Leu Pro Val Ala Ala Tyr Xaa Leu Ile Leu Met Ala Met Leu
1 5 10 15
Trp Arg Gly Leu Ala Gln Gly Gly Ser Ala Gly Trp Gly Ala Leu Leu
20 25 30
Phe Thr Leu Ser Asp Gly Val Leu Ala Trp Asp Thr Phe Ala Gln Pro
35 40 45
Leu Pro His Ala Arg Leu Val Ile Met Thr Thr Tyr Tyr Ala Ala Gln
50 55 60
Leu Leu Ile Thr Leu Ser Ala Leu Arg Ser Pro Val Pro Lys Thr Asp
65 70 75 80

<210> 359
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(324)

<400> 359
atg aag agc acc tgt ggt tcc ctt gtg gcc atg agt gtt gtg gtg gga 48
Met Lys Ser Thr Cys Gly Ser Leu Val Ala Met Ser Val Val Val Gly
1 5 10 15

cca gca tca agc gca aga gat ctg ccg agt cca cgt gga tac act atg 96
Pro Ala Ser Ser Ala Arg Asp Leu Pro Ser Pro Arg Gly Tyr Thr Met
20 25 30

acc ccg cag acc atg aag gta gat gag gag gta atg gca ttc cgt ggt 144
Thr Pro Gln Thr Met Lys Val Asp Glu Glu Val Met Ala Phe Arg Gly
35 40 45

gcc cga tgt gat ggc atc agg gtt ctt cct agc agc gtg gaa gac act 192
Ala Arg Cys Asp Gly Ile Arg Val Leu Pro Ser Ser Val Glu Asp Thr
50 55 60

cct gcc ctc aag agg gct aag tcc agt aaa acc caa cca aca gga gac 240
Pro Ala Leu Lys Arg Ala Lys Ser Ser Lys Thr Gln Pro Thr Gly Asp
65 70 75 80

agt tgg gca gga aga ctc att ctg agt gta gat ggc tct ggg ttt tgt 288

Ser Trp Ala Gly Arg Leu Ile Leu Ser Val Asp Gly Ser Gly Phe Cys
85 90 95

gag agg gtg aaa tct ttg gtc gtt aaa caa ttc tag 324
Glu Arg Val Lys Ser Leu Val Val Lys Gln Phe *
100 105

<210> 360
<211> 107
<212> PRT
<213> Homo sapiens

<400> 360
Met Lys Ser Thr Cys Gly Ser Leu Val Ala Met Ser Val Val Val Gly
1 5 10 15
Pro Ala Ser Ser Ala Arg Asp Leu Pro Ser Pro Arg Gly Tyr Thr Met
20 25 30
Thr Pro Gln Thr Met Lys Val Asp Glu Glu Val Met Ala Phe Arg Gly
35 40 45
Ala Arg Cys Asp Gly Ile Arg Val Leu Pro Ser Ser Val Glu Asp Thr
50 55 60
Pro Ala Leu Lys Arg Ala Lys Ser Ser Lys Thr Gln Pro Thr Gly Asp
65 70 75 80
Ser Trp Ala Gly Arg Leu Ile Leu Ser Val Asp Gly Ser Gly Phe Cys
85 90 95
Glu Arg Val Lys Ser Leu Val Val Lys Gln Phe
100 105

<210> 361
<211> 252
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(252)

<400> 361
atg gag gaa gga ggc ggc ggc gta cgg agt ctg gtc ccg ggc ggg ccg 48
Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
1 5 10 15

gtg tta ctg gtc ctc tgc ggc ctc ctg gag gcg tcc ggc ggc ggc cga 96

Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg
20 25 30

gcc ctt cct caa ctc agc gat gac atc cct ttc cga gtc aac tgg ccc 144
Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
35 40 45

ggc acc gag ttc tct ctg ccc aca act gga gtt tta tat aaa gaa gat 192
Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
50 55 60

aat tat gtc atc atg aca act gca cat aaa gaa aaa tat aaa aaa aaa 240
Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Lys Lys
65 70 75 80

aaa aaa aac taa 252
Lys Lys Asn *

<210> 362
<211> 83
<212> PRT
<213> Homo sapiens

<400> 362
Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
1 5 10 15
Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg
20 25 30
Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
35 40 45
Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
50 55 60
Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Lys Lys
65 70 75 80
Lys Lys Asn

<210> 363
<211> 459
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(459)

<400> 363
atg gat gga aca caa cag cag att ttt aaa atg tta gca gag gta cta      48
Met Asp Gly Thr Gln Gln Gln Ile Phe Lys Met Leu Ala Glu Val Leu
 1               5                  10                  15

gga gga atc aat tgt gta aaa gcc tcg gtt ctt acg cct tat tac cac      96
Gly Gly Ile Asn Cys Val Lys Ala Ser Val Leu Thr Pro Tyr Tyr His
            20                  25                  30

aaa gta gat ttt gag tgt atc ttg gat aaa aga aaa aaa cct ctt ccg     144
Lys Val Asp Phe Glu Cys Ile Leu Asp Lys Arg Lys Lys Pro Leu Pro
        35                  40                  45

tat gga agc cat aat ata gca ttg gga caa cta cca gaa atg ccc tgg     192
Tyr Gly Ser His Asn Ile Ala Leu Gly Gln Leu Pro Glu Met Pro Trp
    50                  55                  60

gaa tca aat atc gaa ata gtt gga tca agg ctg cca cca ggg gct gaa     240
Glu Ser Asn Ile Glu Ile Val Gly Ser Arg Leu Pro Pro Gly Ala Glu
65                  70                  75                  80

agg att gct ttg gaa ttt ttg gat tca aaa gca ctt tgt aga aat atc     288
Arg Ile Ala Leu Glu Phe Leu Asp Ser Lys Ala Leu Cys Arg Asn Ile
                85                  90                  95

cct cac atg aaa gga aaa tct gct atg aaa aaa cga cat ttg gaa att     336
Pro His Met Lys Gly Lys Ser Ala Met Lys Lys Arg His Leu Glu Ile
            100                 105                 110

ctg ggg tat cgt gta att cag att tcc cag ttt gaa tgg aac tct atg     384
Leu Gly Tyr Arg Val Ile Gln Ile Ser Gln Phe Glu Trp Asn Ser Met
        115                 120                 125

gca ctg tca aca aag gat gct cgg atg gac tac ctg aga gaa tgt ata     432
Ala Leu Ser Thr Lys Asp Ala Arg Met Asp Tyr Leu Arg Glu Cys Ile
    130                 135                 140

ttt gga gaa gtc aag tca tgt ttg tag                                 459
Phe Gly Glu Val Lys Ser Cys Leu  *
145                 150
```

<210> 364
<211> 152
<212> PRT
<213> Homo sapiens

<400> 364
Met Asp Gly Thr Gln Gln Gln Ile Phe Lys Met Leu Ala Glu Val Leu
1 5 10 15
Gly Gly Ile Asn Cys Val Lys Ala Ser Val Leu Thr Pro Tyr Tyr His
20 25 30
Lys Val Asp Phe Glu Cys Ile Leu Asp Lys Arg Lys Lys Pro Leu Pro
35 40 45
Tyr Gly Ser His Asn Ile Ala Leu Gly Gln Leu Pro Glu Met Pro Trp
50 55 60
Glu Ser Asn Ile Glu Ile Val Gly Ser Arg Leu Pro Pro Gly Ala Glu
65 70 75 80
Arg Ile Ala Leu Glu Phe Leu Asp Ser Lys Ala Leu Cys Arg Asn Ile
85 90 95
Pro His Met Lys Gly Lys Ser Ala Met Lys Lys Arg His Leu Glu Ile
100 105 110
Leu Gly Tyr Arg Val Ile Gln Ile Ser Gln Phe Glu Trp Asn Ser Met
115 120 125
Ala Leu Ser Thr Lys Asp Ala Arg Met Asp Tyr Leu Arg Glu Cys Ile
130 135 140
Phe Gly Glu Val Lys Ser Cys Leu
145 150

<210> 365
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(600)

<400> 365
atg gtg tgg cgc cgg ctt ctg cgg aag agg tgg gtg ctc gcc ctg gtc 48
Met Val Trp Arg Arg Leu Leu Arg Lys Arg Trp Val Leu Ala Leu Val
1 5 10 15

ttc ggg ctg tcg ctc gtc tac ttc ctc agc agc acc ttc aag cag gag 96

Phe Gly Leu Ser Leu Val Tyr Phe Leu Ser Ser Thr Phe Lys Gln Glu
20 25 30

gag agg gca gtg aga gat agg aat ctc ctc cag gtt cat gac cat aat 144
Glu Arg Ala Val Arg Asp Arg Asn Leu Leu Gln Val His Asp His Asn
35 40 45

cag ccc atc ccg tgg aaa gtg cag ttt aac ttg ggc aat agc agt cgt 192
Gln Pro Ile Pro Trp Lys Val Gln Phe Asn Leu Gly Asn Ser Ser Arg
50 55 60

ccg agc aat cag tgc cgc aac tcc att caa ggg aag cac ctc atc acg 240
Pro Ser Asn Gln Cys Arg Asn Ser Ile Gln Gly Lys His Leu Ile Thr
65 70 75 80

gat gaa ctc ggc tac gtt tgc gag agg aag gat ttg ctg gta aat ggc 288
Asp Glu Leu Gly Tyr Val Cys Glu Arg Lys Asp Leu Leu Val Asn Gly
85 90 95

tgc tgt aat gtc aac gtc cct agc acg aag cag tac tgc tgt gat ggc 336
Cys Cys Asn Val Asn Val Pro Ser Thr Lys Gln Tyr Cys Cys Asp Gly
100 105 110

tgc tgg ccc aac ggc tgc tgc agc gcc tat gag tac tgt gtc tcc tgc 384
Cys Trp Pro Asn Gly Cys Cys Ser Ala Tyr Glu Tyr Cys Val Ser Cys
115 120 125

tgc ctg cag ccc aac aag caa ctt ctc ctg gag cgc ttc ctc aac cgg 432
Cys Leu Gln Pro Asn Lys Gln Leu Leu Leu Glu Arg Phe Leu Asn Arg
130 135 140

gca gcc gtg gca ttc cag aac ctc ttc atg gca gtc gaa gat cac ttt 480
Ala Ala Val Ala Phe Gln Asn Leu Phe Met Ala Val Glu Asp His Phe
145 150 155 160

gag ttg tgc ctg gcc aaa tgc agg acc tca tct cag agc gtg cag cat 528
Glu Leu Cys Leu Ala Lys Cys Arg Thr Ser Ser Gln Ser Val Gln His
165 170 175

gag aac acc tac cgg gac ccc ata gca aag tat tgc tat gga gaa agc 576
Glu Asn Thr Tyr Arg Asp Pro Ile Ala Lys Tyr Cys Tyr Gly Glu Ser
180 185 190

ccg ccc gag ctc ttc ccc gct tga 600

Pro Pro Glu Leu Phe Pro Ala *
195

<210> 366
<211> 199
<212> PRT
<213> Homo sapiens

<400> 366
Met Val Trp Arg Arg Leu Leu Arg Lys Arg Trp Val Leu Ala Leu Val
1 5 10 15
Phe Gly Leu Ser Leu Val Tyr Phe Leu Ser Ser Thr Phe Lys Gln Glu
20 25 30
Glu Arg Ala Val Arg Asp Arg Asn Leu Leu Gln Val His Asp His Asn
35 40 45
Gln Pro Ile Pro Trp Lys Val Gln Phe Asn Leu Gly Asn Ser Ser Arg
50 55 60
Pro Ser Asn Gln Cys Arg Asn Ser Ile Gln Gly Lys His Leu Ile Thr
65 70 75 80
Asp Glu Leu Gly Tyr Val Cys Glu Arg Lys Asp Leu Leu Val Asn Gly
85 90 95
Cys Cys Asn Val Asn Val Pro Ser Thr Lys Gln Tyr Cys Cys Asp Gly
100 105 110
Cys Trp Pro Asn Gly Cys Cys Ser Ala Tyr Glu Tyr Cys Val Ser Cys
115 120 125
Cys Leu Gln Pro Asn Lys Gln Leu Leu Leu Glu Arg Phe Leu Asn Arg
130 135 140
Ala Ala Val Ala Phe Gln Asn Leu Phe Met Ala Val Glu Asp His Phe
145 150 155 160
Glu Leu Cys Leu Ala Lys Cys Arg Thr Ser Ser Gln Ser Val Gln His
165 170 175
Glu Asn Thr Tyr Arg Asp Pro Ile Ala Lys Tyr Cys Tyr Gly Glu Ser
180 185 190
Pro Pro Glu Leu Phe Pro Ala
195

<210> 367
<211> 249
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1)...(249)

<400> 367

```
atg agc aaa tac aag cac aag agc agc cct tta ttg cct ctt ctt atc      48
Met Ser Lys Tyr Lys His Lys Ser Ser Pro Leu Leu Pro Leu Leu Ile
 1               5                  10                  15

ttt cat aat gtt tgc ttc agt cct gca aat aaa ccc aag atc ctg gct      96
Phe His Asn Val Cys Phe Ser Pro Ala Asn Lys Pro Lys Ile Leu Ala
            20                  25                  30

aat gaa aaa gtc att act gtg ctt gct gcc tgt ctg gaa agt gag aat     144
Asn Glu Lys Val Ile Thr Val Leu Ala Ala Cys Leu Glu Ser Glu Asn
        35                  40                  45

caa aat gct cag agg att gga gca gct gcc ctt ggc tct gat tta caa     192
Gln Asn Ala Gln Arg Ile Gly Ala Ala Ala Leu Gly Ser Asp Leu Gln
    50                  55                  60

tta tca gaa ggc aaa aac agc ttt gaa aag ccc atc agt aaa aag aag     240
Leu Ser Glu Gly Lys Asn Ser Phe Glu Lys Pro Ile Ser Lys Lys Lys
65                  70                  75                  80

agt gga tga                                                         249
Ser Gly  *
```

<210> 368
<211> 82
<212> PRT
<213> Homo sapiens

<400> 368

```
Met Ser Lys Tyr Lys His Lys Ser Ser Pro Leu Leu Pro Leu Leu Ile
 1               5                  10                  15
Phe His Asn Val Cys Phe Ser Pro Ala Asn Lys Pro Lys Ile Leu Ala
            20                  25                  30
Asn Glu Lys Val Ile Thr Val Leu Ala Ala Cys Leu Glu Ser Glu Asn
        35                  40                  45
Gln Asn Ala Gln Arg Ile Gly Ala Ala Ala Leu Gly Ser Asp Leu Gln
    50                  55                  60
Leu Ser Glu Gly Lys Asn Ser Phe Glu Lys Pro Ile Ser Lys Lys Lys
65                  70                  75                  80
```

Ser Gly

<210> 369
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(285)

<400> 369
atg gac ggc cgc ggg gct ttc tgg aca gtg gcc att ccc aga gcc agg 48
Met Asp Gly Arg Gly Ala Phe Trp Thr Val Ala Ile Pro Arg Ala Arg
1 5 10 15

cag gaa ggc ctc ggg agg ctg ggg ctc ccg ttc ccg gtg aag cgg acg 96
Gln Glu Gly Leu Gly Arg Leu Gly Leu Pro Phe Pro Val Lys Arg Thr
20 25 30

ccg cca gcg ccc cag aac cca gga gga agc aca cag gcc cca cag aga 144
Pro Pro Ala Pro Gln Asn Pro Gly Gly Ser Thr Gln Ala Pro Gln Arg
35 40 45

gtg gtt ggc aag agt cac tcg ggg att agg atg ccg gcc aaa tcg cgg 192
Val Val Gly Lys Ser His Ser Gly Ile Arg Met Pro Ala Lys Ser Arg
50 55 60

aat ttg agg ctg gaa tcc aag ctc aac agg act gct gtg tgt gaa gca 240
Asn Leu Arg Leu Glu Ser Lys Leu Asn Arg Thr Ala Val Cys Glu Ala
65 70 75 80

ctc aag agg gcc cct aca acc aac ctg cca gga gtc ggc tcc tga 285
Leu Lys Arg Ala Pro Thr Thr Asn Leu Pro Gly Val Gly Ser *
85 90

<210> 370
<211> 94
<212> PRT
<213> Homo sapiens

<400> 370

```
Met Asp Gly Arg Gly Ala Phe Trp Thr Val Ala Ile Pro Arg Ala Arg
 1               5                  10                  15
Gln Glu Gly Leu Gly Arg Leu Gly Leu Pro Phe Pro Val Lys Arg Thr
            20                  25                  30
Pro Pro Ala Pro Gln Asn Pro Gly Gly Ser Thr Gln Ala Pro Gln Arg
        35                  40                  45
Val Val Gly Lys Ser His Ser Gly Ile Arg Met Pro Ala Lys Ser Arg
    50                  55                  60
Asn Leu Arg Leu Glu Ser Lys Leu Asn Arg Thr Ala Val Cys Glu Ala
65                  70                  75                  80
Leu Lys Arg Ala Pro Thr Thr Asn Leu Pro Gly Val Gly Ser
                85                  90
```

<210> 371
<211> 249
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(249)

<400> 371

```
atg cgc gac tgc gac atc aac gac gac gaa ttc ctg cac ctg ccg gcg      48
Met Arg Asp Cys Asp Ile Asn Asp Asp Glu Phe Leu His Leu Pro Ala
 1               5                  10                  15

cat ttg cgg gtg gtc ggg ccc cag cag ctg cat tcc gag acc aac gag      96
His Leu Arg Val Val Gly Pro Gln Gln Leu His Ser Glu Thr Asn Glu
            20                  25                  30

cgg ctc ttc gat gag aag tac aag cct gtc gtg ctc acc gac gat cag     144
Arg Leu Phe Asp Glu Lys Tyr Lys Pro Val Val Leu Thr Asp Asp Gln
        35                  40                  45

gtg gac cag gcg ctg tgg gag gag cag gtc ttg cag aag gag aag aag     192
Val Asp Gln Ala Leu Trp Glu Glu Gln Val Leu Gln Lys Glu Lys Lys
    50                  55                  60

gac agg ctc gcc ctg agc cag gcc cac tcg ctg gtg cag gcg gag gcc     240
Asp Arg Leu Ala Leu Ser Gln Ala His Ser Leu Val Gln Ala Glu Ala
65                  70                  75                  80

ccg aga tga                                                         249
```

Pro Arg *

<210> 372
<211> 82
<212> PRT
<213> Homo sapiens

<400> 372
Met Arg Asp Cys Asp Ile Asn Asp Asp Glu Phe Leu His Leu Pro Ala
1 5 10 15
His Leu Arg Val Val Gly Pro Gln Gln Leu His Ser Glu Thr Asn Glu
20 25 30
Arg Leu Phe Asp Glu Lys Tyr Lys Pro Val Val Leu Thr Asp Asp Gln
35 40 45
Val Asp Gln Ala Leu Trp Glu Glu Gln Val Leu Gln Lys Glu Lys Lys
50 55 60
Asp Arg Leu Ala Leu Ser Gln Ala His Ser Leu Val Gln Ala Glu Ala
65 70 75 80
Pro Arg

<210> 373
<211> 219
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(219)

<221> misc_feature
<222> (1)...(219)
<223> n = A.T.C or G

<400> 373
atg ggc cga gcg ctg ccc ccc ggg ggt cct cgg cgc cgg gcg can tta 48
Met Gly Arg Ala Leu Pro Pro Gly Gly Pro Arg Arg Arg Ala Xaa Leu
1 5 10 15

nga gcg can gca gca ggc tcc att ccc ggc cgc cgc cgc tca gcc cat 96
Xaa Ala Xaa Ala Ala Gly Ser Ile Pro Gly Arg Arg Arg Ser Ala His
20 25 30

tac gca aac ctg gcg ggt cca acc aac ccc gct ctg ccg ccg ctg ctg 144
Tyr Ala Asn Leu Ala Gly Pro Thr Asn Pro Ala Leu Pro Pro Leu Leu
35 40 45

gaa ccc agg agg cgt gct tgc agg ctt cgg gca cta cgc ggg gct gga 192
Glu Pro Arg Arg Arg Ala Cys Arg Leu Arg Ala Leu Arg Gly Ala Gly
50 55 60

aat acc acg cac tgc ccc ttc gcc tag 219
Asn Thr Thr His Cys Pro Phe Ala *
65 70

<210> 374
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(72)
<223> Xaa = Any Amino Acid

<400> 374
Met Gly Arg Ala Leu Pro Pro Gly Gly Pro Arg Arg Arg Ala Xaa Leu
1 5 10 15
Xaa Ala Xaa Ala Ala Gly Ser Ile Pro Gly Arg Arg Arg Ser Ala His
20 25 30
Tyr Ala Asn Leu Ala Gly Pro Thr Asn Pro Ala Leu Pro Pro Leu Leu
35 40 45
Glu Pro Arg Arg Arg Ala Cys Arg Leu Arg Ala Leu Arg Gly Ala Gly
50 55 60
Asn Thr Thr His Cys Pro Phe Ala
65 70

<210> 375
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(579)

<400> 375

atg gcc ccc aag ccg ggg gcc gag tgg agc aca gcc ctg tcc cat ctg 48
Met Ala Pro Lys Pro Gly Ala Glu Trp Ser Thr Ala Leu Ser His Leu
1 5 10 15

gtg ctg gga gtg gtg tct ctg cac gca gcc gtg agc aca gcc gag gca 96
Val Leu Gly Val Val Ser Leu His Ala Ala Val Ser Thr Ala Glu Ala
20 25 30

agt cga ggg gct gct gct ggc ttc ctg ctc cag gtc ttg gct gcc acc 144
Ser Arg Gly Ala Ala Ala Gly Phe Leu Leu Gln Val Leu Ala Ala Thr
35 40 45

acc acg ctg gcc cca ggg ctg agc aca cat gaa gac tgc ctt gct gga 192
Thr Thr Leu Ala Pro Gly Leu Ser Thr His Glu Asp Cys Leu Ala Gly
50 55 60

gcc tgg gtg gcc acc gtc atc ggc ctt ccc ctt ctg gcc ttc gat ttc 240
Ala Trp Val Ala Thr Val Ile Gly Leu Pro Leu Leu Ala Phe Asp Phe
65 70 75 80

cac tgg gtg aat ggg gac cgc tcc tct gcc aac ctg ctc ctg gga gga 288
His Trp Val Asn Gly Asp Arg Ser Ser Ala Asn Leu Leu Leu Gly Gly
85 90 95

ggc atg gtg ctg gca gtg gct ggc ggc cac ctc ggc cct gag ggc cgc 336
Gly Met Val Leu Ala Val Ala Gly Gly His Leu Gly Pro Glu Gly Arg
100 105 110

tct gtg gct ggt cag gca atg ctg ttg gtg gtc gca gtg acc atc ctc 384
Ser Val Ala Gly Gln Ala Met Leu Leu Val Val Ala Val Thr Ile Leu
115 120 125

att gta gct gtc ttc acg gcc aac act tat ggg atg tgg ggg ggg gcg 432
Ile Val Ala Val Phe Thr Ala Asn Thr Tyr Gly Met Trp Gly Gly Ala
130 135 140

atg ctg ggt gtg gca ggc ctc ctg agc cgg ctg gag gag gac agg ctg 480
Met Leu Gly Val Ala Gly Leu Leu Ser Arg Leu Glu Glu Asp Arg Leu
145 150 155 160

ctg ctg cta ccg aag gag gat gtc tgt cgc tgg gcc ttg gct gta ggc 528
Leu Leu Leu Pro Lys Glu Asp Val Cys Arg Trp Ala Leu Ala Val Gly

165 170 175

agc tgg gct tac tgc cgg gcc ctg cat aca cag cgc ctc cag tgg gag 576
Ser Trp Ala Tyr Cys Arg Ala Leu His Thr Gln Arg Leu Gln Trp Glu
180 185 190

tga 579
*

<210> 376
<211> 192
<212> PRT
<213> Homo sapiens

<400> 376
Met Ala Pro Lys Pro Gly Ala Glu Trp Ser Thr Ala Leu Ser His Leu
1 5 10 15
Val Leu Gly Val Val Ser Leu His Ala Ala Val Ser Thr Ala Glu Ala
20 25 30
Ser Arg Gly Ala Ala Ala Gly Phe Leu Leu Gln Val Leu Ala Ala Thr
35 40 45
Thr Thr Leu Ala Pro Gly Leu Ser Thr His Glu Asp Cys Leu Ala Gly
50 55 60
Ala Trp Val Ala Thr Val Ile Gly Leu Pro Leu Leu Ala Phe Asp Phe
65 70 75 80
His Trp Val Asn Gly Asp Arg Ser Ser Ala Asn Leu Leu Leu Gly Gly
85 90 95
Gly Met Val Leu Ala Val Ala Gly Gly His Leu Gly Pro Glu Gly Arg
100 105 110
Ser Val Ala Gly Gln Ala Met Leu Leu Val Val Ala Val Thr Ile Leu
115 120 125
Ile Val Ala Val Phe Thr Ala Asn Thr Tyr Gly Met Trp Gly Gly Ala
130 135 140
Met Leu Gly Val Ala Gly Leu Leu Ser Arg Leu Glu Glu Asp Arg Leu
145 150 155 160
Leu Leu Leu Pro Lys Glu Asp Val Cys Arg Trp Ala Leu Ala Val Gly
165 170 175
Ser Trp Ala Tyr Cys Arg Ala Leu His Thr Gln Arg Leu Gln Trp Glu
180 185 190

<210> 377
<211> 606

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(606)

<400> 377

```
atg acc gtg cag aga ctc gtg gcc gcg gcc gtg ctg gtg gcc ctg gtc      48
Met Thr Val Gln Arg Leu Val Ala Ala Ala Val Leu Val Ala Leu Val
 1               5                  10                  15

tca ctc atc ctc aac aac gtg gcg gcc ttc acc tcc aac tgg gtg tgc      96
Ser Leu Ile Leu Asn Asn Val Ala Ala Phe Thr Ser Asn Trp Val Cys
            20                  25                  30

cag acg ctg gag gat ggg cgc agg cgc agc gtg ggg ctg tgg agg tcc     144
Gln Thr Leu Glu Asp Gly Arg Arg Arg Ser Val Gly Leu Trp Arg Ser
        35                  40                  45

tgc tgg ctg gtg gac agg acc cgg gga ggg ccg agc cct ggg gcc aga     192
Cys Trp Leu Val Asp Arg Thr Arg Gly Gly Pro Ser Pro Gly Ala Arg
    50                  55                  60

gcc ggc cag gtg gac gca cat gac tgt gag gcg ctg ggc tgg ggc tcc     240
Ala Gly Gln Val Asp Ala His Asp Cys Glu Ala Leu Gly Trp Gly Ser
65                  70                  75                  80

gag gca gcc ggc ttc cag gag tcc cga ggc acc gtc aaa ctg cag ttc     288
Glu Ala Ala Gly Phe Gln Glu Ser Arg Gly Thr Val Lys Leu Gln Phe
                85                  90                  95

gac atg atg cgc gcc tgc aac ctg gtg gcc acg gcc gcg ctc acc gca     336
Asp Met Met Arg Ala Cys Asn Leu Val Ala Thr Ala Ala Leu Thr Ala
            100                 105                 110

ggc cag ctc acc ttc ctc ctg ggg ctg gtg ggc ctg ccc ctg ctg tca     384
Gly Gln Leu Thr Phe Leu Leu Gly Leu Val Gly Leu Pro Leu Leu Ser
        115                 120                 125

ccc gac gcc ccg tgc tgg gag gag gcc atg gcc gct gca ttc caa ctg     432
Pro Asp Ala Pro Cys Trp Glu Glu Ala Met Ala Ala Ala Phe Gln Leu
    130                 135                 140
```

gcg agt ttt gtc ctg gtc atc ggg ctc gtg act ttc tac aga att ggc 480
Ala Ser Phe Val Leu Val Ile Gly Leu Val Thr Phe Tyr Arg Ile Gly
145 150 155 160

cca tac acc aac ctg tcc tgg tcc tgc tac ctg aac att ggc gcc tgc 528
Pro Tyr Thr Asn Leu Ser Trp Ser Cys Tyr Leu Asn Ile Gly Ala Cys
165 170 175

ctt ctg gcc acg ctg gcg gca gca tgc tca tct gga aca ttc tcc aca 576
Leu Leu Ala Thr Leu Ala Ala Ala Cys Ser Ser Gly Thr Phe Ser Thr
180 185 190

aga ggg agg act gca tgg ccc ccc ggg tga 606
Arg Gly Arg Thr Ala Trp Pro Pro Gly *
195 200

<210> 378
<211> 201
<212> PRT
<213> Homo sapiens

<400> 378
Met Thr Val Gln Arg Leu Val Ala Ala Ala Val Leu Val Ala Leu Val
1 5 10 15
Ser Leu Ile Leu Asn Asn Val Ala Ala Phe Thr Ser Asn Trp Val Cys
20 25 30
Gln Thr Leu Glu Asp Gly Arg Arg Arg Ser Val Gly Leu Trp Arg Ser
35 40 45
Cys Trp Leu Val Asp Arg Thr Arg Gly Gly Pro Ser Pro Gly Ala Arg
50 55 60
Ala Gly Gln Val Asp Ala His Asp Cys Glu Ala Leu Gly Trp Gly Ser
65 70 75 80
Glu Ala Ala Gly Phe Gln Glu Ser Arg Gly Thr Val Lys Leu Gln Phe
85 90 95
Asp Met Met Arg Ala Cys Asn Leu Val Ala Thr Ala Ala Leu Thr Ala
100 105 110
Gly Gln Leu Thr Phe Leu Leu Gly Leu Val Gly Leu Pro Leu Leu Ser
115 120 125
Pro Asp Ala Pro Cys Trp Glu Glu Ala Met Ala Ala Ala Phe Gln Leu
130 135 140
Ala Ser Phe Val Leu Val Ile Gly Leu Val Thr Phe Tyr Arg Ile Gly
145 150 155 160
Pro Tyr Thr Asn Leu Ser Trp Ser Cys Tyr Leu Asn Ile Gly Ala Cys

```
                165                 170                 175
Leu Leu Ala Thr Leu Ala Ala Ala Cys Ser Ser Gly Thr Phe Ser Thr
            180                 185                 190
Arg Gly Arg Thr Ala Trp Pro Pro Gly
        195                 200

      <210> 379
      <211> 297
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(297)

      <221> misc_feature
      <222> (1)...(297)
      <223> n = A,T,C or G

      <400> 379
atg gnc ncg acg ctg gtg gtc atc tgc aca gca gtc atc gtg gtg gtc      48
Met Xaa Xaa Thr Leu Val Val Ile Cys Thr Ala Val Ile Val Val Val
 1               5                  10                  15

gcg ttg act aga aag aaa gcc ctc aga atc cat tct gtg gaa ggt gac      96
Ala Leu Thr Arg Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp
            20                  25                  30

ctc agg aga aaa tca gct gga cag gag gaa tgg agc ccc agt gct ccc     144
Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro
        35                  40                  45

tca ccc cca gga agc tgt gtc cag gca gaa gct gca cct gct ggg ctc     192
Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu
    50                  55                  60

tgt gga gag cag cgg gga gag gac tgt gcc gag ctg cat gac tac ttc     240
Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe
65                  70                  75                  80

aat gtc ctg agt tac aga agc ctg ggt aac tgc agc ttc ttc aca gag     288
Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu
                85                  90                  95
```

act ggt tag 297
Thr Gly *

<210> 380
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(98)
<223> Xaa = Any Amino Acid

<400> 380
Met Xaa Xaa Thr Leu Val Val Ile Cys Thr Ala Val Ile Val Val Val
1 5 10 15
Ala Leu Thr Arg Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp
20 25 30
Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro
35 40 45
Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu
50 55 60
Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe
65 70 75 80
Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu
85 90 95
Thr Gly

<210> 381
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(264)

<400> 381
atg gct gtc tta gta ctt cgc ctg aca gtt gtc ctg gga ctg ctt gtc 48
Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
1 5 10 15

```
tta ttc ctg acc tgc tat gca gac gac aaa cca gac aag cca gac gac        96
Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
            20                  25                  30

aag cca gac gac tcg ggc aaa gac cca aag cca gac ttc ccc aaa ttc       144
Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
        35                  40                  45

cta agc ctc ctg ggc aca gag atc att gag aat gca gtc gag ttc atc       192
Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile
    50                  55                  60

ctc cgc tcc atg tcc agg agc aca gga ttt atg gaa ttt gat gat aat       240
Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn
65                  70                  75                  80

gaa gga aaa cat tca tca aag tga                                       264
Glu Gly Lys His Ser Ser Lys  *
                85
```

<210> 382
<211> 87
<212> PRT
<213> Homo sapiens

<400> 382

```
Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
1               5                   10                  15
Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
            20                  25                  30
Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
        35                  40                  45
Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile
    50                  55                  60
Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn
65                  70                  75                  80
Glu Gly Lys His Ser Ser Lys
                85
```

<210> 383
<211> 225
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(225)

<400> 383
```
atg act gcc ctc acc tcc tgg cac ctg gcc tat ctc atc act tgg acc      48
Met Thr Ala Leu Thr Ser Trp His Leu Ala Tyr Leu Ile Thr Trp Thr
 1               5                  10                  15

acc tgc ctg gcc tcc cac ctg ctg cag gct gcc ttt gag cac acg acc      96
Thr Cys Leu Ala Ser His Leu Leu Gln Ala Ala Phe Glu His Thr Thr
            20                  25                  30

cag ctt gcc gag gcc cag gag gtt gaa ccc cag gag gtc tca ggg tct      144
Gln Leu Ala Glu Ala Gln Glu Val Glu Pro Gln Glu Val Ser Gly Ser
        35                  40                  45

tcc ttg ctg ccc tca ctg tct gcg tcc tcg gac tca gag tct gga aca      192
Ser Leu Leu Pro Ser Leu Ser Ala Ser Ser Asp Ser Glu Ser Gly Thr
    50                  55                  60

gtt ttg cca gag caa gaa act ccc aga gaa taa                          225
Val Leu Pro Glu Gln Glu Thr Pro Arg Glu  *
 65                  70
```

<210> 384
<211> 74
<212> PRT
<213> Homo sapiens

<400> 384
```
Met Thr Ala Leu Thr Ser Trp His Leu Ala Tyr Leu Ile Thr Trp Thr
 1               5                  10                  15
Thr Cys Leu Ala Ser His Leu Leu Gln Ala Ala Phe Glu His Thr Thr
            20                  25                  30
Gln Leu Ala Glu Ala Gln Glu Val Glu Pro Gln Glu Val Ser Gly Ser
        35                  40                  45
Ser Leu Leu Pro Ser Leu Ser Ala Ser Ser Asp Ser Glu Ser Gly Thr
    50                  55                  60
Val Leu Pro Glu Gln Glu Thr Pro Arg Glu
65                  70
```

<210> 385
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(288)

<221> misc_feature
<222> (1)...(288)
<223> n = A,T,C or G

<400> 385
atg gcc ccc ccg cnc gcg tnc cgg tcc ccg atg tca ccn cng ncg nng 48
Met Ala Pro Pro Xaa Ala Xaa Arg Ser Pro Met Ser Xaa Xaa Xaa Xaa
1 5 10 15

ntg ctg ctg ctg ctg ctg ctg agt ctg gcg ctg ctg ggc gcc cgg gcc 96
Xaa Leu Leu Leu Leu Leu Leu Ser Leu Ala Leu Leu Gly Ala Arg Ala
20 25 30

cgc gcc gag ccc gcc ggg agt gcc gtc ccc gcg cag agc cgc cca tgc 144
Arg Ala Glu Pro Ala Gly Ser Ala Val Pro Ala Gln Ser Arg Pro Cys
35 40 45

gtg gac tgc cac gcc ttc gag ttc atg cag cgc gcc ctg cag gac ctg 192
Val Asp Cys His Ala Phe Glu Phe Met Gln Arg Ala Leu Gln Asp Leu
50 55 60

cgg aag aca gcc tgc agc ctg gac gcg cgg acg gag acc cta ctg ctg 240
Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg Thr Glu Thr Leu Leu Leu
65 70 75 80

cag gca gag cgc cgt gcc ctg tgt gcc tgc tgg cca gcg ggg cac tga 288
Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys Trp Pro Ala Gly His *
85 90 95

<210> 386
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(95)
<223> Xaa = Any Amino Acid

<400> 386
Met Ala Pro Pro Xaa Ala Xaa Arg Ser Pro Met Ser Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Leu Leu Leu Leu Leu Leu Ser Leu Ala Leu Leu Gly Ala Arg Ala
20 25 30
Arg Ala Glu Pro Ala Gly Ser Ala Val Pro Ala Gln Ser Arg Pro Cys
35 40 45
Val Asp Cys His Ala Phe Glu Phe Met Gln Arg Ala Leu Gln Asp Leu
50 55 60
Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg Thr Glu Thr Leu Leu Leu
65 70 75 80
Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys Trp Pro Ala Gly His
85 90 95

<210> 387
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(351)

<400> 387
atg aag gga ctc aga agt ctg gca gca aca acc ttg gct ctt ttc ctg 48
Met Lys Gly Leu Arg Ser Leu Ala Ala Thr Thr Leu Ala Leu Phe Leu
1 5 10 15

gtg ttt gtt ttc ctg gga aac tcc agc tgc gct ccg cag aga ctg ttg 96
Val Phe Val Phe Leu Gly Asn Ser Ser Cys Ala Pro Gln Arg Leu Leu
20 25 30

gag aga agg aac tgg act cct caa gct atg ctc tac ctg aaa ggg gca 144
Glu Arg Arg Asn Trp Thr Pro Gln Ala Met Leu Tyr Leu Lys Gly Ala
35 40 45

cag ggt cgc cgc ttc atc tcc gac cag agc cgg aga aag gac ctc tcc 192
Gln Gly Arg Arg Phe Ile Ser Asp Gln Ser Arg Arg Lys Asp Leu Ser

50 55 60

gac cgg cca ctg ccg gaa aga cga agc cca aat ccc caa cta cta act 240
Asp Arg Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr
65 70 75 80

att ccg gag gca gca acc atc tta ctg gcg tcc ctt cag aaa tca cca 288
Ile Pro Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro
85 90 95

gaa gat gaa gaa aaa aac ttt gat caa acc aga ttc ctg gaa gac agt 336
Glu Asp Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser
100 105 110

ctg ctt aac tgg tga 351
Leu Leu Asn Trp *
115

<210> 388
<211> 116
<212> PRT
<213> Homo sapiens

<400> 388
Met Lys Gly Leu Arg Ser Leu Ala Ala Thr Thr Leu Ala Leu Phe Leu
1 5 10 15
Val Phe Val Phe Leu Gly Asn Ser Ser Cys Ala Pro Gln Arg Leu Leu
20 25 30
Glu Arg Arg Asn Trp Thr Pro Gln Ala Met Leu Tyr Leu Lys Gly Ala
35 40 45
Gln Gly Arg Arg Phe Ile Ser Asp Gln Ser Arg Arg Lys Asp Leu Ser
50 55 60
Asp Arg Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr
65 70 75 80
Ile Pro Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro
85 90 95
Glu Asp Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser
100 105 110
Leu Leu Asn Trp
115

<210> 389
<211> 318

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(318)

<400> 389
```
atg aac ttg ggg gtc agc atg ctg agg atc ctc ttc ctc ctg gat gta        48
Met Asn Leu Gly Val Ser Met Leu Arg Ile Leu Phe Leu Leu Asp Val
 1               5                  10                  15

gga gga gct caa gtg ctg gca aca ggc aag acc cct ggg gct gaa att        96
Gly Gly Ala Gln Val Leu Ala Thr Gly Lys Thr Pro Gly Ala Glu Ile
            20                  25                  30

gat ttc aag tac gcc ctc atc ggg act gct gtg ggt gtc gcc ata tct       144
Asp Phe Lys Tyr Ala Leu Ile Gly Thr Ala Val Gly Val Ala Ile Ser
        35                  40                  45

gct ggc ttc ctg gcc ctg aag atc tgc atg atc agg agg cac tta ttt       192
Ala Gly Phe Leu Ala Leu Lys Ile Cys Met Ile Arg Arg His Leu Phe
    50                  55                  60

gac gac gac tct tcc gac ctg aaa agc acg cct ggg ggc ctc agt gac       240
Asp Asp Asp Ser Ser Asp Leu Lys Ser Thr Pro Gly Gly Leu Ser Asp
65                  70                  75                  80

acc atc ccg cta aag aag aga gcc cca agg cga aac cac aat ttc tcc       288
Thr Ile Pro Leu Lys Lys Arg Ala Pro Arg Arg Asn His Asn Phe Ser
                85                  90                  95

aaa aga gat gca cag gtg att gag ctg tag                               318
Lys Arg Asp Ala Gln Val Ile Glu Leu  *
            100                 105
```

<210> 390
<211> 105
<212> PRT
<213> Homo sapiens

<400> 390
```
Met Asn Leu Gly Val Ser Met Leu Arg Ile Leu Phe Leu Leu Asp Val
```

```
 1               5                   10                  15
Gly Gly Ala Gln Val Leu Ala Thr Gly Lys Thr Pro Gly Ala Glu Ile
            20                  25                  30
Asp Phe Lys Tyr Ala Leu Ile Gly Thr Ala Val Gly Val Ala Ile Ser
        35                  40                  45
Ala Gly Phe Leu Ala Leu Lys Ile Cys Met Ile Arg Arg His Leu Phe
    50                  55                  60
Asp Asp Asp Ser Ser Asp Leu Lys Ser Thr Pro Gly Gly Leu Ser Asp
65                  70                  75                  80
Thr Ile Pro Leu Lys Lys Arg Ala Pro Arg Arg Asn His Asn Phe Ser
                85                  90                  95
Lys Arg Asp Ala Gln Val Ile Glu Leu
            100                 105

      <210> 391
      <211> 150
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(150)

      <221> misc_feature
      <222> (1)...(150)
      <223> n = A,T,C or G

      <400> 391
atg gcc atc ctc cag gtc act gcg ggc nac ccc ctg gcc atg gcc cag      48
Met Ala Ile Leu Gln Val Thr Ala Gly Xaa Pro Leu Ala Met Ala Gln
 1               5                   10                  15

ggc ccc cac ccc ctg gtc cac atc act gag gaa gta gaa gaa aac agg      96
Gly Pro His Pro Leu Val His Ile Thr Glu Glu Val Glu Glu Asn Arg
            20                  25                  30

aca caa gat ggc aag cct gag aga att gcc cag ctg acc tgg aat gag     144
Thr Gln Asp Gly Lys Pro Glu Arg Ile Ala Gln Leu Thr Trp Asn Glu
        35                  40                  45

gcc taa                                                             150
Ala  *
```

<210> 392
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(49)
<223> Xaa = Any Amino Acid

<400> 392
Met Ala Ile Leu Gln Val Thr Ala Gly Xaa Pro Leu Ala Met Ala Gln
1 5 10 15
Gly Pro His Pro Leu Val His Ile Thr Glu Glu Val Glu Glu Asn Arg
20 25 30
Thr Gln Asp Gly Lys Pro Glu Arg Ile Ala Gln Leu Thr Trp Asn Glu
35 40 45
Ala

<210> 393
<211> 294
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(294)

<400> 393
atg gat cct gag gtg acc ttg ctg ctg cag tgc cct ggc ggg ggc ctg 48
Met Asp Pro Glu Val Thr Leu Leu Leu Gln Cys Pro Gly Gly Gly Leu
1 5 10 15

ccc cag gag cag ata cag gcc gag ctg agc ccc gcc cat gac cgt cgc 96
Pro Gln Glu Gln Ile Gln Ala Glu Leu Ser Pro Ala His Asp Arg Arg
20 25 30

cca ctg cca ggt ggg gac gag gcc atc act gcc atc tgg gag acc cgg 144
Pro Leu Pro Gly Gly Asp Glu Ala Ile Thr Ala Ile Trp Glu Thr Arg
35 40 45

cta aag gcc caa ccc tgg ctc ttc gac gcc ccc aag ttc cgc ctg cac 192

Leu Lys Ala Gln Pro Trp Leu Phe Asp Ala Pro Lys Phe Arg Leu His
50 55 60

tca gcc acc ctg gcg cct att ggc tct cgg ggg cca cag ctg ctc ctg 240
Ser Ala Thr Leu Ala Pro Ile Gly Ser Arg Gly Pro Gln Leu Leu Leu
65 70 75 80

cgc ctg ggc ctt act tcc tgc cga gtt cta tgt cca gtg cag cct gac 288
Arg Leu Gly Leu Thr Ser Cys Arg Val Leu Cys Pro Val Gln Pro Asp
85 90 95

ttc tga 294
Phe *

<210> 394
<211> 97
<212> PRT
<213> Homo sapiens

<400> 394
Met Asp Pro Glu Val Thr Leu Leu Leu Gln Cys Pro Gly Gly Gly Leu
1 5 10 15
Pro Gln Glu Gln Ile Gln Ala Glu Leu Ser Pro Ala His Asp Arg Arg
20 25 30
Pro Leu Pro Gly Gly Asp Glu Ala Ile Thr Ala Ile Trp Glu Thr Arg
35 40 45
Leu Lys Ala Gln Pro Trp Leu Phe Asp Ala Pro Lys Phe Arg Leu His
50 55 60
Ser Ala Thr Leu Ala Pro Ile Gly Ser Arg Gly Pro Gln Leu Leu Leu
65 70 75 80
Arg Leu Gly Leu Thr Ser Cys Arg Val Leu Cys Pro Val Gln Pro Asp
85 90 95
Phe

<210> 395
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1)...(303)

<400> 395
atg cga caa gtt ttt ggt gat gag aag aag tac tgg ttg cta ccc att 48
Met Arg Gln Val Phe Gly Asp Glu Lys Lys Tyr Trp Leu Leu Pro Ile
1 5 10 15

ttt tca agt cta ggt gat ggc tgc tcc ttt cca act tgc ctt gtt aac 96
Phe Ser Ser Leu Gly Asp Gly Cys Ser Phe Pro Thr Cys Leu Val Asn
20 25 30

cag gat cct gaa caa gca tct act cct gca ggg ctg aat tcc aca gct 144
Gln Asp Pro Glu Gln Ala Ser Thr Pro Ala Gly Leu Asn Ser Thr Ala
35 40 45

aaa aat ctc gaa aac cat cag ttt cct gca aag cca ttg aga gag tcc 192
Lys Asn Leu Glu Asn His Gln Phe Pro Ala Lys Pro Leu Arg Glu Ser
50 55 60

cag agc cac ctt ctt act gat tct cag tct tgg acg gag agc agc ata 240
Gln Ser His Leu Leu Thr Asp Ser Gln Ser Trp Thr Glu Ser Ser Ile
65 70 75 80

aac cca gga aaa tgc aaa gct ggt atg agc aat cct gca tta acc atg 288
Asn Pro Gly Lys Cys Lys Ala Gly Met Ser Asn Pro Ala Leu Thr Met
85 90 95

gaa aat gag act taa 303
Glu Asn Glu Thr *
100

<210> 396
<211> 100
<212> PRT
<213> Homo sapiens

<400> 396
Met Arg Gln Val Phe Gly Asp Glu Lys Lys Tyr Trp Leu Leu Pro Ile
1 5 10 15
Phe Ser Ser Leu Gly Asp Gly Cys Ser Phe Pro Thr Cys Leu Val Asn
20 25 30
Gln Asp Pro Glu Gln Ala Ser Thr Pro Ala Gly Leu Asn Ser Thr Ala
35 40 45

Lys Asn Leu Glu Asn His Gln Phe Pro Ala Lys Pro Leu Arg Glu Ser
50 55 60
Gln Ser His Leu Leu Thr Asp Ser Gln Ser Trp Thr Glu Ser Ser Ile
65 70 75 80
Asn Pro Gly Lys Cys Lys Ala Gly Met Ser Asn Pro Ala Leu Thr Met
85 90 95
Glu Asn Glu Thr
100

<210> 397
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(141)

<400> 397
atg ctc tcc ttc ctg ccc ttc ctg gtg ctg ctg gtt ttc atc agg aac 48
Met Leu Ser Phe Leu Pro Phe Leu Val Leu Leu Val Phe Ile Arg Asn
1 5 10 15

ctc cga gcc ctg tcc atc ttc tcc ctg ttg gcc aac atc acc atg ctg 96
Leu Arg Ala Leu Ser Ile Phe Ser Leu Leu Ala Asn Ile Thr Met Leu
20 25 30

gtc agc ttg gtc atg atc tac cag ttc att gtt cag atc ctg tga 141
Val Ser Leu Val Met Ile Tyr Gln Phe Ile Val Gln Ile Leu *
35 40 45

<210> 398
<211> 46
<212> PRT
<213> Homo sapiens

<400> 398
Met Leu Ser Phe Leu Pro Phe Leu Val Leu Leu Val Phe Ile Arg Asn
1 5 10 15
Leu Arg Ala Leu Ser Ile Phe Ser Leu Leu Ala Asn Ile Thr Met Leu
20 25 30
Val Ser Leu Val Met Ile Tyr Gln Phe Ile Val Gln Ile Leu
35 40 45

<210> 399
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(360)

<400> 399
atg cag agc agc cac gcc tac tgc aca cct ctc aat gca gct tta cag 48
Met Gln Ser Ser His Ala Tyr Cys Thr Pro Leu Asn Ala Ala Leu Gln
1 5 10 15

gct tca atg gct gag aat agt ata cct cta tac act acc gct tcc atg 96
Ala Ser Met Ala Glu Asn Ser Ile Pro Leu Tyr Thr Thr Ala Ser Met
20 25 30

gga aat ccc act ctg ggc aac tta gcc agc gca ata cgg gaa gag ctg 144
Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser Ala Ile Arg Glu Glu Leu
35 40 45

aac ggg gca atg gag cat acc aac agc aac gag agt gac agc agt cca 192
Asn Gly Ala Met Glu His Thr Asn Ser Asn Glu Ser Asp Ser Ser Pro
50 55 60

ggc aga tct cct atg caa gcc gtg cat cct gta cac gtc aaa gaa gag 240
Gly Arg Ser Pro Met Gln Ala Val His Pro Val His Val Lys Glu Glu
65 70 75 80

ccc ctc gat cca gag gaa gct gaa ggg ccc ctg tcc tta gtg aca aca 288
Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro Leu Ser Leu Val Thr Thr
85 90 95

gcc aac cac agt cca gat ttt gac cat gac aga gat tac gaa gat gaa 336
Ala Asn His Ser Pro Asp Phe Asp His Asp Arg Asp Tyr Glu Asp Glu
100 105 110

cca gta aac gag gac atg gag tga 360
Pro Val Asn Glu Asp Met Glu *
115

<210> 400
<211> 119
<212> PRT
<213> Homo sapiens

<400> 400
Met Gln Ser Ser His Ala Tyr Cys Thr Pro Leu Asn Ala Ala Leu Gln
1 5 10 15
Ala Ser Met Ala Glu Asn Ser Ile Pro Leu Tyr Thr Thr Ala Ser Met
20 25 30
Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser Ala Ile Arg Glu Glu Leu
35 40 45
Asn Gly Ala Met Glu His Thr Asn Ser Asn Glu Ser Asp Ser Ser Pro
50 55 60
Gly Arg Ser Pro Met Gln Ala Val His Pro Val His Val Lys Glu Glu
65 70 75 80
Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro Leu Ser Leu Val Thr Thr
85 90 95
Ala Asn His Ser Pro Asp Phe Asp His Asp Arg Asp Tyr Glu Asp Glu
100 105 110
Pro Val Asn Glu Asp Met Glu
115

<210> 401
<211> 474
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(474)

<400> 401
atg tcg aaa agc tgt gga aat aat tta gcg gcc att tct gta gga att 48
Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile
1 5 10 15

tcg ctt ctt tta ctc tta gtg gtt tgt gga att ggg tgt gtt tgg cac 96
Ser Leu Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His
20 25 30

tgg aaa cac cgt gtt gcc aca cga ttt acc tta ccg agg ttt tta caa 144
Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln
35 40 45

agg aga agc agc agg aga aaa gtc tgt act aaa aca ttc ttg ggc ccc 192
Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro
50 55 60

cgc atc att ggc tta agg cat gaa atc tca gtt gaa acc caa gac cac 240
Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His
65 70 75 80

aaa tct gct gtc agg gga aat aac aca cac gac aac tat gaa aat gtg 288
Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val
85 90 95

gaa gca ggt cct ccc aaa gct aaa gga aaa acc gat aag gaa cta tat 336
Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr
100 105 110

gaa aac aca ggg cag tct aat ttc gag gag cat atc tat gga aat gag 384
Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu
115 120 125

aca tct tct gac tat tat aac ttc cag aag cct cgt cct tct gaa gtt 432
Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val
130 135 140

cct caa gat gaa gat ata tac att ctt cca gat tca tat tag 474
Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr *
145 150 155

<210> 402
<211> 157
<212> PRT
<213> Homo sapiens

<400> 402
Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile
1 5 10 15
Ser Leu Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His
20 25 30
Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln
35 40 45
Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro
50 55 60

Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His
65 70 75 80
Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val
85 90 95
Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr
100 105 110
Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu
115 120 125
Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val
130 135 140
Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr
145 150 155

<210> 403
<211> 279
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(279)

<400> 403
atg tgg cct gtg ttt tgg acc gtg gtt cgt acc tat gct cct tat gtc 48
Met Trp Pro Val Phe Trp Thr Val Val Arg Thr Tyr Ala Pro Tyr Val
1 5 10 15

aca ttc cct gtt gcc ttc gtg gtc ggg gct gtg ggt tac cac ctg gaa 96
Thr Phe Pro Val Ala Phe Val Val Gly Ala Val Gly Tyr His Leu Glu
20 25 30

tgg ttc atc agg gga aag gac ccc cag ccc gtg gag gag gaa aag agc 144
Trp Phe Ile Arg Gly Lys Asp Pro Gln Pro Val Glu Glu Glu Lys Ser
35 40 45

atc tca gag cgc cgg gag gat cgc aag ctg gat gag ctt cta ggc aag 192
Ile Ser Glu Arg Arg Glu Asp Arg Lys Leu Asp Glu Leu Leu Gly Lys
50 55 60

gac cac acg cag gtg gtg agc ctt aag gac aag cta gaa ttt gcc ccg 240
Asp His Thr Gln Val Val Ser Leu Lys Asp Lys Leu Glu Phe Ala Pro
65 70 75 80

aaa gct gtg ctg aac aga aac cgc cca gag aag aat taa 279

Lys Ala Val Leu Asn Arg Asn Arg Pro Glu Lys Asn *
85 90

<210> 404
<211> 92
<212> PRT
<213> Homo sapiens

<400> 404
Met Trp Pro Val Phe Trp Thr Val Val Arg Thr Tyr Ala Pro Tyr Val
1 5 10 15
Thr Phe Pro Val Ala Phe Val Val Gly Ala Val Gly Tyr His Leu Glu
20 25 30
Trp Phe Ile Arg Gly Lys Asp Pro Gln Pro Val Glu Glu Glu Lys Ser
35 40 45
Ile Ser Glu Arg Arg Glu Asp Arg Lys Leu Asp Glu Leu Leu Gly Lys
50 55 60
Asp His Thr Gln Val Val Ser Leu Lys Asp Lys Leu Glu Phe Ala Pro
65 70 75 80
Lys Ala Val Leu Asn Arg Asn Arg Pro Glu Lys Asn
85 90

<210> 405
<211> 255
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(255)

<400> 405
atg agt gaa ttc tgg ttg tgt ttc aac tgc tgt att gca gaa cag cct 48
Met Ser Glu Phe Trp Leu Cys Phe Asn Cys Cys Ile Ala Glu Gln Pro
1 5 10 15

cag cct aaa agg cga cgg cgg att gac aga agt atg att gga gag ccc 96
Gln Pro Lys Arg Arg Arg Arg Ile Asp Arg Ser Met Ile Gly Glu Pro
20 25 30

aca aac ttt gtg cat aca gct cat gtt gga tca gga gac ctg ttc agt 144
Thr Asn Phe Val His Thr Ala His Val Gly Ser Gly Asp Leu Phe Ser
35 40 45

gga atg aat tca gtt agc tcc att cag aac caa atg cag tcc aag gga 192
Gly Met Asn Ser Val Ser Ser Ile Gln Asn Gln Met Gln Ser Lys Gly
50 55 60

ggt tat gga ggt gga atg cct gcc aat gtc cag atg cag ctc gtg gat 240
Gly Tyr Gly Gly Gly Met Pro Ala Asn Val Gln Met Gln Leu Val Asp
65 70 75 80

acg aag gcg gga tag 255
Thr Lys Ala Gly *

<210> 406
<211> 84
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Glu Phe Trp Leu Cys Phe Asn Cys Cys Ile Ala Glu Gln Pro
1 5 10 15
Gln Pro Lys Arg Arg Arg Arg Ile Asp Arg Ser Met Ile Gly Glu Pro
20 25 30
Thr Asn Phe Val His Thr Ala His Val Gly Ser Gly Asp Leu Phe Ser
35 40 45
Gly Met Asn Ser Val Ser Ser Ile Gln Asn Gln Met Gln Ser Lys Gly
50 55 60
Gly Tyr Gly Gly Gly Met Pro Ala Asn Val Gln Met Gln Leu Val Asp
65 70 75 80
Thr Lys Ala Gly

<210> 407
<211> 249
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(249)

<400> 407
atg gcg agt agc ggc ggt gct ggg gcg gcg gcg gcg gcc gcg gcg gcg 48

Met Ala Ser Ser Gly Gly Ala Gly Ala Ala Ala Ala Ala Ala Ala Ala
1 5 10 15

aat ctg aat gcg gtg cgg gag acc atg gac gtt ctg ctt gag att tca 96
Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu Leu Glu Ile Ser
20 25 30

aga att ttg aat act ggc tta gat atg gaa act ctg tct att tgt gta 144
Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu Ser Ile Cys Val
35 40 45

cgg ctt tgt gaa caa gga att aac cca gaa gct tta tca tcg gtt att 192
Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu Ser Ser Val Ile
50 55 60

aag gag ctt cgc aag gct act gaa gca ctg aag gct gct gaa aat atg 240
Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala Ala Glu Asn Met
65 70 75 80

aca agc tga 249
Thr Ser *

<210> 408
<211> 82
<212> PRT
<213> Homo sapiens

<400> 408
Met Ala Ser Ser Gly Gly Ala Gly Ala Ala Ala Ala Ala Ala Ala Ala
1 5 10 15
Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu Leu Glu Ile Ser
20 25 30
Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu Ser Ile Cys Val
35 40 45
Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu Ser Ser Val Ile
50 55 60
Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala Ala Glu Asn Met
65 70 75 80
Thr Ser

<210> 409

<211> 156
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(156)

<400> 409
```
atg cag tgc tgc ctg ctg ctg cgc tgg ctg gca tct gcc ctc ctc cgt        48
Met Gln Cys Cys Leu Leu Leu Arg Trp Leu Ala Ser Ala Leu Leu Arg
 1               5                  10                  15

ctc ctg ggt gct gcc aca gag aag aga gag aga gtg aag cgg gca gag        96
Leu Leu Gly Ala Ala Thr Glu Lys Arg Glu Arg Val Lys Arg Ala Glu
            20                  25                  30

act ggc tgt tgc cat cac aca act gag ggc gga cct gga gct cac cgg       144
Thr Gly Cys Cys His His Thr Thr Glu Gly Gly Pro Gly Ala His Arg
        35                  40                  45

ctg agg gtt tga                                                       156
Leu Arg Val  *
    50
```

<210> 410
<211> 51
<212> PRT
<213> Homo sapiens

<400> 410
```
Met Gln Cys Cys Leu Leu Leu Arg Trp Leu Ala Ser Ala Leu Leu Arg
 1               5                  10                  15
Leu Leu Gly Ala Ala Thr Glu Lys Arg Glu Arg Val Lys Arg Ala Glu
            20                  25                  30
Thr Gly Cys Cys His His Thr Thr Glu Gly Gly Pro Gly Ala His Arg
        35                  40                  45
Leu Arg Val
    50
```

<210> 411
<211> 420
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(420)

<221> misc_feature
<222> (1)...(420)
<223> n = A,T,C or G

<400> 411
atg cac gtc act gag gct ctg cac cag aac atg cag gct ctg ttt agc 48
Met His Val Thr Glu Ala Leu His Gln Asn Met Gln Ala Leu Phe Ser
1 5 10 15

acc ctg gct cag gcg gag gag cag cag ccc tac ctg gag ggc tcc acc 96
Thr Leu Ala Gln Ala Glu Glu Gln Gln Pro Tyr Leu Glu Gly Ser Thr
20 25 30

gtt atg cgc ggg act cgc tgt ctg gca gag tac cac ctg ggg gat tat 144
Val Met Arg Gly Thr Arg Cys Leu Ala Glu Tyr His Leu Gly Asp Tyr
35 40 45

gga cac gcc tgg aac agg tgt tgg gtg ctg gac agg gtg gac acc tgg 192
Gly His Ala Trp Asn Arg Cys Trp Val Leu Asp Arg Val Asp Thr Trp
50 55 60

gct gtg gtc atg ttc att gat ttt gga cag ttg gcc acc atc cct gtg 240
Ala Val Val Met Phe Ile Asp Phe Gly Gln Leu Ala Thr Ile Pro Val
65 70 75 80

cag tct ctg cgc anc tna gac agc gac gac ttc tgg acc atc cca ccc 288
Gln Ser Leu Arg Xaa Xaa Asp Ser Asp Asp Phe Trp Thr Ile Pro Pro
85 90 95

ctg act cag cca ttc atg ctg gag aaa gac att ttg agt tcg tat gag 336
Leu Thr Gln Pro Phe Met Leu Glu Lys Asp Ile Leu Ser Ser Tyr Glu
100 105 110

gtt gtc cat cga atc ctc aaa ggg aaa atc act ggt gct ttg aac tcg 384
Val Val His Arg Ile Leu Lys Gly Lys Ile Thr Gly Ala Leu Asn Ser
115 120 125

gcg ttg cac atc cta aag ttt gaa gag tct aaa taa 420

Ala Leu His Ile Leu Lys Phe Glu Glu Ser Lys *
130 135

<210> 412
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(139)
<223> Xaa = Any Amino Acid

<400> 412
Met His Val Thr Glu Ala Leu His Gln Asn Met Gln Ala Leu Phe Ser
1 5 10 15
Thr Leu Ala Gln Ala Glu Glu Gln Gln Pro Tyr Leu Glu Gly Ser Thr
20 25 30
Val Met Arg Gly Thr Arg Cys Leu Ala Glu Tyr His Leu Gly Asp Tyr
35 40 45
Gly His Ala Trp Asn Arg Cys Trp Val Leu Asp Arg Val Asp Thr Trp
50 55 60
Ala Val Val Met Phe Ile Asp Phe Gly Gln Leu Ala Thr Ile Pro Val
65 70 75 80
Gln Ser Leu Arg Xaa Xaa Asp Ser Asp Asp Phe Trp Thr Ile Pro Pro
85 90 95
Leu Thr Gln Pro Phe Met Leu Glu Lys Asp Ile Leu Ser Ser Tyr Glu
100 105 110
Val Val His Arg Ile Leu Lys Gly Lys Ile Thr Gly Ala Leu Asn Ser
115 120 125
Ala Leu His Ile Leu Lys Phe Glu Glu Ser Lys
130 135

<210> 413
<211> 795
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(795)

<400> 413

```
atg ttc gtt ccc tgc ggg gag tcg gcc ccc gac ctt gcc ggc ttc acc      48
Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe Thr
 1               5                  10                  15

ctc cta atg cca gca gta tct gtt gga aat gtt ggc cag ctt gca atg      96
Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala Met
             20                  25                  30

gat ctg att att tct aca ctg aat atg tct aag att ggt tac ttc tat     144
Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr
         35                  40                  45

acc gat tgt ctt gtg cca atg gtt gga aac aat cca tat gcg acc aca     192
Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr
     50                  55                  60

gaa gga aat tca aca gaa ctt agc ata aat gct gaa gtg tat tca ttg     240
Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu
 65                  70                  75                  80

cct tca aga aag ctg gtg gct cta cag tta aga tcc att ttt att aag     288
Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys
                 85                  90                  95

tat aaa tca aag cca ttc tgt gaa aaa ctg ctt tcc tgg gtg aaa agc     336
Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser
            100                 105                 110

agt ggc tgt gcc aga gtc att gtt ctt tca agc agt cat tca tat cag     384
Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln
        115                 120                 125

cgt aat gat ctg cag ctt cgt agt act ccc ttc cgg tac cta ctt aca     432
Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr
    130                 135                 140

cct tcc atg caa aaa agt gtt caa aat aaa ata aag agc ctt aac tgg     480
Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp
145                 150                 155                 160

gaa gaa atg gaa aaa agc cgg tgc att cct gaa ata gat gat tcc gag     528
Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu
                165                 170                 175
```

ttt tgt atc cgc att ccg gga gga ggt atc aca aaa aca ctc tat gat 576
Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
180 185 190

gaa agc tgt tct aaa gaa atc caa atg gca gtt ctg ctg aaa ttt gtt 624
Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
195 200 205

tca gaa ggg gac aac atc cca gat gca tta ggt ctt gtt gag tat ctt 672
Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
210 215 220

aat gag tgg ctt cag ata ctc aaa cca ctt agc gat gac ccc aca gta 720
Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
225 230 235 240

tct gcc tca cgg tgg aaa ata cca agt tct tgg aga tta ctc ttt ggc 768
Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe Gly
245 250 255

agt ggt ctt ccc cct gca ctt ttc tga 795
Ser Gly Leu Pro Pro Ala Leu Phe *
260

<210> 414
<211> 264
<212> PRT
<213> Homo sapiens

<400> 414
Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe Thr
1 5 10 15
Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala Met
20 25 30
Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr
35 40 45
Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr
50 55 60
Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu
65 70 75 80
Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys
85 90 95
Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser

```
            100                 105                 110
Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln
        115                 120                 125
Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr
    130                 135                 140
Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp
145                 150                 155                 160
Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu
                165                 170                 175
Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
            180                 185                 190
Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
        195                 200                 205
Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
    210                 215                 220
Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
225                 230                 235                 240
Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe Gly
                245                 250                 255
Ser Gly Leu Pro Pro Ala Leu Phe
            260
```

<210> 415
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(225)

<400> 415

```
atg ggg aaa tta ttc tgg att ata cag atg gac tgt gtt cag tca cag       48
Met Gly Lys Leu Phe Trp Ile Ile Gln Met Asp Cys Val Gln Ser Gln
 1               5                  10                  15

gag ctc tta aaa gca gag acg ctt tcc cag ctt ggg tca gag aga ttc       96
Glu Leu Leu Lys Ala Glu Thr Leu Ser Gln Leu Gly Ser Glu Arg Phe
            20                  25                  30

atc atg aga aga tct cca cta gct gtt gct gga ttt cag gat gga gga      144
Ile Met Arg Arg Ser Pro Leu Ala Val Ala Gly Phe Gln Asp Gly Gly
        35                  40                  45
```

aga ctc aag cag aga gac ctg gtg gcc act aga agc ttg gaa cag ccc 192
Arg Leu Lys Gln Arg Asp Leu Val Ala Thr Arg Ser Leu Glu Gln Pro
50 55 60

tca gtt gat agc aag gaa atg agg act cag tga 225
Ser Val Asp Ser Lys Glu Met Arg Thr Gln *
65 70

<210> 416
<211> 74
<212> PRT
<213> Homo sapiens

<400> 416
Met Gly Lys Leu Phe Trp Ile Ile Gln Met Asp Cys Val Gln Ser Gln
1 5 10 15
Glu Leu Leu Lys Ala Glu Thr Leu Ser Gln Leu Gly Ser Glu Arg Phe
20 25 30
Ile Met Arg Arg Ser Pro Leu Ala Val Ala Gly Phe Gln Asp Gly Gly
35 40 45
Arg Leu Lys Gln Arg Asp Leu Val Ala Thr Arg Ser Leu Glu Gln Pro
50 55 60
Ser Val Asp Ser Lys Glu Met Arg Thr Gln
65 70

<210> 417
<211> 414
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(414)

<400> 417
atg gag tac ata cag cag ttg aag gac ttt act acc gat gac ctg ttg 48
Met Glu Tyr Ile Gln Gln Leu Lys Asp Phe Thr Thr Asp Asp Leu Leu
1 5 10 15

cag cta tta atg tca tgt ccc caa gtt gaa tta att cag tgt ctc act 96
Gln Leu Leu Met Ser Cys Pro Gln Val Glu Leu Ile Gln Cys Leu Thr
20 25 30

aaa gag ttg aat gag aaa caa cca tct tta tct ttt ggt ctt gct ata 144
Lys Glu Leu Asn Glu Lys Gln Pro Ser Leu Ser Phe Gly Leu Ala Ile
35 40 45

ctt cat ctg ttc tct gca gac atg aaa aaa gtt ggc att aag cta ctt 192
Leu His Leu Phe Ser Ala Asp Met Lys Lys Val Gly Ile Lys Leu Leu
50 55 60

caa gaa atc aat aaa ggt ggg ata gat gca gta gaa agt ctt atg ata 240
Gln Glu Ile Asn Lys Gly Gly Ile Asp Ala Val Glu Ser Leu Met Ile
65 70 75 80

aat gat tcc ttt tgc tcc ata gaa aag tgg caa gaa gtg gca aat ata 288
Asn Asp Ser Phe Cys Ser Ile Glu Lys Trp Gln Glu Val Ala Asn Ile
85 90 95

tgt tca cag aat ggc ttt gac aaa tta tct aat gac atc acg tct att 336
Cys Ser Gln Asn Gly Phe Asp Lys Leu Ser Asn Asp Ile Thr Ser Ile
100 105 110

ctt cga tct cag gct gca gtt aca gaa att tct gaa gag gat gac gca 384
Leu Arg Ser Gln Ala Ala Val Thr Glu Ile Ser Glu Glu Asp Asp Ala
115 120 125

gtc aac cta atg gaa cat gtg ttt tgg tag 414
Val Asn Leu Met Glu His Val Phe Trp
130 135

<210> 418
<211> 137
<212> PRT
<213> Homo sapiens

<400> 418
Met Glu Tyr Ile Gln Gln Leu Lys Asp Phe Thr Thr Asp Asp Leu Leu
1 5 10 15
Gln Leu Leu Met Ser Cys Pro Gln Val Glu Leu Ile Gln Cys Leu Thr
20 25 30
Lys Glu Leu Asn Glu Lys Gln Pro Ser Leu Ser Phe Gly Leu Ala Ile
35 40 45
Leu His Leu Phe Ser Ala Asp Met Lys Lys Val Gly Ile Lys Leu Leu
50 55 60
Gln Glu Ile Asn Lys Gly Gly Ile Asp Ala Val Glu Ser Leu Met Ile

```
65                  70                  75                  80
Asn Asp Ser Phe Cys Ser Ile Glu Lys Trp Gln Glu Val Ala Asn Ile
                85                  90                  95
Cys Ser Gln Asn Gly Phe Asp Lys Leu Ser Asn Asp Ile Thr Ser Ile
            100                 105                 110
Leu Arg Ser Gln Ala Ala Val Thr Glu Ile Ser Glu Glu Asp Asp Ala
        115                 120                 125
Val Asn Leu Met Glu His Val Phe Trp
    130                 135

      <210> 419
      <211> 285
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(285)

      <400> 419
atg act aca gtt ccc acg tgc gca act ctg ccc ttg gct caa gga ttc        48
Met Thr Thr Val Pro Thr Cys Ala Thr Leu Pro Leu Ala Gln Gly Phe
 1               5                  10                  15

cgt gat gtt cat ttt ggt ttt cta agc gag agg ctc cga gcc ttc caa        96
Arg Asp Val His Phe Gly Phe Leu Ser Glu Arg Leu Arg Ala Phe Gln
            20                  25                  30

cct ctg act ggc tgg tcc tgt gag acc cct cga tca ggg atg ctg ctg       144
Pro Leu Thr Gly Trp Ser Cys Glu Thr Pro Arg Ser Gly Met Leu Leu
        35                  40                  45

caa gtg gtc atg gca gtt gct gac acc tct gcg aag gcc gtg gag acc       192
Gln Val Val Met Ala Val Ala Asp Thr Ser Ala Lys Ala Val Glu Thr
    50                  55                  60

gtg aag aag cag caa ggc gag cag atc tgc tgg ggt ggc agc agc tcc       240
Val Lys Lys Gln Gln Gly Glu Gln Ile Cys Trp Gly Gly Ser Ser Ser
 65                  70                  75                  80

gtc atg agt cta gct acc aag atg aat gaa cta atg gag aaa tag           285
Val Met Ser Leu Ala Thr Lys Met Asn Glu Leu Met Glu Lys  *
                85                  90
```

<210> 420
<211> 94
<212> PRT
<213> Homo sapiens

<400> 420
Met Thr Thr Val Pro Thr Cys Ala Thr Leu Pro Leu Ala Gln Gly Phe
1 5 10 15
Arg Asp Val His Phe Gly Phe Leu Ser Glu Arg Leu Arg Ala Phe Gln
20 25 30
Pro Leu Thr Gly Trp Ser Cys Glu Thr Pro Arg Ser Gly Met Leu Leu
35 40 45
Gln Val Val Met Ala Val Ala Asp Thr Ser Ala Lys Ala Val Glu Thr
50 55 60
Val Lys Lys Gln Gln Gly Glu Gln Ile Cys Trp Gly Gly Ser Ser Ser
65 70 75 80
Val Met Ser Leu Ala Thr Lys Met Asn Glu Leu Met Glu Lys
85 90

<210> 421
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(240)

<400> 421
atg cag ggc cgg ctg gag ctc gtg ggc agg ggc tgc cga cct ctg agc 48
Met Gln Gly Arg Leu Glu Leu Val Gly Arg Gly Cys Arg Pro Leu Ser
1 5 10 15

tgg gtg tgc tgg gag cca ggg atc act ggg tgc cgg cca cag agg aag 96
Trp Val Cys Trp Glu Pro Gly Ile Thr Gly Cys Arg Pro Gln Arg Lys
20 25 30

gtc cct gag gac aca gta ccg aag tct gat ccc aga gga gga agg aag 144
Val Pro Glu Asp Thr Val Pro Lys Ser Asp Pro Arg Gly Gly Arg Lys
35 40 45

gtg ggc cgg gga gaa ggt ctg agt gca ggg atg gtc cag gag gag gac 192
Val Gly Arg Gly Glu Gly Leu Ser Ala Gly Met Val Gln Glu Glu Asp

```
     50                 55                 60

tgg aag ctg cag gat ggc tgc agg ggg ccg tgg acc ctc ctg gcc tga        240
Trp Lys Leu Gln Asp Gly Cys Arg Gly Pro Trp Thr Leu Leu Ala  *
 65                 70                  75
```

<210> 422
<211> 79
<212> PRT
<213> Homo sapiens

<400> 422

```
Met Gln Gly Arg Leu Glu Leu Val Gly Arg Gly Cys Arg Pro Leu Ser
 1               5                  10                  15
Trp Val Cys Trp Glu Pro Gly Ile Thr Gly Cys Arg Pro Gln Arg Lys
            20                  25                  30
Val Pro Glu Asp Thr Val Pro Lys Ser Asp Pro Arg Gly Gly Arg Lys
        35                  40                  45
Val Gly Arg Gly Glu Gly Leu Ser Ala Gly Met Val Gln Glu Glu Asp
    50                  55                  60
Trp Lys Leu Gln Asp Gly Cys Arg Gly Pro Trp Thr Leu Leu Ala
65                  70                  75
```

<210> 423
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide tag

<400> 423

```
Glu Tyr Met Pro Met Glu
 1               5
```